CBAB
CROP BREEDING AND
APPLIED BIOTECHNOLOGY

ARTICLE

Crop Breeding and Applied Biotechnology
19: 8-14, 2019
Brazilian Society of Plant Breeding.
Printed in Brazil
http://dx.doi.org/10.1590/1984-70332019v19n1a02

Agronomic evaluation of a *Hancornia speciosa* Gomes germplasm collection from the Brazilian Cerrado

Gabriella Queiroz de Almeida[1*], Lázaro José Chaves[2], Muza do Carmo Vieira[3] and Rita Maria Devós Ganga[2]

Abstract: *Hancornia speciosa Gomes is a fruit tree native to Brazil with potential for use in cropping systems. The objective of this study was to characterize accessions of a germplasm collection by evaluating agronomic traits. The collection was planted in 2005, in an experiment with 57 progenies and four replications, totaling 192 individual accessions from 29 natural subpopulations of four botanical varieties, from the Brazilian Cerrado. The components of variance were estimated using the restricted maximum likelihood (REML) procedure. Heritability coefficients show the potential of the collection as base population for selection programs. The trait number of fruits per plant presented the highest estimated selection gain. The accessions of H. speciosa var. cuyabensis are the ones with the greatest potential for selection based on plant size and productivity. Progenies with greater development in the juvenile phase are potentially more productive in the adult phase, allowing the early selection of superior genotypes.*

Keywords: *Mangaba, genetic resources, ex situ conservation, early selection.*

INTRODUCTION

The Cerrado biome occurs in 13 Brazilian states and the Federal District, representing 23% of the national territory. It has great biodiversity, particularly in the flora, which is considered the richest among the savannas of the world, with more than 12,000 vascular species (Mendonça et al. 2008).

Native fruits, which are often consumed fresh or used for the production of sweets, jams, juices, and liqueurs, are highlighted among the natural richness of this biome. These native fruit species can be used successfully in the recovery of deforested or degraded areas, erosion control, intercropping, reforestation, plant enrichment, planting in parks and gardens, and in environmental protection or conservation. In addition, many of these species are part of the bee flora of the Cerrado, with their leaves and bark being used in folk medicine (Agostini-Costa et al. 2010).

Hancornia speciosa Gomes (mangaba tree) presents great phenotypic variation under natural conditions. The literature on the taxonomy of the species reports the occurrence of six botanical varieties based on the article by Monachino (1945). *H. speciosa* var. *speciosa* (Gomes) has small leaves and long petioles and occurs from the Northeast towards the Middle-West and

***Corresponding author:**
E-mail: gabriellaqueirozalmeida@hotmail.com
ORCID: 0000-0002-0340-7346

Received: 05 February 2018
Accepted: 28 March 2018

[1] Universidade Federal de Viçosa, Departamento de Fitotecnia, Campus Universitário, 36.570-900, Viçosa, MG, Brazil
[2] Universidade Federal de Goiás, Departamento de Genética e Melhoramento Vegetal, Campus Samambaia, Escola de Agronomia, 74.690-900, Goiânia, GO, Brazil
[3] Instituto Federal Goiano, Laboratório de Biotecnologia, Rodovia Geraldo Silva Nascimento Km-12,5 - Zona Rural, 75.790-000, Urutaí, GO, Brazil

North Brazil; *H. speciosa* var. *Maximiliani* (A. DC.) occurs in Southeast Brazil and also has small leaves with long petioles; *H. speciosa* var. *lundii* (A. DC.) also occurs in Southeast Brazil and has medium leaves and short petiole; *H. speciosa* var. *cuyabensis* (Malme) occurs in the West part of the Brazilian Cerrado and has medium leaves and short petiole; *H. speciosa* var. *gardneri* (A. DC. Muell. Arg.) and *H. speciosa* var. *pubescens* (Nees & Martius) Muell. Arg. occur in Central Brazil, sometimes in sympatry, and have large leaves and short petiole, although the last one has pubescent leaves and young braches. More details on variety differentiation can be found in Silva Junior and Lédo (2006). However, the list of species of the Flora Brazil 2020 project recognizes only two botanical varieties: *H. speciosa* var. *pubescens* and *H. speciosa* var. *speciosa*, with the latter including the other varieties (Koch et al. 2015).

