

## Selection of *Pinus caribaea* var. *bahamensis* progenies based on the predicted genetic value

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**ABSTRACT** - *Pinus caribaea* var. *bahamensis* progenies were selected by mixed models using the estimate of the genetic parameters by REML for the prediction of additive genetic values by BLUP. The experimental design was a 11 x 11 partially balanced square lattice containing 119 progenies and two commercial controls. After 13 years, the diameter at breast height (DBH), height and volume were evaluated. The progenies presented good mean performance (18.83 m, 20.80 cm and 0.462 m<sup>3</sup> tree<sup>-1</sup>), and heritability estimates of 0.12, 0.20 and 0.21 for height, DBH and volume, respectively. The trait with greatest variability was the volume with a genetic variation coefficient of 22.60% while the genetic variation for height was lower (3.73%). A genetic gain of 14.5% was obtained for DBH with a selection of 250 trees from 56 progenies, with a mean of 4.46 trees selected per progeny and an effective population size of 72.

**Key words:** REML/BLUP, *Pinus*, improvement of perennial plant species, genetic parameters, selection.

### INTRODUCTION

The social-economic development of diverse regions in Brazil has been boosted by exotic forest species introduced into the country, particularly in areas where the soil and climate characteristics daunt agricultural activities. The increase of raw material to supply the paper and cellulose industries and more recently, for resin extraction, is one of these noteworthy benefits. The genus *Pinus* is of great importance for regions of temperate and tropical climate in particular, since it serves for the reforestation or recovery of degraded areas, as well as for the achievement of raw material for paper and cellulose industries and of wood. For the implantation of commercial *Pinus*

plantations, primary need is a seed orchard with a high yield potential for the establishment of vigorous seedlings with good uniformity.

Genetic improvement of the genus *Pinus* has focused on paper, long-fiber cellulose, saw logs, and resin extraction, namely. Among the contributions to this improvement are the increase of the volumetric yield and the yield of trees with straight trunks, with a lower number of crotches and of thick branches, which improves the wood's industrial utility.

Estimates of genetic parameters provide information about the nature of the genic action involved in the trait heritability and are base for the evaluation of improvement programs (Vencovsky and Barriga 1992). There are several studies relating

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such estimates in *Pinus* (Kageyama et al. 1977, Cotterill and Zed 1980, Dean et al. 1983, Dean et al. 1986, Otegbeye 1988, Gurgel Garrido and Kageyama 1993, Sebbenn et al. 1994, Sebbenn et al. 1995, Gurgel Garrido et al. 1996, Sampaio et al. 2000, 2002, Moura and Dvorak 2001, Johnston et al. 2003, Missio et al. 2003).

An optimum procedure for the estimation/prediction of genetic values in the improvement of perennial species is the REML/BLUP (Restricted Maximum Likelihood estimation/Best Linear Unbiased Prediction). However, when dealing with balanced data, the estimate of variance components by the least-square method applied in analyses of variance is equal to that obtained by REML, and the prediction of genetic values by the multi-effect index is equal to the individual BLUP (Resende 2002a). The REML/BLUP procedure has been successfully applied in perennial plant improvement in Brazil of species such as peach palm (Farias Neto and Resende 2001), Barbados cherry (Paiva et al. 2002), cacao (Resende and Dias 2000, Dias and Resende 2001), coffee (Resende et al. 2001), rubber (Costa et al. 2000, Kalil Filho et al. 2000, Costa et al. 2002a, Costa et al. 2002b), tea (Simeão et al. 2002), cupuaçu (Souza et al. 2002), *Eucalyptus* (Resende et al. 1993), and *Pinus* (Resende et al. 1996a, b).

On this background, our study had the objective of selecting *Pinus caribaea* var. *bahamensis* progenies using mixed models by means of the estimation of the genetic parameters by REML and their use in the BLUP prediction of additive genetic values.

