Genetic variability and progeny selection of peach palm via mixed models (REML / BLUP)

Haroldo Silva Rodrigues[1*], Cosme Damião Cruz[1], Jeferson Luis Vasconcelos de Macêdo[2], Marcos Deon Vilela de Resende[3], Ricardo Lopes[2] and Aluízio Borém[1]

¹Departamento de Fitotecnia, Universidade Federal de Viçosa, Av. Peter Henry Rolfs, s/n, 36570-900, Campus Universitário, Viçosa, Minas Gerais, Brazil. ²Embrapa Amazônia Ocidental, Manaus, Amazonas, Brazil. ³Embrapa Florestas, Colombo, Paraná, Brazil. *Author for correspondence. E-mail: roldoagro@hotmail.com

ABSTRACT. Heart of palm harvesting and exploitation has reduced the natural reserves of açaí and juçara; hence, the peach palm is an excellent option as source of heart of palm that can reduce the pressure on these two species. The peach palm has high tillering and no post-harvest oxidation. An experiment in a randomized block design with 72 progenies of peach palm, 36 replications and a single tree plot was performed for five years at the experimental field of Embrapa in the Western Amazon. Genetic parameters were estimated using two mixed models, one based on progeny means and the second on joint information from crops. A repeatability analysis, genotype selection, and progeny selection were performed; the Mulamba and Mock selection index was determined; and Tocher's clustering method was applied. The repeatability analysis revealed the existence of genetic variability, low repeatability, which ranged from 0.3307 to 0.6698 for five years. The analysis performed through the progeny means showed a heritability that varied from 51% to 23% for in all variables; the clustering revealed two groups. The progeny selection should be the main selection strategy, and crosses of superior progenies of different groups should be emphasized.

Keywords: heart of palm, perennial breeding, amazon.

Variabilidade genética e seleção de progênies de pupunheira via modelos mistos (REML/BLUP)

RESUMO. A coleta de palmito via extrativismo vem reduzindo as reservas naturais de açaí e juçara, sendo o palmito de pupunha uma excelente opção para obtenção de palmito plantado, pois além de diminuir a pressão da exploração extrativista sobre essas duas espécies, possui alto grau de perfilhamento e não apresenta oxidação pós-colheita. Foram testadas 72 progênies de pupunheira, em cinco anos, no campo experimental da Embrapa Amazônia Ocidental, em delineamento blocos casualizados com 36 repetições e uma planta por parcela. Os parâmetros genéticos foram estimados através de modelos mistos (REML/BLUP), foram também realizadas análises de repetibilidade, seleção de progênies, seleção de indivíduos por meio de BLUP individual, índice de seleção Mulamba-Rank e agrupamento de otimização de Tocher. As análises realizadas revelaram a existência de variabilidade genética, baixa repetibilidade, variando de 0,3307 até 0,6698 para cinco anos e herdabilidades variando de 51% a 23% para seleção de progênies nas variáveis analisadas, o agrupamento revelou dois grupos distintos. A seleção de progênies deve ser a principal estratégia de seleção e cruzamentos entre progênies superiores de grupos diferentes devem ser enfatizados.

Palavras-chave: palmito, melhoramento de perenes, amazônia.

Introduction

Brazil is the world's largest producer and consumer of heart of palm, the main way to obtain such good is through exploitation of juçara (*Euterpe edulis* Mart.) and açaí (*Euterpe oleracea* Mart.) (Sousa, Soares, Cordeiro, & Silva, 2011). Because the natural reserves of these two species in southern Brazil are running out, the exploitation of Amazonian acai and juçara has increased; these plants may also be depleted by predatory exploitation without good management practices.

The peach palm (*Bactris gasipaes* Kunth.) is proving to be a promising species and an alternative for heart of palm production. It shows desirable features for this sector. It is a native species, has high rusticity, is heat resistant, and has high tillering capacity, which reduces the need for land

mechanization and replanting after several harvests. The heart of palm extracted from peach palm has a sweetish taste, is slightly yellowish in color, has good palatability, a doughy texture, low fibrousness, and does not show post cut darkening by oxidative enzymes, as noted in heart of palm extracted from juçara and açaí, which contributes to its commercialization as a minimally processed product (Kapp, Pinheiro, Silva Raupp, & Chaimsohn, 2003).

Breeding programs to increase heart of palm productivity are conducted through successive cycles of selection and require evaluations over several years in field conditions, and a precise estimation of the variance components is imperative to maximize the accuracy of progeny selection. Then, it becomes necessary to use estimation methods that may fit certain experimental conditions and unbalanced data (Farias Neto & Resende, 2001; Farias Neto et al., 2007; Farias Neto, Clement, & Resende, 2013).

The restricted maximum likelihood/best linear unbiased prediction procedure (REML / BLUP) has been successfully used in peach palm breeding (Farias Neto & Resende, 2001). According to Resende (2000), the prediction of additive genetic values and genotypic values through mixed model values is essential. Comparing this method with the least squares estimation method for variance components and the multi-effects indexes method for genotypes genetic values estimation, this method leads to similar results in cases of small imbalances. However, in conditions of highly unbalanced data, it provides more accurate results.