Genetic resources of perennial native species such as *H. speciosa* should be conserved, primarily, in *in situ* conditions, assuring the evolutionary and ecological processes and avoiding genetic erosion. The *ex situ* conservation has a complementary role, and priority should be given to collections in areas of greater risk of genetic erosion (Chaves 2006). Because the mangaba tree has recalcitrant seeds, and so far, *in vitro* conservation techniques are not available, *ex situ* conservation should be done through *in vivo* collections. This type of collection, in addition to its conservation purpose, also can be used for genetic-agronomic studies and as a working collection for breeding. The well-conducted characterization and evaluation of a germplasm collection greatly simplifies the work of breeders and is a basic requirement for the measurement of genetic variability, essential for beginning a selection program (Valls 2007).

Controlled pollination experiment demonstrated that the species is self-incompatible (Darrault and Schlidwein 2005) that was corroborated by pollen dispersal study (Collevatti et al. 2016). Some works have shown the existence of genetic variability among and/or within botanical varieties based on quantitative traits (Ganga et al. 2009), allozymes (Martins et al. 2012), DNA molecular markers (Moura et al. 2005, Silva et al. 2011, Rodrigues et al. 2015, Collevatti et al. 2016, Costa et al. 2017) and chemical components (Flores et al. 2018).

The germplasm collection of *H. speciosa* at the Federal University of Goiás (UFG) was evaluated for developmental traits in the nursery and juvenile phase (Ganga et al. 2009) and by microsatellite markers (Collevatti et al. 2016). The objective of this work was to study the genetic variability of agronomic traits of plants and fruits in their adult phase and the potential for selection of the UFG germplasm collection of *H. speciosa*, in addition to a correlation study on growth traits of the initial and juvenile phases.

MATERIAL AND METHODS

The experimental data were obtained from the UFG germplasm collection of *H. speciosa* Gomes (mangaba tree) at the city of Goiânia, Goiás, Brazil (lat 16º 35’ 39’’ S, long 49º 17’ 26’’ W, alt 720 m asl). According to the classification of Köppen the climate in the region is Aw, tropical with a rainy season from October to April and a dry season from May to September. The average annual rainfall is 1,481 mm and the average annual air temperature is 22.1 ºC (Lobato 2016). The soil of the experimental area is a Dark Red Latosol (Hapludox), originally recovered by upland forest.

The collection was performed in natural subpopulations (local populations) of *H. speciosa* Gomes in the states of Goiás, Tocantins, Mato Grosso, Mato Grosso do Sul, Bahia, and Minas Gerais. The collection area represents almost the area of occurrence of the species in the Brazilian Cerrado with latitudes varying from 10° 24’ 31” S (Mateiro – TO) to 18° 36’ 57” S (Coxim – MS), longitudes from 45° 55’ 13” W (São Desidério – BA) to 55° 17’ 27” W (Chapada dos Guimarães – MT) and altitudes from 261 m (Coxim MS) to 970 m (Alexânia – GO) (Ganga et al. 2009, 2010). The most collection areas were in fragments of the native vegetation, including some subpopulations in the road borders. Only three subpopulations were collected in large areas, continuously covered by native vegetation. There were no apparent signs of extractive exploitation of fruits in the sampled areas.

The germplasm collection was installed in the field in December 2005 (Ganga et al. 2009) in a randomized complete block design with 58 treatments (progenies) and four blocks, with one plant per plot with a spacing of 6 m x 5 m, totaling an area of 6960 m^2 and including 232 individual accessions. No artificial fertilizing was done. Currently, 191 individual accessions of 57 open-pollinated progenies from the sampled mother trees remain, representing 29 subpopulations of *H. speciosa* var. *pubescens*, *H. speciosa* var. *gardneri*, *H. speciosa* var. *speciosa*, and *H. speciosa* var. *cuyabensis*. Henceforth, varieties will be referred to only by the term differentiator, for simplification, using the classification by Monachino (1945). The collection also has 274 individual accessions not included in the experiment. A study of gene flow carried out in the complete collection showed a reproductive system with 100% outcrossing rate and no barriers to crosses between varieties (Collevatti et al. 2016).