**MATERIAL AND METHODS**

**Plant material**

The seeds of the progenies used for the trial came from a clonal seed orchard of the Centro de Conservação Genética e Melhoramento de Pinheiros Tropicais (Center of Genetic Conservation and Improvement of Tropical Pine) - CCGMPT, in Aracruz, State of Espírito Santo (lat 19° 48' S; long 40° 17' W; altitude 50 m asl). These seeds were provided by the Instituto de Pesquisas e Estudos Florestais (Institute of Forest Research and Studies) - IPEF-ESALQ/USP, Piracicaba, State of São Paulo. Besides the progenies, two commercial controls originated from tree matrixes of the Duratex company in Agudos, state of São Paulo (lat 22° 22' S, long 48° 52' W; altitude 550 m asl) were included.

The progeny test was conducted in the period from March 20 to 21, 1990, on the Fazenda de Ensino e Pesquisa da Faculdade de Engenharia (Farm of Education and Research of the Faculty of Engineering) - Campus of Ilha Solteira - of the Universidade Estadual Paulista “Júlio de Mesquita Filho” - UNESP, in Selvíria, state of Mato Grosso do Sul (lat 20° 20' S; long 51° 23' W;

altitude 370 m asl). The experimental design was a 11 x 11 partially balanced square lattice, with 119 progenies from the CCGMPT and two commercial controls provided by Duratex. The row plots contained six plants in a spacing of 3.0 x 3.0 meters. The progenies were evaluated after 13 years for the diameter at breast height (DBH, in cm) and the tree height (in m) and volume (m<sup>3</sup> tree<sup>-1</sup>).

**Methods - Mixed linear model**

The mixed linear model applied to half-sib progenies in the lattice design with several plants per plots and one measurement per individual is described by Resende (2002a) as:

$$y = Xb + Za + Wc + H\delta + e,$$

where

*y*, *b*, *a*, *c*,  $\delta$  and *e* are data vectors of the replication effects (fixed), of the additive genetic effects (random), of the plot effects of (random), of the random effects of blocks within replications and of the random errors, respectively.

*X*, *Z*, *W* and *H* are the matrixes of incidence for *b*, *a*, *c* and  $\delta$ , respectively.

Distributions and structures of means and variances:

$$\begin{aligned} y|b, V &\sim N(Xb, V) \\ a|A, \sigma_a^2 &\sim N(0, A \sigma_a^2) \\ c| \sigma_c^2 &\sim N(0, I \sigma_c^2) \\ \delta| \sigma_\delta^2 &\sim N(0, I \sigma_\delta^2) \\ e| \sigma_e^2 &\sim N(0, I \sigma_e^2) \end{aligned}$$

The covariances among all random effects of the model are considered zero. So:

$$\begin{bmatrix} y \\ a \\ c \\ \delta \\ e \end{bmatrix} = \begin{bmatrix} Xb \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix} \text{ and } \begin{bmatrix} y \\ a \\ c \\ \delta \\ e \end{bmatrix} = \begin{bmatrix} V & ZG & WC & HB & R \\ GZ' & G & 0 & 0 & 0 \\ CW' & 0 & C & 0 & 0 \\ BH' & 0 & 0 & B & 0 \\ R & 0 & 0 & 0 & R \end{bmatrix} \text{ Var, where}$$

$$\begin{aligned} G &= A \sigma_a^2 \\ C &= I \sigma_c^2 \\ B &= I \sigma_\delta^2 \\ R &= I \sigma_e^2 \\ V &= ZA \sigma_a^2 Z' + W I \sigma_c^2 W' + H' I \sigma_\delta^2 H + I \sigma_e^2 = ZGZ' + WCW' + HBH' + R \end{aligned}$$

