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Genetic parameters and selection gains in open-pollination progenies of bacabi palm tree (*Oenocarpus mapora*)

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Abstract

The Bacabi (*Oenocarpus mapora* Karsten) is an Amazonian palm whose fruit is widely used in the food industry due to its organoleptic properties and excellent nutritional quality. The objective of this work was to estimate genetic parameters and selection gains in the selection of open pollinated bacabi progenies. The experiment was carried out in the district of Campo Limpo, in the municipality of Santo Antônio do Tauá, state of Pará. The study assessed 38 progenies from open-pollination under an agroforestry system in a randomized block design with five replicates and two plants per plot. At Seventeen, Twenty-four and Thirty months after planting, data were collected on the following traits: stem height (SH), plant diameter (DIAM), number of live leaves (NLL), length of the leaf rachis (LLR), number of leaflet pairs (NLP) and leaflet length (LL). Genetic variety was observed among and within progenies for all evaluated traits. The broad-sense heritability estimates varied between 0.13 and 72.81%. High values were found for NLP (72.81%), DIAM (52.01%), LLR (62.64%), and SH (66.16%). Selection gains can be achieved for all the traits evaluated, with selection of 30% among progenies and 20% inside progenies.

Keywords: Amazonian palm, Genetic differences, Native species, phytotechnics

Introduction

Native to the Amazon region, the bacabi palm (*Oenocarpus mapora* Karsten) has great economic importance for the region. The plant provides raw material for food, medicines, fibers, building materials, and other products. It is a multi-stemmed, early producing palm tree (Costa et al., 2021). *O. mapora* fruits are mainly used in the food industry to make non-alcoholic beverages, popsicles, ice cream, and fresh consumption. The palm oil extracted from the fruit as well as other derived products with excellent nutritional qualities (Oliveira & Moura 2010). The bacabi oil has similar properties to olive oil and its industrialization and trade could reduce foreign exchange losses with olive oil imports. Palm trees (Arecaceae) can be considered plant species with too much potential to produce vegetable oils (Lahlou et al., 2022; Khatiwari et al., 2021). However, there are no records of the extractive production of this species.

Genetic differences have been found in various traits of palm trees, among populations and/or progenies (Oliveira & Moura, 2010). This may be the result of small differences in environmental conditions (Villanueva-Almanza et al., 2021).

In addition, in Arecaceae species, morphological characters are widely used to characterize diversity, such as plant height, rachis length, number of rachillae, fruit circumference and mass, number of clusters, fruit production per cluster and the mass of 100 fruits to help describe dissimilarity within groups (Domiciano et al. 2015; Elsafy et al. 2015; Sobral et al.2018).

Progenies are genetic entities used to estimate population variability and to explain the nature of phenotypic variation. Important traits for breeding are evaluated in the progenies and tested in experimental designs, allowing the estimation of genetic parameters that can assist the choice of the base population and

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selection method. Understanding genetic diversity precedes the achievement of effective conservation and management strategies for plant species (Khadivi et al. 2020).

Knowing the variability due to genetic differences based on genetic parameters and environmental influences (interaction genotype x environment) is crucial in breeding programs. Conserving the present genetic pool and using it efficiently depends on a comprehensive analysis of diversity, which is done by distinguishing materials within species (Souza et al., 2023). Thus, considering that *O. mapora* is yet to be domesticated, this study estimated the genetic parameters and the selection gains in open-pollination progenies of bacabi (*O. mapora*).

Material and Methods

An experiment using 38 progenies of *O. mapora* was conducted in an agroforestry system, in the community of Campo Limpo, Municipality of Santo Antônio do Tauá, Pará, Brazil (1°02'22.9"S and 48°08'55.1"W), in April 2011. Ripe fruits samples were collected from open-pollinated mother plants, from different municipalities: 22 samples from Santo Antônio do Tauá, 12 from Belém, and 4 from Colares, municipalities belonging to the state of Pará, Brazil. The samples and their respective progenies were identified with numbers (**Table 1**).