For the purpose of this study, the evaluations of the plants began in September 2013, and the individual accessions were characterized for the agronomical quantitative traits: plant height (PH); canopy diameter (CD); stem circumference (SC), up to 10 cm from the soil surface and below the lower branch; lower branching height (BH); and primary branching number (BN). At the time of production, the diameter (FD) and length (FL) of the fruit were determined directly on the trees, and five fruits were sampled per accession. Then, five to 10 fruits were collected per accession (according to availability), and data were collected on the fruit mass (FM), number of seeds per fruit (NS), and seed mass per fruit (SM). The number of fruits per plant (FN) was also evaluated, with collections being undertaken every three days, the number of fruits fallen per accession being counted and removed from the area. The fruit data was taken from September to December 2013 – the period of greatest yield.

The estimates of variance components were obtained by the restricted maximum likelihood (REML) method, based on the random hierarchical model: $Y_{ijkl} = m + v_l + s_{i(l)} + p_{j(il)} + b_k + e_{ijkl}$, where Y_{ijkl} is the phenotypic value of the plant of block *k* of progeny *j* of subpopulation *i* of variety *l*; *m* is the general mean; v_l is the random effect of varieties; $s_{i(l)}$ is the random effect of subpopulations within varieties; $p_{j(il)}$ is the random effect of progenies within subpopulations; b_k is the random effect of blocks and e_{ijkl} is the experimental error associated to Y_{ijkl}. The analysis was performed in R environment using Ime4 package and Imer procedure (R Core Team 2017).

The potential for selection was assessed by evaluation of the genetic parameters, considering the set of progenies and disregarding the structure in varieties and subpopulations. The estimated parameters were the mean (m), residual variance (σ^2), genetic variance among progenies (σ^2_{prog}), phenotypic variance among progenies (σ^2_{pbp}), heritability at progeny level (h^2_{prog}), coefficient of genetic variation (*CVg*), and coefficient of residual variation (*CVe*). Gain was also estimated by selection at the progeny level (SG_{prog}), with a selection intensity of 20% (standardized selection differential equal to 1.40). To select the best progenies and keep the collection intact, only the female parent was considered for selection, using the formula $SG_{prog} = k \frac{\frac{1}{2}\sigma^2_{prog}}{\sigma_{pbp}}$, where *k* is the standardized selection differential. The selection gain was presented as percentage of the mean of each trait. The genetic parameters were estimated in Excel® spreadsheet using the variance components from the previous analysis.

The phenotypic (r_F) and genotypic (r_G) correlation coefficients were estimated between the 11 agronomic traits in pairs and also with six juvenile traits of plant growth (Ganga et al. 2009). For this, common data of the 162 plants were considered. The variables considered for the juvenile plants were stem diameter growth rate (DGR), plant height growth rate (HGR), stem diameter in the nursery (SDN), stem diameter in the field (SDF), plant height in the nursery (PHN), and plant height in the field (PHF). The phenotypic correlation was based on the individual phenotypic values and the genotypic correlation for the predicted individual genotypic values, which was obtained by the "ranef" procedure of the "lme4" package, but the two correlations were estimated in the correlation coefficients were estimated in R environment using ds package ds and dscor procedure, (R Core Team 2017).

RESULTS AND DISCUSSION

Descriptive statistics

The descriptive analysis showed great variation among the accessions of *H. speciosa* for the 11 agronomic traits evaluated (Table 1). The following traits related to the production are highlighted: FN, with variation from zero to 1744, and FM, with variation from 1.6 g to 52.3 g. At the time of the collections that generated the germplasm collection, the evaluation of the mother trees under natural conditions showed that the mean number of fruits per plant was 83.8, and the maximum value was 830 fruits (Ganga et al. 2010). The mean and maximum values found in this work (202.6 and 1744) were much higher, showing the good adaptation of the mangaba tree to the growing conditions of the collection. Although no fertilizing was done in the collection, the soil naturally has better nutritional conditions than the soil of most areas of natural occurrence of the mangaba tree. On the other hand, the mean mass of the fruits collected in the

Table 1. Minimum and maximum values, overall mean, means by botanical variety, and genetic value (*Blup*) of the evaluated agronomic traits of the UFG germplasm collection of *Hancornia speciosa* Gomes