**Mixed model equations (MME)**

$$\begin{bmatrix} X'X & X'Z & X'W & X'H \\ Z'X & Z'Z + A^{-1}\lambda_1 & Z'W & Z'H \\ W'X & W'Z & W'W + I\lambda_2 & W'H \\ H'X & H'Z & H'W & H'H + I\lambda_3 \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{a} \\ \hat{c} \\ \hat{\delta} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \\ W'y \\ H'y \end{bmatrix}, \text{ where}$$

$$\lambda_1 = \frac{\hat{\sigma}_c^2}{\hat{\sigma}_a^2} = \frac{1 - \hat{h}^2 - \hat{c}^2 - \hat{\delta}^2}{\hat{h}^2}; \lambda_2 = \frac{\hat{\sigma}_c^2}{\hat{\sigma}_e^2} = \frac{1 - \hat{h}^2 - \hat{c}^2 - \hat{\delta}^2}{\hat{c}^2}; \lambda_3 = \frac{\hat{\sigma}_c^2}{\hat{\sigma}_\theta^2} = \frac{1 - \hat{h}^2 - \hat{c}^2 - \hat{\delta}^2}{\hat{\delta}^2};$$

$\hat{h}^2 = \frac{\hat{\sigma}_a^2}{\hat{\sigma}_a^2 + \hat{\sigma}_c^2 + \hat{\sigma}_e^2 + \hat{\sigma}_\theta^2}$  is the individual narrow-sense heritability in the replication;

$\hat{c}^2 = \frac{\hat{\sigma}_c^2}{\hat{\sigma}_a^2 + \hat{\sigma}_c^2 + \hat{\sigma}_e^2 + \hat{\sigma}_\theta^2}$  is the correlation due to the common environment of the plot;

$\hat{\delta}^2 = \frac{\hat{\sigma}_\theta^2}{\hat{\sigma}_a^2 + \hat{\sigma}_c^2 + \hat{\sigma}_e^2 + \hat{\sigma}_\theta^2}$  is the correlation due to the common environment of the block within the replication;

$\hat{\sigma}_a^2$  is the additive genetic variance;

$\hat{\sigma}_c^2$  is the variance among plots;

$\hat{\sigma}_e^2$  is the variance among blocks within replications;

$\hat{\sigma}_\theta^2$  is the residual variance (environmental within plots plus the non-additive genetic variance);

A is the matrix of additive genetic correlation between the individuals in evaluation.

The heritability coefficients of progeny mean ( $\hat{h}_m^2$ ) and within progeny ( $\hat{h}_d^2$ ) were estimated by:

$$\hat{h}_m^2 = \frac{0.25 \hat{\sigma}_a^2}{0.25 \hat{\sigma}_a^2 + \hat{\sigma}_c^2 / b + \hat{\sigma}_e^2 / (nb)}$$

$$\hat{h}_d^2 = \frac{0.75 \hat{\sigma}_a^2}{0.75 \hat{\sigma}_a^2 + \hat{\sigma}_c^2}$$

Iterative estimators of the components of variance by REML via algorithm EM

$$\hat{\sigma}_a^2 = [y'y - b' X' y - \hat{a}' Z' y - \hat{c}' W' y - \hat{\delta}' H' y] / [N - r(x)]$$

$$\hat{\sigma}_c^2 = [\hat{a}' A^{-1} \hat{a} + \hat{\sigma}_c^2 \text{tr}(A^{-1} C^{22})] / q$$

$$\hat{\sigma}_e^2 = [\hat{c}' c + \hat{\sigma}_e^2 \text{tr} C^{33}] / s, \text{ where:}$$

$$\hat{\sigma}_\theta^2 = [\hat{\delta}' \hat{\delta} + \hat{\sigma}_\theta^2 \text{tr} C^{44}] / \eta, \text{ where:}$$

$C^{22}$ ,  $C^{33}$  and  $C^{44}$  are derived from the inverse of the matrix of the coefficients of the mixed model equations;

tr is the trace operator of a matrix;

r(x) is the rank of matrix X;

N, q, s,  $\eta$  are the number data, trees, plots and blocks, respectively.

The genetic parameter estimates and predictions of additive and genotypic genetic values were obtained using Selegen-REML/BLUP (Resende 2002b), a software that works with algorithm EM.