The study area has a plain relief with a secondary vegetation (*capoeira)*. The climate in the municipality is moist megathermal due to the influence of the low latitudes. The average temperatures are high throughout the year (25°C), with monthly averages between 24°C and 26°C. The average annual rainfall is 2,350 mm and concentrated between January and June, corresponding to 80% of the rainfall. The soil in the region is Yellow-Latosol characterized by medium texture and low fertility (Rodrigues et al., 2004).

The soil in the experimental area had the following chemical characteristics: pH = 5.0; N = 0.11%; P = 2 mg.dm^{-1}; K = 45 mg.dm^{-1}; Na = 17 mg.dm^{-1}; Ca = 1.3 cmolc dm^{-1}; Mg = 0.4 cmolc dm^{-1}; Al = 0.6 cmolc dm^{-1}; H+Al = 5.78 cmolc dm^{-1}; MO = 14,44 g/kg; Chemical and organic fertilizations were applied according to the recommendations by *Embrapa Amazônia Oriental* for the cultivation of açaí (*Euterpe oleracea*) (Cravo et al., 2007). The fertilizers were applied every 6 or 3 months, with the first application at the beginning of the rainy season. Three applications of 100 g of 10-28-20 NPK formula were carried out in the first year. The fertilizer was evenly spread around the plant 30 cm from the base. In the second year, 150 g of the same mixture was applied to each clump, 50cm from the plant base, with 10 L of cattle manure.

Progenies were assessed 30 months after planting. Data on vegetative traits were collected using an assessment form created by the Embrapa Active Germplasm Bank (AGB) for bacabi. The following traits were analyzed: stem height (SH) measured from the root-initiation zone at the bottom of the stem to the base of the newest emerging leaf in the crown (cm); plant diameter (DIAM at 10 centimeters above ground; number of live leaves (NLL); count of all live leaves; leaf rachis length (LRL) measured on leaf 1 (cm); number of leaflet pairs (NLP); leaflet length (LL) measured on the third pair, from top to bottom in relation to their position in the leaf rachis; number of offhoots (NS) counted as described by Clement & Bovi (2000) for peach palm (*Bactris gasipaes*).

The O. mapora progenies were evaluated in a randomized block experimental design, with 38 treatments (38 progenies) and 5 (replications) at a spacing of 4 x 4 meters, with each replication consisting of two plants. In total, 380 plants were evaluated. Estimates of plot means as well as means of individual plants (within plots) were expressed per Y_{ij}, where *i*th progeny and *j*th repetition (or blocks) (Cruz et al., 2004).

Variance analysis was carried out for each trait and all the effects were considered random (except the mean), to verify the homogeneity of the variances. The analyses used the software GENES (Cruz, 2013), which uses the estimators of genetic and phenotypic parameters and the expected selection gains as described by Vencovsky & Barriga (1992).

The values of NLL and NLP were transformed into $\sqrt{X}$ for the analysis of variance, according to Steel & Torrie (1980). The absolute growth rate for height and the absolute growth rate for seedling diameter (AGRH and AGRD) were transformed as described by Benincasa (1988). Evaluations were carried out in three campaigns, at 17, 24 and 30 months after planting. Based on the analysis of variance, estimates were made for phenotypic and genetic variances, phenotypic and genetic covariances, heritability coefficient, and "b" index between the coefficients of genetic and environmental variation.

Results and Discussion

Most of the traits evaluated in the 38 progenies of *O. mapora* showed differences by the F test at 1% significance, indicating a significant genetic variability among and within progenies, which may help to identify individuals with desirable traits (**Table 2**).

According to the coefficient of genetic variation, the values between progenies and within progenies

Table 1. Identification of bacabi (*Oenocarpus mapora*) progenies used in the study. Belém, Pará, Brazil.