Statistics	**PH** (m)	**SD** (m)	**SC** (cm)	**BH** (m)	**BN**	**FN**	**FL** (mm)	**FD** (mm)	**FM** (g)	**SN**	**SM** (g)
Minimum	2.20	0.44	8.00	0.00	0.00	0	15.39	14.49	1.61	1.00	0.02
Maximum	11.70	10.83	72.00	1.86	5.00	1744	53.73	54.14	52.31	30.00	6.51
Overall mean	5.95	5.59	40.58	0.38	1.40	202.6	37.69	34.22	22.66	8.05	2.71
H. s. var. *cuyabensis* (C)	6.66	6.17	45.50	0.32	1.54	444.1	38.54	35.27	23.72	8.55	2.88
H. s. var. *gardineri* (G)	6.21	5.76	42.54	0.42	1.37	203.9	37.75	34.39	22.58	8.04	2.79
H. s. var. *pubescens* (P)	4.65	5.18	35.63	0.33	1.39	65.7	38.17	33.90	22.66	7.91	2.28
H. s. var. *speciosa* (S)	5.17	3.89	25.07	0.33	1.36	12.5	26.76	24.58	12.33	3.00	0.85
Blup (C)	0.39	0.65	5.15	0.00	0.00	203.6	1.93	0.00	0.00	0.00	0.00
Blup (G)	0.19	0.34	3.35	0.00	0.00	5.0	1.20	0.00	0.00	0.00	0.00
Blup (P)	-0.47	-0.09	-0.90	0.00	0.00	-86.6	1.31	0.00	0.00	0.00	0.00
Blup (S)	-0.11	-0.90	-7.61	0.00	0.00	-122.0	-4.44	0.00	0.00	0.00	0.00

PH: plant height; CD: canopy diameter; SC: stem circumference; BH: lower branching height; BN: primary branching number; FN: fruit number; FL: fruit length; FD: fruit diameter; FM: fruit mass; SN: seed number; SM: seed mass. *Blup* values equals to 0.00 indicates not significant effects of varieties.

mother trees plants was 27.9 g (Ganga et al. 2010), a value slightly higher than the FM value of this work (22.7 g). This difference may be related to the higher number of fruits per plant in the collection, without discarding the hypothesis of some upward bias regarding the size of the fruits collected under natural conditions, since the main objective was to obtain sufficient seeds for seedling formation for implementation of the germplasm collection.

The traits related to the size of the plant are mostly in agreement with descriptions of other studies with *H. speciosa* (Silva Junior and Lédo 2006, Ganga et al. 2010, Freitas et al. 2012). A remarkable exception occurs when comparing the size of fruits of the *speciosa* variety of this work with the values found for the same variety in the northeastern coast of Brazil (Silva Junior et al. 2007), where the fruits showed greater development, highlighting once again, lower adaptation of this variety to the conditions of the UFG germplasm collection.

The genetic values (*blup;* Best Linear Unbiased Prediction) (Table 1) indicate that no significant genetic variation (zero values) was detected among the botanical varieties for the traits BH, BN, FD, FM, SN, and SM. The *cuyabensis* variety had the highest *blup* values for all other traits, and FN was highlighted with a superiority of 203.6 relative to the overall mean. On the other hand, the *speciosa* variety was not very productive under cultivation conditions, with a negative *blup* value of -122.0. As no significant effect of the FM was observed between varieties, the number of fruits is the determining factor in the estimated yield difference. Therefore, the *cuyabensis* botanical variety presents the greatest yield potential, followed by the *gardneri* variety.

Genetic parameters and expected selection gain

The analysis by the REML procedure revealed a significant genetic variation among the botanical varieties (Table 2) for the traits CD, SC, and FN. For the source subpopulations within varieties, the variables PH, CD, SC, and FN presented significant genetic variation. This significant variation of FN shows the existence of a potential difference in yield among the subpopulations within the varieties, in addition to the difference among varieties. Among the progenies within the subpopulations, significant genetic variation exists for the BH, BN, FL, and FD. For all variables, the highest percentage of variation occurred for the residue, which corresponds to the phenotypic variation among individuals within progenies, discounting the block effect.