This study aimed to estimate genetic parameters in individual and joint analysis, conduct heritability and repeatability studies to guide the progeny selection, and estimate genotype genetic values of half-sibs of peach palm through BLUP and the application of Mulamba and Mock selection index, as well as study the genetic diversity by grouping progenies through Tocher's clustering method (Neto et al., 2013; Barbosa et al., 2014).

Material and methods

Experiment location

The experiment was conducted at the experimental station of the Agroforestry Research Center of the Western Amazon - Embrapa/CPAA, located at the AM-010 highway, km 29, in the coordinates of 2° 51 'S latitude and 59° 52' W longitude. The data were collected in 2009, 2010, 2011, 2012, and 2013. The area's soil is classified as clayey alic yellow latosol; it has a clay content of approximately 80% on the surface horizon, is acidic and shows low cation exchange capacity, high aluminum saturation and low phosphorus content. To characterize the area, two soil compound samples (20 single samples in each half of the area) were collected for physical (particle size) and chemical analysis (fertility; Table 1).

In October 2006, the area was tilled to incorporate plant residues and limed (1.5 tons of dolomitic limestone ha^{-1}). In January 2007, the seedlings were transplanted *in situ*; fertilization at planting and five topdressing fertilizations at 2, 6, 12, 24, and 36 months were performed according to Embrapa's technical recommendations.

Genetic resource

The progenies used in the study originated from the city of Benjamin Constant, Amazonas, Brazil, selected for two generations, and from Yurimaguas, a city in the Peruvian Amazon; all came from the RECA Project (Economical Condensed Intercropped Reforestation) in the municipality of Extrema, RO - Brazil.

Number of progenies

The number of progenies was selected by number of seedlings acquired at the end of the production period, considering vigor, nutritional aspects, the absence of pests and diseases and especially the total absence of thorns on the stipe. Thus, from 100 progenies, 72 progenies were selected and transplanted *in situ*.

Table 1. Physical and chemical characteristics, base saturation, micronutrients, total cation exchange capacity (T), effective cation exchange capacity (t), base saturation index (V) and aluminum saturation index (m) in the experimental area soil for peach palm progeny selection.

Sample	Depth (cm)	Particle size (g kg^{-1})					pH (H$_2$O)	Base saturation (cmol$_c$ dm^{-3})					Micronutrients (mg dm^{-3})			
		Sand		Silt	Clay	Silt/Clay		Ca	Mg	Al	H+Al		Fe	Zn	Mn	Cu
		Coarse	Fine													
A1	20	110.15	31.45	211.90	646.50	0.33	4.22	0.60	0.33	0.84	7.11		264	1.93	2.98	0.63
A2	20	111.45	30.43	230.62	627.50	0.37	4.32	0.56	0.33	0.82	7.75		191	1.78	2.58	0.56
		P	K	Na	SB	T	t		V		m	Carbon		Organic matter		
		(mg dm^{-3})						(%)				(g kg^{-1})				
A1	20	10	72	5	1.14	8.25	1.98		13.77		42.63	17.41		29.95		
A2	20	8	70	5	1.09	8.84	1.91		12.34		43.03	16.64		28.61		

Number of replications, experimental sketch and analyzed traits

The peach palms plants were arranged in a 2.0 m x 1.0 m space (density of 5,000 plants ha^{-1}). The experiment was conducted in a randomized block design with single tree plots. The treatments consisted of 72 progenies of peach palms in 36 replications (a total of 2,592 plants), which occupied an area of 0.8 hectares. Six traits directly related to the productivity and yield of heart of palm were measured: heart of palm basal weight (HPBW), heart of palm apical weight (HPAW), and heart of palm weight (HPW), which were measured in grams (g) using a high precision scale; billets number (BN), which is the number of billets produced in the tussock with a standard size of 9 cm; heart of palm diameter (HPD), measured in millimeters (mm); and heart of palm length (HPL), expressed in centimeters (cm) and measured with an electronic paquimeter. The measurements were taken after harvest and cleaning of the product in the field

Genotype and progeny selection

To estimate the genotype genetic parameters, we used the SELEGEN-REML/BLUP model 15. The estimations of the variance components and genetic values predictions via a suitable linear mixed model were equivalent to:

$\gamma = Xf + Za + Wc + e,$ where:

γ, f, a, c, e are the data vectors, fixed effects (general average), additive effects (random), block effects (random events) and random errors, respectively, and X, Z and W are the incidence matrices associating f, a and c to the data vector γ, respectively.

The f value was estimated through generalized least squares prediction and a and c through BLUP, the values were obtained by solving the linear equations system, which is called mixed model equation (MME):

$$\begin{bmatrix} \hat{f} \\ \hat{a} \\ \hat{c} \end{bmatrix} = \begin{bmatrix} X'X & X'Z & X'W \\ Z'X & Z'Z + A^{-1}\lambda_1 & Z'W \\ W'X & W'Z & W'W + I\lambda_2 \end{bmatrix}^{-1} \begin{bmatrix} X'y \\ Z'y \\ W'y \end{bmatrix}$$

where,

$$\lambda_1 = \frac{1-h^2-c^2}{h^2} = \frac{\sigma_e^2}{\sigma_a^2}; \quad \lambda_2 = \frac{1-h^2-c^2}{c^2} = \frac{\sigma_e^2}{\sigma_C^2};$$

A and I = additive kinship and identity matrix, respectively.