Progeny	Origin	Locality
001	Belém	Embrapa Active Germplasm Bank (AGB)
002	Belém	Embrapa Active Germplasm Bank (AGB)
003	Belém	Embrapa Active Germplasm Bank (AGB)
004	Belém	Embrapa Active Germplasm Bank (AGB)
005	Stº Antônio do Tauá	Comunidade Campo Limpo
006	Belém	Federal Rural University of Amazon
007	Belém	Federal Rural University of Amazon
008	Belém	Embrapa Active Germplasm Bank (AGB)
009	Belém	Embrapa Active Germplasm Bank (AGB)
010	Belém	Embrapa Active Germplasm Bank (AGB)
011	Belém	Embrapa Active Germplasm Bank (AGB)
012	Belém	Embrapa Active Germplasm Bank (AGB)
013	Stº Antônio do Tauá	Mr. Takanori's Farm
014	Stº Antônio do Tauá	Vila do Remédio District
015	Stº Antônio do Tauá	Vila São Tomé District
016	Stº Antônio do Tauá	Vila Trombeta District
017	Stº Antônio do Tauá	Vila Trombeta District
018	Stº Antônio do Tauá	Vila Stª Maria District
019	Colares	Vila Quaxinguba District
020	Colares	Vila Penha Longa District
021	Colares	Vila Penha Longa District
022	Colares	Vila Penha Longa District
023	Stº Antônio do Tauá	Mr. Takanori's Farm
024	Stº Antônio do Tauá	Mr. Takanori's Farm
025	Stº Antônio do Tauá	Mr. Takanori's Farm
026	Stº Antônio do Tauá	Mr. Takanori's Farm
027	Stº Antônio do Tauá	Mr. Takanori's Farm
028	Stº Antônio do Tauá	Mr. Takanori's Farm
029	Stº Antônio do Tauá	Mr. Takanori's Farm
030	Stº Antônio do Tauá	Mr. Takanori's Farm
031	Stº Antônio do Tauá	Mr. Takanori's Farm
032	Stº Antônio do Tauá	Mr. Takanori's Farm
033	Stº Antônio do Tauá	Mr. Takanori's Farm
034	Stº Antônio do Tauá	Mr. Takanori's Farm
035	Stº Antônio do Tauá	Mr. Takanori's Farm
036	Stº Antônio do Tauá	Mr. Takanori's Farm
037	Stº Antônio do Tauá	Mr. Takanori's Farm
038	Belém	Embrapa Active Germplasm Bank (AGB)

Table 2. Genetic, phenotypic, and environmental parameters for eight traits evaluated in the 38 progenies of bacabi (*Oenocarpus mapora*). Belém, Pará, Brazil.

Genetic parameter	Trait							
	SH	DIAM	NLL	LRL	NLP	LL	AGRH	AGRD
			cm				cm/cm.day	mm/mm.day
σ^2_g	373.3115	15.1583	0.2678	283.8203	13.4574	2.3546	0.0024	0.00007
σ^2_{gd}	1119.9345	45.47516	0.803573	851.4609	40.3724	7.0639	0.0073	0.00024
σ^2_f	564.3167	29.143	0.5366	453.0385	18.4828	9.4212	0.0034	0.0001
σ^2_d	1242.9492	57.4401	1.8775	831.1831	36.8114	33.5297	0.0082	0.0002
σ^2_e	89.0296	14.4299	0.0949	142.5146	1.3736	6.2061	0.0005	6.9174
CV_g (%)	19.65	22.52	8.96	22.83	26.69	4.75	20.22	30.56
CV_{gd} (%)	34.04	38.47	15.52	39.55	44.15	8.21	37.15	52.94
h^2m (%)	66.15	52.01	49.91	62.64	72.81	24.99	66	0.13
hd (%)	0.9	0.79	0.42	1.02	1.09	0.21	0.88	0.86
b among	2.04	1.03	1.67	1.41	3.13	0.61	2.06	1.42
b within	3.54	1.77	2.9	2.44	5.17	1.066	3.79	2.47

σ^2g: genetic variance among progeny; σ^2e: environmental variance; σ^2f: phenotypic variance; CVg (%): coefficient of genetic variation among progenies; h^2m: mean heritability coefficient; hd: heritability; b among: CVg/CVe; b within: CVgd/CVe. SH: stem height; DIAM: plant diameter; NLL: number of live leaves; LRL: leaf rachis length; NLP: number of leaflet pairs; LL: leaflet length; AGRH: absolute growth rate for height; AGRD: absolute growth rate for seedling diameter.

varied, with the lowest value for LL and the highest value for AGRD. On the other hand, the "b" index, which measures the relationship between genetic variance and environmental variance, was higher than 1 for most of the traits, except for LL. This indicates that, for this trait, selection is not favorable. The b values within progenies were higher than among progenies. The coefficients of genetic variation within plots were almost the double of the coefficients of genetic variation among progenies (Table 2).