The nonhierarchical analysis, performed only for the effect of the progenies, showed no significant difference between progenies only for the traits BH, FD, and SM (Table 2). The coefficients of experimental variation (*CVe*) presented high values for most of the traits. This was expected due to the variation between plants within progenies, which accumulated environmental variation between plots and genetic variation within progenies, corresponding to ¾ additive variance plus all dominance variance, assuming progenies of half sibs. The coefficients of genetic variation (*CVg*) show good selection potential for the traits with significant σ^2_{prog}. Importantly, the FN with coefficient of genetic variation of 94.5% is notable. The high *CVe* value for the same characteristic may also indicate high genetic variation within progenies. For these same

Table 2. Components of variance as a percentage of the total variation and genetic parameters of the agronomic traits of the UFG germplasm collection of *Hancornia speciosa* Gomes

Sources of variation	**Variance components** (%)										
	PH (m)	**CD** (m)	**SC** (cm)	**BH** (cm)	**BN**	**FN**	**FL** (mm)	**FD** (mm)	**FM** (g)	**SN**	**SM** (g)
Botanical Variety	7.41	19.26^{**}	21.11^{**}	0.00	0.00	27.57^{**}	23.57	0.00	0.00	0.00	0.00
Population/Variety	30.10^{**}	14.15^{**}	19.98^{**}	8.43	0.00	15.50^{**}	0.00	6.40^{*}	1.50	0.00	0.00
Progeny/Population	0.00	5.15	3.93	20.89^{**}	18.80^{**}	0.87	25.04^{**}	29.96^{**}	7.53	15.00	4.75
Error	62.48	61.44	54.97	70.68	81.20	56.06	51.39	63.64	90.97	84.99	95.24
Genetic parameters											
σ^2_{prog}	1.442^{**}	0.797^{**}	78.879^{**}	0.000	0.070^{**}	44348^{**}	8.975^{**}	0.552	9.177^{*}	3.392^{*}	0.145
CVg %	20.18	15.96	21.15	0.00	18.34	94.46	8.95	2.31	12.78	22.88	14.03
CVe %	26.60	24.62	34.28	202.76	36.96	93.48	12.59	68.50	34.82	56.27	53.41
h^2_m %	65.84	58.44	56.02	0.00	44.26	77.39	62.17	0.37	32.82	33.41	17.31
SG_{prog}%	11.46	8.54	11.08	0.00	8.54	58.17	4.94	0.09	5.35	9.26	4.09

**, *: Significant at 0.01 and 0.05 probability levels, respectively; σ^2_{prog}: Total genetic variance among progenies; *CVg* %: Genetic coefficient of variation; *CVe* %: Experimental coefficient of variation; h^2_m %: heritability coefficient at progeny means level; SG_{prog} %: Selection gain at progeny level (20% selection intensity; female parents only). PH: plant height; CD: canopy diameter; SC: stem circumference; BH: lower branching height; BN: primary branching number; FN: fruit number; FL: fruit length; FD: fruit diameter; FM: fruit mass; SN: seed number; SM: seed mass.

traits, heritability at the progeny level (h^2_m) ranged from 32.8% to 77.4%. Once again, the FN with the highest heritability coefficient stands out. Estimates of genetic gain expected by selection among progenies reinforce the great potential of the collection as a basis for the selection of progenies with higher fruit yield, corresponding to 58.2% increase in the mean of the trait in one recurrent selection cycle. In addition to this, the traits PH and SD show potential gains greater than 10% relative to the mean.

The proposed strategy of selection among the progenies, disregarding the structuring of the botanical varieties and subpopulations, follows genetic and practical criteria. A previous selection among varieties could restrict the genetic basis of the population, since only four botanical varieties are in the collection. Selection among the subpopulations (provenances) also presents constraints due to an imbalance in the number of subpopulations by varieties and progenies by subpopulation. In a random hierarchical model with three levels of structuring, as in this collection, the variance among progenies, when the higher levels are disregarded, accumulates all the variance between progenies within subpopulations and accumulates a considerable part of the variances between subpopulations within and among varieties. The expected selection gains selection attest to this potential. In addition to selection among progenies, the selection of one or two best individuals from each selected progeny is recommended. Given the large genetic variability expected within progenies, this selection, although not predicted in this study, could considerably increase the total gains.