To obtaining the random effects variance, REML estimators applying the EM algorithm (Expectation-Maximization) are:

$$\hat{\sigma}_e^2 = [y'y - \hat{f}'X'y - \hat{a}'Z'y - \widehat{C}'W'y]/[N - r(x)]$$

$$\hat{\sigma}_a^2 = [\hat{a}'A^{-1}\hat{a} + \sigma_e^2 tr A^{-1}C^{22}]/q$$

$$\hat{\sigma}_c^2 = [\hat{c}'c + \hat{\sigma}_e^2 tr C^{33}]/S$$

where:
tr = matrix trace;
$r(x)$ = X matrix's rank;
N- $r(x)$ = Error degrees of freedom;
q = individuals number;
s = block number;
N = total data number.

C^{22} e C^{33} = comes from: $C = \begin{bmatrix} C^{11} & C^{12} & C^{13} \\ C^{21} & C^{22} & C^{23} \\ C^{31} & C^{32} & C^{33} \end{bmatrix}$,

which is the coefficient matrix's generalized inverse of the MME.

The joint analysis, along with the repeatability analysis and progeny BLUP, were obtained through model 8 (Resende, 2007).

$\gamma = Xm + Za + Wp + Qi + Ts + e$, where:

γ, m, a, p, i, s, e are the data vectors, vector of the effects of the measuring-repetition combinations (fix) added to the general mean, vector of the individual additive genetic effects (random), plot effects vector (random), effects of the genotype measuring interaction vector (random), vector of the permanent effects (random), vector of residues (random), respectively, and X, Z, W, Q, and T are the incidence matrices associating m, a, p, i and s to the data vector γ, respectively.

Simultaneous trait selection

The Mulamba and Mock selection index was used (Resende, Silva, & Azevedo, 2014).

Genetic diversity study

To study the genetic diversity among genotypes, we adopted a multivariate methodology. Through this methodology, a dissimilarity matrix was generated by a modified Mahalanobis generalized distance applied to the genotypic values estimated by:

$D^2_{ii'} = \delta R \delta$ where:
$D^2_{ii'}$ = Mahalanobis distance between i and i' genotypes;
R = genotypic variance and covariance matrix;
$\delta = [d_1 d_2 \dots d_v]$, where $d_j = Y_{ij} - Y_{i'j}$;
Y_{ij} = genotypic mean of the ith progeny in the jth trait.

The cluster of progeny was performed using Tocher's method, as described by Cruz, Ferreira, and Pessoni (2011), where the estimated intragroup distance must be smaller than the intergroup distance. Because a large group was established, the

same method was applied to split it into subgroups.

All analysis were performed in SELEGEN-REML / BLUP (Resende, 2007).

Results and discussion

The genetic parameters estimation for individual analysis are shown in Table 2; low values for additive genetic variance (σ^2a) can be observed. The residual variance (σ^2) was greater than σ^2a for all traits, which may mask the phenotypic selection. This fact is reflected in the narrow sense heritability based on genotype selection (h^2a); it is observed that the highest heritability was estimated in the years 2010 and 2013, in which we also observed the highest concentration of significant additive genetic variance. The heritability based in progeny selection (h^2pa) seems more suitable to selection; this heritability ranged from 51 to 23% for the traits with statistically significant additive genetic variance. Padilha, Oliveira, and Mota (2003) found CV% values of 49.25, 46.20, 56.45 8.15, 22.50 and 18.14 for HPBW, HPAW, HPW, BN, HPD, and HPL, respectively. These authors analyzed 14-year-old plants; the high coefficients of variation found in this study may be due to the use of young plants that have not reached production stability yet.

A joint analysis showed low h^2a for all studied traits, which ranged from 1% to 3% for HPBW, HPAW, BN, HPD, and HPL (Table 2). The low heritability values found can be attributed to the fact that the tested progeny were at the third selection cycle. The heritability for progeny selection is much higher than the heritability based on the genotypes either in the individual or joint analysis; thus, progeny selection is the best way to obtain meaningful gains. Aiming at the rapid availability of superior genetic materials for farmers, genotypes from the best progenies can be selected and cloned. The difference observed between means was due to the destruction required for the data collection: the trees were cut to gain accesses to the heart of palm.

The analyzed correlations between years (r) showed a low magnitude (Table 2), which indicates a complex genotype-environment interaction (Vencovsky & Barriga, 1992) and means that the genotype ranking changes over time, which is not a positive situation if the genotypes show unstable behavior over time.

Table 2. Individual analysis, joint analysis and genetic parameters estimative for the traits heart of palm basal weight (HPBW), heart of palm apical weight (HPAW), heart of palm weight (HPW), billets number (BN), heart of palm diameter (HPD) and heart of palm length (HPL) of half-sibs of peach palm (Bactris gasipaes Kunth.) progenies grown in EMBRAPA Western Amazon in Manaus, Amazonas.