The average heritability for most of the traits between progenies was higher than within progenies (table 2). Estimates of overall heritability revealed high values for NLP, SH, LRL and DIAM.

The genetic gains were calculated using ¼ of the additive variance for the selection among progenies and ¾ for the selection within progenies. The selection gains were higher for the traits SH, LRL, NLP, and DIAM, which was expected considering the information on genetic variance and broad-sense heritability (**Table 3**). Based on these findings, the study selected progenies that stood out for the traits evaluated: 001, 002, 003, and 009 (identification in table 1) presented the best results for all the traits assessed. Progenies 007 and 008 provided good performances for LL and NLL. Progeny 016 stood out for SH, DIAM, and NLL. Progenies 017, 019, 026, and 028 stood out for LL, AGRH, and AGRD. Progeny 029 showed good performances for NLL, LRL, NLP, LL, and AGRD. Progeny 030 showed high potential for NLL, NLP, and AGRD. Progeny 031 stood out only for DIAM and progeny 038 for SH, NLP, and AGRH (Table 3).

During growth, selection gains achieved were 5.40% for SH, with the population mean increasing from 98.28 to 103.59 cm; gains of 5.65% for DIAM, with the population mean increasing from 17.52 to 18.51 mm; 6.56% of selection gains for LRL, with the population mean increasing from 73.77 cm to 78.61 cm, 5.52% for AGRH, with the population mean increasing from 0.24 to 0.25 cm/day, and 7.08% of selection gains for AGRD, with the population mean increasing from 0.028 to 0.030 mm/day (Table 3).

The "b" index, which measures the relationship between genetic variance and environmental variance, was above 1.00 for most characters. The coefficients of genetic variation within plots were almost the double of the coefficients of genetic variation among progenies. This is because the *O. mapora* progenies were considered half-sibling, even though the fruits were originated from open pollination and harvested directly from the mother plants.

The pattern of genetic variance distribution among populations assessed by half-sibling progenies follows the model of ¼ of additive genetic variance among progenies. While ¾ of the variance and the whole dominance variance is available within the respective progenies (Vencovsky, 1987), which indicates that additional genetic gains are possible using methods that combine selection within progenies. Luistri et al. (2021) High phenotypic variation was observed for all the descriptors analyzed in the *Acrocomia aculeata* palm, both within and between progeny averages.

The estimates for broad-sense heritability varied from 0.13 to 72.81%. Considering these traits, these values are highly favorable to selection and provide a better use of the additive effects in this type of progeny, since similarly to half-sibling progenies, open pollinated progenies use only ¼ of the available additive genetic variance (Hallauer & Miranda Filho, 1981). These results agree with the findings of Silva et al. (2009) who estimated broad-sense heritability of agronomic traits above 50% in *O. mapora* progenies. The only exception among the bacabi (*Oenocarpus distichus* Mart.) progenies was for AGRD, with heritability estimates under 50%.

In this work, of all traits, AGRD had the lowest

Table 3. Genetic gain and mean ($\bar{X}$) ± standard error (EP) population for the traits stem height (SH), stem diameter (DIAM), number of living leaves (NLL), leaf rachis length (LRL), number of leaflet pairs (NLP), leaflet length (LL), absolute growth rate height and absolute growth rate diameter (AGRH and AGRD) in bacabi (*Oenocarpus mapora*). Belém, Pará, Brazil.