Correlation analysis

Of the 55 correlation coefficients estimated between the agronomic traits, 24 phenotype correlations and 21 genotype correlations were significant (Table 3). The final goal in a *H. speciosa* breeding program would be the improvement of the production of fruit per area. Here we didn’t focus on latex production. The high positive correlation of the FN with PH, CD, and SC is highlighted, showing that more vigorous plants are more productive. A relevant aspect to be defined in a pre-breeding program of *H. speciosa* would be the desirable size of the plant. The data from this study clearly show that taller plants with larger canopies are more productive. However, larger plants require greater plant spacing, which would reduce the number of plants per unit area. An alternative to exclusive plantings would be pruning for growth conduction and maintenance, which would require further studies. For intercropping with annual small crops or with pasture, the larger size would be no problem, since the spacing would be naturally larger.

Of the 66 correlations found between the juvenile and adult traits, 24 phenotypic correlations and 39 genotypic correlations were significant (Table 4), with emphasis on the traits of the adult plants, FN, PH, DB, and SC compared to juvenile traits such as DGR, HGR, SDF, and PHF. Genetic correlations, however, may be overestimated by the constant environmental effects of the experimental plots, since they were estimated with the same plants in the same environments

Table 3. Estimates of the phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients at the level of the individual (N = 192) between agronomic traits of the UFG germplasm collection of *Hancornia speciosa* Gomes

	PH	CD	SC	BH	BN	FN	FL	FD	FM	SN	SM
PH	-	0.566**	0.344**	0.161*	0.093	0.127	0.124	0.124	-0.074	0.079	0.188*
CD	0.399*	-	0.336**	0.038	0.254**	0.217	0.283	0.283	0.062	0.142	0.182*
SC	0.169	0.304*	-	-0.014	0.159*	0.504**	0.171	0.171	0.062	-0.006	0.084
BH	0.166	0.122	-0.120	-	-0.076	0.025	0.135	0.135	-0.019	-0.089	-0.124
BN	0.036	0.366*	0.297*	-0.169	-	0.450*	0.105	0.105	-0.037	0.028	0.023
FN	0.443**	0.464**	0.402**	0.028	0.203**	-	0.134	0.134	-0.032	0.034	0.144
FL	0.091	0.287**	0.079	0.016	-0.052	0.140	-	0.928**	0.498**	0.260**	0.291**
FD	0.073	0.281**	0.067	0.048	0.002	0.141	1.000**	-	0.514**	0.225**	0.285**
FM	0.075	0.304*	0.233	0.129	0.139	0.153	0.845**	0.845**	-	0.510**	0.612**
SN	0.201	0.363*	0.324*	0.136	0.036	0.200	0.708**	0.708**	0.849**	-	0.861**
SM	0.156	0.331*	0.302*	0.158	-0.002	0.205	0.738**	0.738**	0.879**	0.977**	-

**, *: Significant at 0.01 and 0.05 probability levels, respectively. PH: plant height; CD: canopy diameter; SC: stem circumference; BH: lower branching height; BN: primary branching number; FN: fruit number; FL: fruit length; FD: fruit diameter; FM: fruit mass; SN: seed number; SM: seed mass.

Table 4. Estimates of the phenotypic and genotypic correlation coefficient of traits in the juvenile stage$^{1/}$ (columns) with the biometric data of the adult plants (rows) of the UFG germplasm collection of *H. speciosa* Gomes (N = 162)