	2009						2010					
	HPBW	HPAW	HPW	BN	HPD	HPL	HPBW	HPAW	HPW	BN	HPD	HPL
σ^2a	76.46[ns]	2.63[ns]	426.26★	0.03[ns]	0.03★	2.48[ns]	7354.46★	118.09★	2254.05[nss]	2.38★	0.01[ns]	193.16★
σ^2b B	833.71	53.61	454.45	0.05	0.01	4.42	9789.11	131.54	1074.77	1.49	0.03	120.68
σ^2	2850.68	880.06	6842.85	1.22	0.16	99.14	96387.40	1841.60	43315.08	21.04	0.40	1704.03
σ^2p F	3760.84	936.29	7723.56	1.31	0.19	106.05	113530.97	2091.22	46643.89	24.91	0.43	2017.86
h^2a	0.02±0.01	0.002±0.06	0.05±0.02	0.02±0.01	0.13±0.04	0.02±0.01	0.06±0.03	0.05±0.03	0.05±0.02	0.10±0.04	0.01±0.01	0.10±0.04
h^2pa	0.16	0.02	0.30	0.15	0.51	0.15	0.30	0.25	0.23	0.38	0.08	0.38
CVe%	28.51	63.71	54.53	36.99	16.28	36.99	79.59	80.19	77.81	69.95	26.89	69.95
$\bar{X}$	189.14	46.61	155.21	3.02	2.59	27.17	401.07	54.79	272.64	6.83	2.36	61.47
	2011						2012					
	HPBW	HPAW	HPW	BN	HPD	HPL	HPBW	HPAW	HPW	BN	HPD	HPL
σ^2a	87.38[ns]	14.25[ns]	230.05[ns]	0.02[ns]	0.01[ns]	1.72[ns]	18.94[ns]	30.39[ns]	251.25[ns]	0.01[ns]	0.01[ns]	0.87[ns]
σ^2b B	1823.79	27.23	727.15	0.03	0.00	2.66	251.89	54.07	1500.18	0.03	0.02	2.03
σ^2	13624.22	1599.08	34431.77	2.19	0.21	177.58	6702.92	1404.04	43433.63	3.20	1.14	259.15
σ^2p F	15535.40	1640.56	35388.97	2.25	0.23	181.97	6973.75	1488.51	45185.05	3.24	1.16	262.05
h^2a	0.01±0.01	0.01±0.01	0.01±0.01	0.01±0.01	0.06±0.04	0.01±0.01	0.00±0.01	0.02±0.02	0.01±0.01	0.00±0.01	0.01±0.01	0.00±0.01
h^2pa	0.02	0.03	0.02	0.03	0.17	0.03	0.01	0.07	0.02	0.01	0.03	0.01
CVe%	62.49	73.67	60.52	57.64	16.29	57.64	57.22	68.64	61.48	57.99	38.56	57.99
$\bar{X}$	187.23	54.46	307.36	2.58	2.87169	23.20	143.23	55.03	339.71	3.09	2.77	27.79
	2013						Joint analysis					
	HPBW	HPAW	HPW	BN	HPD	HPL	HPBW	HPAW	HPW	BN	HPD	HPL
σ^2a	154.33★	9.51[ns]	536.71[ns]	0.20★	0.01[ns]	16.46★	540.72★	38.01★	822.89★	0.19★	0.01★	15.48★
σ^2b B	406.43	111.28	1227.05	0.59	0.01	48.19	1372.157	32.21	390.69	0.11	0.01	9.03
σ^2	1504.53	1564.62	30898.42	2.14	0.36	173.38	26057.087	1378.22	27766.39	6.74	0.34	546.11
σ^2p F	2065.28	1685.41	32662.19	2.94	0.39	238.03	30111.129	1514.44	31636.27	7.41	0.47	600.43
h^2a	0.07±0.03	0.01±0.01	0.02±0.01	0.07±0.03	0.03±0.02	0.07±0.03	0.01±0.01	0.03±0.01	0.02±0.01	0.03±0.01	0.03±0.01	0.03±0.01
h^2pa	0.35	0.03	0.09	0.33	0.17	0.33	0.31	0.36	0.38	0.39	0.36	0.39
CVe%	61.41	77.00	69.64	59.63	22.99	59.63	82.33	71.02	62.91	72.08	21.97	72.08
$\bar{X}$	65.55	51.49	254.04	2.54	2.65	22.86	196.07	52.28	264.87	3.60	2.64	32.42
r	-	-	-	-	-	-	0.02	0.09	0.12	0.09	0.28	0.09

σ^2a: additive genetic variance, σ^2b: block variance, σ^2: residual variance, σ^2p: individual phenotypic variance, h^2a: narrow sense heritability based in genotypes and its standard errors represented by ±, h^2pa: heritability based in progeny means, CV(%): experimental coefficient of variation, $\bar{X}$: average, ★/ns: statistically significant through Deviance test [χ^2(1, 5%) = 3.,84] and not statistically significant, respectively, r: correlation between years.