Trait	Genetic gain GS$_e$				$\bar{X}$ ± EP
	Among	Within	Total	%	
SH (cm)	1.10	4.20	5.30	5.40	103.59±16.5
DIAM (cm)	0.19	0.79	0.99	5.65	18.51±2.8
NLL (√x)	0.025	0.077	0.10	1.78	5.87±0.8
LRL (cm)	0.93	3.91	4.84	6.56	78.61±10.7
NLP (√x)	0.21	0.88	1.10	8.01	14.84±2.0
LL (cm)	0.053	0.161	0.21	0.66	32.58±4.2
AGRH (cm/cm.day)	0.0028	0.0106	0.01	5.52	0.25±0.02
AGRD (mm/mm.day)	0.0002	0.0017	0.001	7.08	0.03±0.01

Among progenies: selection of 30% of progenies (k=1.12); Within progenies: selection of 20% of progenies (k=2.12); NLL and NLP transformed to √X heritability (0.13). However, the “b” index was higher than 1.00 among and within progeny, which may validate a possible selection for this trait. For Muller et al. (2005), coefficients of genetic variation allow the comparison of the genetic variance available for the selection in white-açaí palm (*Euterpe oleracea*), mainly between traits. The authors reported that plant height presented the highest CVg (11.64%), followed by the number of live leaves (5.73%), and diameter had the lowest estimate of CVg (4.15%). These results are inferior to those found in this study for *O. mapora*.

Bergo et al. (2004) estimated genetic and phenotypic paramenters in half-sibling progenies of pupunha (*Bactris gasipaes* Kuntn, palm) in the western region of the Amazon and found heritabilities for plant height and plant diameter lower than this study. However et al. (2008) reported high heritabilities for open-pollinated progenies of açaí palm at the individual level and mean of progenies, with estimates of mean progeny heritability of 35.30% and 36.28%, corroborating the results of this study for *O. mapora*.

Carvalho et al. (2008) reported genetic variability for the dwarf coconut traits alive leaf number, emitted leaf number, circumference of stem, length of stem, number of emitted inflorescence and number of feminine flowers for inflorescence, considering the values expressed by the ratio CVg/CVe, which varied between 1.49 and 3.57. The average heritability estimated in the second year was 51% for number of emitted inflorescence and higher than 78% for all the other traits. All of these estimates indicate a favorable scenario for selection in palm trees and are consistent with the results found for *O. mapora*.

Selection between progenies was 30% and within progeny 20%. According to Vencovsky & Barriga (1992). The highest gains were achieved with selection within progenies due to the higher selection intensity, higher coefficients of phenotypic variation within families and higher coefficients of heritability at individual level within families. The relatively high estimates were favored by selection pressure, which was also considered high, ie, one progeny selected (20%) of the five plants in the 38 progenies of *O. mapora*.

These results agree with the findings of Lins et al. (2001), who obtained genetic gains in direct selection among and within families of the genus *Grevillea*, using selection intensity among families of 30% and within families of 10%. It is of note that, whichever the year of the selection, the highest gains will be achieved with selection within family.

Vencovsky (1987) reported that selection gains are favorable when the ratio CVg/CVexp tends to one (1.0) or > 1.0 and, in these cases, the genetic variance exceeds environmental variance. In this sense, when the selection is carried out in the first year, the genetic gains are maximized. However, selection at very early stages is questionable because the individuals may not have developed their full genetic potential. Therefore, a reassessment at a more advanced age is desirable.

In two studies, Farias Neto et al. (2005) and Farias Neto et al. (2008) stated that high selection gains can be achieved when high estimates of heritability exist and the ratio between the coefficients of genetic variation (CV_g%) and coefficients of experimental variation (CV_e%) is higher than the unit. This relationship was confirmed in the work with young açaí progenies, in which higher heritabilities provide higher probability of gains in number of suckers and diameter at breast height (DBH). Height and number of live leaves achieved only moderate gains since the heritability in these traits were below 47.23% and 51.6%, respectively. The authors also reported that a substantial genetic gain of 45%, above the experimental mean, is possible with the selection of the twenty best individuals for the trait total fruit production, which are consistent with the findings for the genetic parameters estimated in this work.

Conclusions

The CVg/CVe ratio (“b” index) indicates that the selection among and within progenies can be efficiently performed for most of the traits evaluated, except for LL, in which the traits height and diameter can be used for the indirect assessment of production and the identification of phenotypically superior plants for the genetic improvement program of bacabi palm (*O. mapora*).

The heritability estimated at the level of family means and at the level of mean among plants from progenies showed higher values for NLP, followed by SH, AGRH, LRL and DIAM, revealing the potential for responses to selection in these traits. Therefore, these traits can be used in the selection of seeds and seedlings aiming at further genetic improvement studies.

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