	Phenotypic correlations						Genotypic correlations					
	DGR	HGR	SDN	SDF	PHN	PHF	DGR	HGR	SDN	SDF	PHN	PHF
PH	0.405**	0.43**	0.405**	0.451**	-0.019	-0.046	0.2914*	0.3768**	0.2687*	0.3959**	0.0788	-0.0762
CD	0.478**	0.426**	0.490**	0.438**	0.227**	0.063	0.4385**	0.2733*	0.4732**	0.3176*	-0.0624	-0.2391*
SC	0.379**	0.386**	0.380**	0.432**	-0.016	-0.114	0.4947**	0.4563**	0.453**	0.4849**	-0.0654	-0.108
BH	0.044	0.092	0.109	0.171*	-0.199	-0.136	0.0824	0.0541	0.1735	0.1572	-0.0129	-0.086
BN	0.197*	0.228**	0.178*	0.175*	-0.051	-0.007	0.1444	0.1007	0.1145	0.0476	-0.1455	-0.0722
FN	0.366**	0.348**	0.381**	0.379**	0.015	-0.019	0.4539**	0.4088**	0.4241**	0.4322**	0.0241	-0.009
FL	0.156	0.088	0.214*	0.138	0.040	-0.043	0.3594**	0.2983*	0.3598**	0.2867*	0.2513*	-0.0096
FD	0.121	0.058	0.171*	0.118	0.022	-0.053	0.3594**	0.2983*	0.3598**	0.2867*	0.2513*	-0.0096
FM	-0.031	-0.085	0.029	-0.026	-0.027	-0.086	0.307*	0.2427*	0.3149*	0.2383*	0.134	0.0108
SN	-0.104	-0.072	-0.083	-0.080	0.131	-0.024	0.3368*	0.2951*	0.3275*	0.2793*	0.1473	-0.0434
SM	-0.007	-0.040	0.041	-0.017	0.111	-0.003	0.3496**	0.2748*	0.3459**	0.27*	0.1298	-0.0469

**, *: Significant at 0.01 and 0.05 probability levels, respectively. PH: plant height; CD: canopy diameter; SC: stem circumference; BH: lower branching height; BN: primary branching number; FN: fruit number; FL: fruit length; FD: fruit diameter; FM: fruit mass; SN: seed number; SM: seed mass; DGR: stem diameter growth rate; HGR: plant height growth rate; SDN: diameter of the seedling in the nursery; SDF: stem diameter in the field; PHN: seedling height in the nursery; PHF: height in the field. ^{1} Data obtained by Ganga et al. (2009).

at different ages. These results indicate the possibility of early selection based on initial plant development. From the point of view of establishment of crops through seed propagation, an alternative would be dense planting with thinning after the first years, of the plants with lower initial development.

On the other hand, no significant genetic correlations were verified among the measured traits in the nursery with the adult plants, showing that the results obtained in the nursery are not the most appropriate to make predictions about the future development of the mangaba trees. Notably, although the progenies are common, the number of plants per progeny in the nursery was much higher than those for plants transplanted to the field, and a visual selection was made of four plants with good development of each progeny to form the field collection. The possible effect of this selection in the nursery could not be predicted with the data from this study.

Concluding remarks

The results of the present study demonstrate the great genetic variability existing in the UFG germplasm collection of *H. speciosa* for most of the evaluated agronomic traits, attesting to the potential use of the collection as a base population for pre-breeding of the species. The botanical variety *H. speciosa* var. *cuyabensis* are superior to the others regarding fruit yield and plant size. Progenies with greater development in the juvenile phase are potentially more productive in the adult phase, allowing the early selection of superior genotypes. For initiating a breeding program in the germplasm collection we suggest a selection strategy based on the selection of the superior progenies, disregarding the structure in varieties and subpopulations, focusing on fruit number and plant architecture. Additionally, it is recommended to select the superior plants within progenies.

REFERENCES

Agostini-Costa TS, Silva DB, Vieira RF, Sano SM and Ferreira FR (2010) Espécies de maior relevância para a região Centro-Oeste. In Vieira RF, Agostini-Costa TS, Silva DB, Sano SM and Ferreira FR (eds) **Frutas nativas da região Centro-Oeste do Brasil**. Embrapa, Brasília, p. 15-30.

Chaves LJ (2006) Recursos genéticos no Cerrado. In Silva Junior JF and Lédo AS (eds) **A cultura da mangaba**. Embrapa, Aracaju, p. 75-84.

Collevatti RG, Olivatti AM, Telles MPC and Chaves LJ (2016) Gene flow among *Hancornia speciosa* (Apocynaceae) varieties and hybrid fitness. **Tree Genetics and Genomes 12**: 74-85.

Costa CF, Collevatti RG, Chaves LJ, Lima JS, Soares TN and Telles MPC (2017) Genetic diversity and fine-scale genetic structure in *Hancornia speciosa* Gomes (Apocynaceae). **Biochemical Systematics and Ecology 72**: 63-67.