Repeatability for five measurements (five years) presented determination coefficients that ranged from 0.3307 to 0.6698, which are associated with accuracies that ranged from 0.2416 to 0.3182 (Table 3). Using five measures, the h^2_a based on the yearly averages were relatively low for all the analyzed traits. Padilha et al. (2003) concluded that repeatability coefficients for all heart of palm production traits are negligible and that several measurements are needed to express a reliable progeny value. Moreover, Bergo, Negreiros, Miqueloni, and Lunz (2013) indicated that seven measurement cycles was sufficient to predict the real value of the progenies and reach an accuracy of 85% by the principal components method. The use of seven measures for all the analyzed traits showed determination coefficient values that ranged from 0.4086 to 0.7396 and accuracies from 0.2616 to 0.3426, while the use of 10 measures showed values that ranged from 0,4987 to 0.8023 for the coefficient of determination and 0.2814 to 0.3802 for accuracy.

The ranking of the best selected progenies (20%) is shown in Table 4. These progenies can compose a seed production orchard and meet the market demand for improved seeds.

The selection based on joint analysis (Table 4) shows that the three best progenies for HPBW, BN and HPL did not change: progenies 157, 158 and 49. These progenies also ranked well in HPAW an HPW. The traits HPBW, BN, and HPL showed constant statistically significant $\sigma^2 a$ over the years. Progeny 157 has high additive genetic value (a) and is well ranked in most of the studied traits; it is expected that its offspring inherit half of the a. Selecting 20% of the analyzed progenies (15 progenies) to assemble a seed production orchard is expected to achieve a gain of 18.43 grams for HPBW, 5.55 grams HPAW, HPW to 25.99 grams, 0.712 billets for BN, and 0.09 cm to 6.38 cm for HPD and HPL. The use of a high number of traits makes selection difficult to perform; using selection indexes that maximize the predicted gain may be a good option in many cases.

The adoption of a selection strategy without overlapping generations in seed production can be positive due to the heterosis, possibly obtained through hybridization. Urpí and Solis (1980) described peach palm as an allogamous species and proposed the existence of a genetic self-incompatibility system. Mossanek, Wendling, Koehler, and Zuffellato-Ribas (2014) mentioned that peach palm pollination happens through crosses, which also suggests allogamy.

Table 3. Repeatability study for the traits heart of palm basal weight (HPBW), heart of palm apical weight (HPAW), heart of palm weight (HPW), billets number (BN), heart of palm diameter (HPD) and heart of palm length (HPL) of half-sibs of peach palm (Bactris gasipaes Kunth.) progenies grown in EMBRAPA Western Amazon in Manaus, Amaazonas, analyzed during 5 years.

HC	$h^2_a ya$	R^2	PA	REHU	HC	$h^2_a ya$	R^2	PA	REHU
	HPBW					HPAW			
1	0.0180	0.1346	0.1340	1.00	1	0.0251	0.0899	0.1584	1.00
2	0.0317	0.2373	0.1779	1.33	2	0.0461	0.1650	0.2146	1.35
3	0.0424	0.3182	0.2060	1.54	3	0.0638	0.2287	0.2526	1.59
4	0.0512	0.3836	0.2262	1.69	4	0.0791	0.2833	0.2812	1.77
5	0.0584	0.4375	0.2416	1.80	5	0.0923	0.3307	0.3038	1.92
6	0.0644	0.4828	0.2538	1.89	6	0.1039	0.3723	0.3223	2.03
7	0.0695	0.5213	0.2637	1.97	7	0.1141	0.4089	0.3378	2.13
8	0.0740	0.5545	0.2720	2.03	8	0.1232	0.4416	0.3510	2.22
9	0.0778	0.5834	0.2789	2.08	9	0.1314	0.4708	0.3624	2.29
10	0.0812	0.6087	0.2849	2.13	10	0.1387	0.4971	0.3724	2.35
	HPW					BN			
1	0.0260	0.1223	0.1613	1.00	1	0.0258	0.0905	0.1606	1.00
2	0.0464	0.2180	0.2153	1.33	2	0.0473	0.1659	0.2174	1.35
3	0.0627	0.2948	0.2504	1.55	3	0.0655	0.2298	0.2559	1.59
4	0.0761	0.3579	0.2759	1.71	4	0.0811	0.2846	0.2848	1.77
5	0.0873	0.4107	0.2955	1.83	5	0.0946	0.3322	0.3076	1.92
6	0.0968	0.4554	0.3112	1.93	6	0.1065	0.3738	0.3263	2.03
7	0.1050	0.4938	0.3240	2.01	7	0.1170	0.4105	0.3420	2.13
8	0.1121	0.5272	0.3348	2.08	8	0.1263	0.4431	0.3553	2.21
9	0.1183	0.5564	0.3440	2.13	9	0.1346	0.4724	0.3669	2.28
10	0.1238	0.5822	0.3519	2.18	10	0.1421	0.4987	0.3769	2.35
	HPD					HPL			
1	0.0285	0.2886	0.1688	1.00	1	0.0360	0.0801	0.1615	1.00
2	0.0442	0.4480	0.2103	1.25	2	0.0462	0.1660	0.2257	1.37
3	0.0542	0.5490	0.2328	1.38	3	0.0756	0.2301	0.2693	1.61
4	0.0611	0.6187	0.2471	1.46	4	0.0711	0.2798	0.2771	1.80
5	0.0661	0.6698	0.2571	1.52	5	0.1016	0.3402	0.3182	1.96
6	0.0700	0.7088	0.2645	1.57	6	0.1103	0.3837	0.3315	2.10
7	0.0730	0.7396	0.2702	1.60	7	0.1190	0.4086	0.3426	2.19
8	0.0755	0.7645	0.2747	1.63	8	0.1282	0.4518	0.3622	2.25
9	0.0775	0.7850	0.2784	1.65	9	0.1339	0.4697	0.3691	2.27
10	0.0792	0.8023	0.2814	1.67	10	0.1419	0.4972	0.3802	2.33

HC: harvest numbers, $h^2_a ya$: individual narrow sense heritability based in year's average, R^2: determination coefficient, PA: phenotypic accuracy and REHU: relative efficiency of one harvest necessary use to achieve certain selective accuracy values.

Table 4. Selection of the fifteen best half-sib progenies of peach palm (Bactris gasipaes Kunth.) for the traits heart of palm basal weight (HPBW), heart of palm apical weight (HPTW), heart of palm weight (HPW), billets number (BN), heart of palm diameter (HPD) and heart of palm length (HPL), grown in EMBRAPA Western Amazon in Manaus, Amazonas.

HPBW				HPAW			
Genitor	a	Gain	New average	Genitor	a	Gain	New average
157	46.65	46.65	242.72	113	9.69	9.69	61.97
49	31.50	39.07	235.14	40	8.45	9.07	61.35
158	29.83	35.99	232.06	6	8.23	8.79	61.07
137	25.74	33.43	229.50	131	8.21	8.65	60.92
48	24.87	31.72	227.79	48	7.15	8.35	60.62
163	22.42	30.17	226.24	85	6.91	8.11	60.38
47	13.39	27.77	223.84	114	6.16	7.83	60.10
131	13.35	25.97	222.04	162	4.82	7.45	59.73
162	11.80	24.39	220.47	157	4.31	7.10	59.38
44	10.81	23.04	219.11	12	4.03	6.80	59.07
85	10.45	21.89	217.96	18	3.45	6.49	58.77
51	10.00	20.90	216.97	137	3.01	6.20	58.48
113	8.80	19.97	216.04	75	2.94	5.95	58.23
12	8.78	19.17	215.24	68	2.92	5.73	58.01
41	8.06	18.43	214.50	163	2.91	5.55	57.82

HPW				BN			
Genitor	a	Gain	New average	Genitor	a	Gain	New average
158	43.78	43.78	308.66	157	0.78	0.78	4.38
88	42.92	43.35	308.23	158	0.65	0.72	4.32
137	41.00	42.57	307.44	49	0.61	0.68	4.29
157	40.63	42.08	306.96	48	0.48	0.63	4.23
48	36.26	40.92	305.79	137	0.47	0.60	4.20
131	29.43	39.00	303.88	41	0.41	0.57	4.17
47	28.26	37.47	302.34	163	0.40	0.54	4.15
46	24.53	35.85	300.73	47	0.38	0.52	4.13
154	19.91	34.08	298.95	162	0.32	0.50	4.10
152	18.84	32.56	297.43	131	0.29	0.48	4.08
49	17.89	31.22	296.10	88	0.29	0.46	4.07
40	12.43	29.66	294.53	85	0.28	0.45	4.05
36	12.05	28.30	293.18	164	0.27	0.43	4.04
41	11.36	27.09	291.97	46	0.26	0.42	4.02
163	10.53	25.99	290.86	51	0.19	0.41	4.01

HPD				HPL			
Genitor	a	Gain	New average	Genitor	a	Gain	New average
156	0.36	0.36	3.00	157	7.04	7.04	39.46
131	0.13	0.24	2.89	158	5.89	6.46	38.89
17	0.10	0.20	2.84	49	5.52	6.15	38.57
81	0.10	0.17	2.82	48	4.29	5.68	38.11
18	0.09	0.16	2.80	137	4.27	5.40	37.82
152	0.09	0.14	2.79	41	3.67	5.11	37.54
88	0.08	0.13	2.78	163	3.63	4.90	37.32
114	0.07	0.13	2.77	47	3.40	4.71	37.14
9	0.06	0.12	2.76	162	2.90	4.51	36.93
123	0.06	0.11	2.76	131	2.64	4.33	36.75
137	0.06	0.11	2.75	88	2.61	4.17	36.59
158	0.06	0.11	2.75	85	2.50	4.03	36.45
75	0.06	0.10	2.75	164	2.45	3.91	36.33
154	0.05	0.10	2.74	46	2.36	3.80	36.22
155	0.05	0.09	2.74	51	1.73	3.66	36.08

a:additive genetic value.