Darrault RO and Schlindwein C (2005) Limited fruit production in *Hancornia speciosa* (Apocynaceae) and pollination by nocturnal and diurnal insects. **Biotropica 37**: 381-388.

Flores IS, Silva AK, Furquim LC, Castro CFS, Chaves LJ, Collevatti RG and Lião LM (2018) HR-MAS NMR allied to chemometric on *Hancornia speciosa* varieties differentiation. **Journal of the Brazilian Chemical Society 29**: 708-714.

Freitas MKC, Coimbra RR, Aguiar GB, Aguiar CBN, Chagas DB, Ferreira WF and Oliveira RJO (2012) Variabilidade fenotípica e caracterização morfológica de uma população natural de *Hancornia speciosa* Gomes. **Bioscience Journal** 28: 833-841.

Ganga RMD, Chaves LJ and Naves RV (2009) Parâmetros genéticos em progênies de *Hancornia speciosa* Gomes do Cerrado. **Scientia Forestalis 37**: 395-404.

Ganga RMD, Ferreira GA, Chaves LJ, Naves RV and Nascimento JL (2010) Caracterização de frutos e árvores de populações naturais de *Hancornia speciosa* Gomes do Cerrado. **Revista Brasileira de Fruticultura 32**: 101-113.

Koch I, Rapini A, Simões AO, Kinoshita LS, Spina AP and Castello ACD (2015) Apocynaceae In **Lista de espécies da flora do Brasil.** Jardim Botânico do Rio de Janeiro. Available at: <http://floradobrasil.jbrj.gov.br/jabot/floradobrasil/FB26452>. Accessed on Nov 21, 2017.

Lobato EJV (2016) **Atlas climatológico do Estado de Goiás**. UFG, Goiânia, 89p.

Martins GV, Martins LSS, Veasey EA, Lederman IE and Silva EF (2012) Diversity and genetic structure in natural populations of *Hancornia speciosa* var. *speciosa* Gomes in Northeastern Brazil. **Revista Brasileira de Fruticultura 34**: 1143-1153.

Mendonça RC, Felfili JM, Walter BMT, Silva Junior MC, Rezende AV, Filgueiras TS, Nogueira PE and Fagg CW (2008) Flora vascular do bioma Cerrado. In Sano SM, Almeida SP and Ribeiro JF (Eds) **Cerrado: ecologia e flora**. Embrapa, Brasília, p. 423-442.

Monachino JA (1945) A revision of *Hancornia* (Apocynaceae). **Lilloa 1**: 19-48.

Moura NF, Chaves LJ, Vencovsky R, Zucchi MI, Pinheiro JB, Morais LK and Moura MF (2005) Seleção de marcadores RAPD para o estudo da estrutura genética de populações de *Hancornia speciosa* Gomes. **Bioscience Journal 21**: 119-125.

R Core Team (2017) **R: A language and environment for statistical computing**. R Foundation for Statistical Computing, Vienna. Available at: <http://www.R-project.org>. Accessed on Nov 21, 2017.

Rodrigues AJL, Yamaguishi AT, Chaves LJ, Coelho ASG, Lima JS and Telles MPC (2015) **Genetics and Molecular Research 14**: 7274-7278.

Silva AVC, Santos ARF, Wickert E, Silva Junior JF and Costa TS (2011) Divergência genética entre acessos de managabeira (*Hancornia speciosa* Gomes). **Revista Brasileira de Ciências Agrárias 6**: 572-578.

Silva Junior JF and Lédo AS (2006) Botânica. In Silva Junior JF and Lédo AS (eds) **A cultura da mangaba**. Embrapa Tabuleiros Costeiros, Aracaju, p. 25-34.

Silva Junior JF, Xavier FRS, Ledo CAS, Neves Junior JS, Mota DM, Schmitz H, Musser RS and Ledo AS (2007) Variabilidade em populações naturais de mangabeira do litoral de Pernambuco. **Magistra 19**: 373-378.

Valls JF (2007) Caracterização de recursos genéticos vegetais. In Nass LL (eds) **Recursos genéticos vegetais**. Embrapa, Brasília, p. 281-306.