Farias Neto and Resende (2001) selected 31 and 53 genotypes for a short and a long peach palm breeding program, respectively. This type of selection is reflected in the effective population size (Ne). Table 5 shows the selection of genotypes based on different Ne values. To achieve a selective ceiling where Ne varies between 19 (Farias Neto & Rezende, 2001), 30 and 60 (Pires, Resende, Silva, & Resende Jr., 2011), a number of genotypes and progenies can be selected. It appears that the genotype of progeny 157 located in block 10 showed phenotypic values much higher than other genotypes for at least half of the studied traits.

As cited above, Farias Neto and Resende (2001) presented a selection of 31 genotypes from 9 progenies that resulted in an Ne of 19 for a short-term breeding program; in this study, the selection that results in an Ne of 19 is the use of 48 to 170 genotypes from 11 to 19 progenies. Table 5 shows that the selection of 226 to 303 genotypes leads to 22 to 32 progenies, maintaining the Ne near 30; in the work of Farias Neto and Resende (2001), 53 genotypes were selected and, consequently, 15 progenies

reached the same Ne in all traits. Focusing on a selective ceiling to reach an Ne of 60, 552 to 600 genotypes should be selected, thus selecting 35 to 49 progenies. The use of a large number of progenies retains the genetic diversity within the breeding population for a longer amount of time; otherwise, results will be obtained in the long term.

To select superior genotypes that simultaneously possess high performance in the desirable traits is usually a difficult task for a breeder. Thus, using selection index theory can be a good effective alternative (Cruz Regazzi, & Carneiro, 2014). The analysis performed on the Mulamba and Mock selection index (Resende et al., 2014) classified the 72 analyzed progenies (Table 6). The best rated progeny was progeny 157, with a gain of 563.6% in relation to all other studied progenies; the last in the rank was progeny 151. Using a selection rate of 20%, it resulted in selecting 15 progenies, which led to an expected gain of 166%.

Table 7 shows the result of Tocher's clustering based on Mahalanobis distance, where the formation of two distinct groups can be observed. Group one is the largest, containing 71 progenies; it was divided into 32 subgroups, also using Tocher's method. The formed group can point to future crosses in breeding programs; an intra-population recurrent selection program could also be started, evaluating general and specific combining ability.

Overall, based on the analyses performed in this study, it is easy to conclude that progeny 157 had a superior performance; it is the best ranked in progeny selection (Table 4), individual BLUP (Table 5), and the selection index (Table 6) and is isolated in a group on the cluster analysis (group 2). Negreiros, Bergo, Miqueloni, and Lunz (2013) found 26 groups when they analyzed 100 progenies of peach palm; they also reported that they found a strong genetic divergence using Tocher's method.

Table 5. Peach palm (Bactris gasipaes Kunth.) genotype selections grown in EMBRAPA Western Amazon in Manaus, Amazonas for the traits heart of palm basal weight (HPBW), heart of palm apical weight (HPAW), heart of palm weight (HPW), billets number (BN), heart of palm diameter (HPD) and heart of palm length (HPL) based on the effective population size.

NGen	Prog	Block	f	a	$u+a$	Gain	New avarege	Ne	d	g	NP
HPBW											
1	157	10	967.3	53.5	250	53.46	250	1	20	73.6	1
157	158	18	202.4	15.3	211.4	21.1	217.1	19.0	0.3	15.6	19
303	48	34	44.5	11.3	207.4	17.3	213.3	30.0	-0.7	10.6	32
588	11	20	341.0	6.0	202.1	12.9	209.0	60.0	4.6	10.6	48
HPAW											
1	6	29	273.5	11.7	64.0	11.7	64.0	1.0	5.1	16.8	1
48	162	18	88.8	5.6	57.9	6.9	59.1	19.0	2.1	7.7	14
226	131	17	40.0	3.8	56.1	5.0	57.3	30.0	-0.2	3.6	22
573	18	35	70.0	2.1	54.4	3.7	56.0	60.1	0.3	2.4	47
HPW											
1	158	2	535.4	40.5	305.3	40.5	305.3	1.0	12.4	52.8	1
76	18	4	579.8	24.5	289.4	30.2	295.1	19.1	12.9	37.5	11
278	51	2	491.8	17.5	282.4	23.1	287.9	30.1	11.7	29.2	25
600	49	17	259.7	10.2	275.1	17.9	282.8	60.0	0.9	11.1	48
BN											
1	157	10	14.4	1.0	4.6	1.0	4.6	1.0	0.4	1.4	1
117	48	27	4.7	0.3	4.0	0.4	4.0	19.1	0.1	0.4	19
244	40	31	11.3	0.3	3.9	0.4	4.0	30.2	0.2	0.4	30
552	74	31	8.5	0.2	3.8	0.3	3.9	60.0	0.1	0.3	49
HPD											
1	156	32	38.5	1.0	3.6	1.0	3.6	1.0	0.5	1.5	1
170	18	21	2.9	0.1	2.7	0.1	2.8	19.1	0.0	0.1	17
266	88	24	3.0	0.0	2.7	0.1	2.7	30.1	0.0	0.1	23
569	155	24	2.8	0.0	2.7	0.1	2.7	60.0	0.0	0.0	35
HPL											
1	157	10	129.4	8.9	41.4	8.9	41.4	1.0	3.6	12.5	1
117	48	27	42.0	3.1	35.6	3.9	36.3	19.1	0.7	3.8	19
244	40	31	101.3	2.5	34.9	3.3	35.7	30.2	1.4	3.9	30
552	74	31	76.5	1.5	33.9	2.5	35.0	60.0	0.8	2.3	48

NGen: number of genotypes, Prog: progeny, f: Phenotypic value, a: additive effect, u+a: additive genetic value, Ne: effective population size, d: dominance effect, g: effect genotypic total NP: number of progenies.

Table 6. Mulamba and Mock selection index for 72 half-sib progenies of peach palm (Bactris gasipaes Kunth.) grown in EMBRAPA Western Amazon in Manaus, Amazonas, based on heart of palm basal weight (HPBW), heart of palm apical weight (HPAW), heart of palm weight (HPW), billets number (BN), heart of palm diameter (HPD) and heart of palm length (HPL).

Prog	Rank	Gain	Gain (%)	Prog	Rank	Gain	Gain (%)	Prog	Rank	Gain	Gain(%)
157	5.5	5.50	563.6	36	27.3	18.11	101.51	118	45.7	28.24	29.3
131	6.7	6.08	500.0	155	28.7	18.52	97.09	123	46.0	28.59	27.7
137	6.7	6.28	481.4	154	30.3	18.96	92.54	68	47.3	28.96	26.0
158	7.8	6.67	447.5	139	32.3	19.43	87.81	74	47.8	29.32	24.5
48	11.5	7.63	378.2	78	32.5	19.89	83.55	73	48.0	29.68	23.0
49	14.5	8.78	315.8	17	33.3	20.33	79.51	35	48.5	30.02	21.6
41	15.5	9.74	274.8	9	34.5	20.79	75.56	81	48.5	30.36	20.2
162	15.5	10.46	249.0	63	35.3	21.24	71.81	165	49.2	30.70	18.9
163	15.7	11.04	230.7	102	36.0	21.69	68.27	145	51.3	31.06	17.5
85	16.3	11.57	215.6	136	38.2	22.18	64.59	43	51.8	31.42	16.2
44	16.8	12.05	203.0	126	38.3	22.64	61.23	125	52.0	31.77	14.9
47	17.0	12.46	193.0	6	38.5	23.08	58.15	71	52.7	32.11	13.7
46	18.5	12.92	182.4	11	39.2	23.51	55.23	107	55.3	32.49	12.3
88	18.7	13.33	173.8	54	40.2	23.95	52.39	84	55.3	32.86	11.1
113	19.2	13.72	166.0	144	40.5	24.38	49.74	39	55.5	33.22	9.9
114	19.3	14.07	159.4	31	41.0	24.79	47.23	156	55.8	33.58	8.7
40	21.2	14.49	151.9	160	41.3	25.20	44.87	7	56.0	33.92	7.6
164	23.7	15.00	143.3	83	42.0	25.60	42.60	69	56.7	34.27	6.5
18	23.8	15.46	136.0	153	43.0	26.00	40.38	70	56.8	34.60	5.5
12	24.0	15.89	129.7	25	43.5	26.40	38.27	14	58.7	34.96	4.4
51	26.5	16.40	122.6	37	43.7	26.78	36.29	65	59.3	35.31	3.4
24	26.8	16.87	116.3	16	43.8	27.15	34.43	149	61.0	35.68	2.3
75	27.2	17.32	110.8	60	44.2	27.51	32.66	108	63.5	36.07	1.2
152	27.2	17.73	105.9	55	44.8	27.88	30.94	151	67.2	36.50	0.0

Prog: progeny, Rank: average progeny rank.

Table 7. Clustering of 72 half-sib progenies of peach palm (Bactris gasipaes Kunth.) through Tocher's method based on the Mahalanobis distance for the traits heart of palm basal weight (HPBW), heart of palm apical weight (HPAW), heart of palm weight (HPW), billets number (BN), heart of palm diameter (HPD) and heart of palm length (HPL).

Group						Progenies							
1	6	9	35	63	164	43	71	55	114	81	74	83	44	156
	40	73	153	25	165	151	131	46	113	68	17	78	139	7
	16	136	160	41	118	47	155	51	158	39	88	11	137	145
	149	154	108	125	24	54	85	75	102	107	163	49	123	162
	144	48	60	37	18	31	84	36	12	65	69	126	14	70
	152													
2	157													

Conclusion

The studied population has low genetic variability. However, the progeny selection can result in significant gains in breeding programs.

A large number of measurements of the production traits of the heart of palm from peach palm are necessary to obtain reliable repeatability values.

The progeny selection by BLUP and the selection index confirmed the superiority of some progenies.

Crossing between genotypes of superior progenies located in different genetic groups can result in heterosis or high specific combined ability.

Acknowledgements

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