## RESULTS AND DISCUSSION

### Genetic and phenotypic parameters

The progenies presented good mean performance (18.83 m, 20.80 cm and 0.462 m<sup>3</sup> tree<sup>-1</sup>) (Table 1) and expressive genetic variability, mainly for volume and DBH, which presented higher coefficients of genotypic variation (22.60% and 9.64%, respectively) than the plant height (3.73%). Volume and DBH also presented higher estimates of heritability (0.21 and 0.20, respectively) than of height (0.12), indicating that the selection based on the first two traits tends to provide larger genetic gains. The heritability indicates the degree with which the individuals pass their traits on to their descendants, making inferences on the genetic control of traits possible. In this context, a high heritability value indicates a good possibility of genetic gain with selection.

**Table 1.** Narrow-sense heritability estimates ( $\hat{h}^2$ ), correlation due to the common environment of the plot ( $\hat{c}^2$ ), correlation due to the common environment of the block within replication ( $\hat{\delta}^2$ ), additive genetic variance ( $\hat{\sigma}_a^2$ ), variance among plots ( $\hat{\sigma}_c^2$ ), variance among blocks within replications ( $\hat{\sigma}_e^2$ ), residual variance ( $\hat{\sigma}_\theta^2$ ), phenotypic variance ( $\hat{\sigma}_p^2$ ), coefficient of genotypic variation (CV<sub>g</sub>), and general mean for height, DBH and volume in 13-year-old progenies of *Pinus caribaea* var. *bahamensis*

Parameters	Traits		
	Height m	DBH cm	Volume m <sup>3</sup> tree <sup>-1</sup>
$\hat{h}^2$	0.12	0.20	0.21
$\hat{c}_p^2$	0.07404	0.02992	0.04224
$\hat{c}_b^2$	0.00158	0.00040	0.00050
$\hat{\sigma}_a^2$	0.49420	4.02069	0.01090
$\hat{\sigma}_c^2$	0.31310	0.59483	0.00222
$\hat{\sigma}_e^2$	0.00669	0.00794	0.00003
$\hat{\sigma}_\theta^2$	3.41505	15.25818	0.03933
$\hat{\sigma}_r^2$	4.22902	19.88163	0.05247
CV <sub>g</sub> (%)	3.73	9.64	22.60
Mean ( $\hat{\mu}$ )	18.83	20.80	0.462

In general, the estimates of heritability found in the present work are lower than those reported by Resende et al. (1996b) for *Pinus maximinoi*, though higher than the mean of the narrow-sense heritabilities estimated by the mixed model methodology (REML/BLUP) for some tree species (Table 2).

In relation to the correlation due to the common environment of the plot ( $\hat{c}_p^2$ ), which measures the variability among the plots in the block, the values varied from 7.40% to 2.99% for height and DBH, respectively (Table 1). According to

Table 2. Estimates of genetic parameters by the mixed model methodology (REML/BLUP) found in literature for some perennial tree species

Crop	Reference	Traits	$h^2$	$h_a^2$	$\hat{\rho}$	$c^2$	$\hat{\sigma}_a^2$	$\hat{\sigma}_p^2$	$\hat{\sigma}_c^2$	$\hat{\sigma}_e^2$	$\hat{\sigma}_f^2$	$\hat{\sigma}_d^2$
Cacao	Resende and Dias (2000)	Number of fruits	0.10	0.38	0.57	0.10	56.99	174.24	58.16	246.01	576.77	-
		Plant heights	0.18	-	-	-	0.0189	-	-	0.00321	-	0.095
Peach palm	Farias Neto and Resende (2001)	Diameter at colo height	0.03	-	-	-	0.0517	-	-	0.00164	-	1.6233
		Basal residue weight	0.06	-	-	-	28.8425	-	-	27.3811	-	434.120
		Apical residue weight	0.00	-	-	-	0.000	-	-	42.6374	-	1105.06
		Palm-heart diameter	0.11	-	-	-	0.0178	-	-	0.00273	-	0.1617
		Palm-heart size	0.43	-	-	-	22.8642	-	-	2.15009	-	45.9681
Erva-mate	Simião et al., 2002	Palm-heart weight	0.06	-	-	-	1015.008	-	-	69.4897	-	17478.41
		Yield of leaf biomass	0.39	-	-	-	0.030	-	-	-	-	-
Rubber	Kadil Filho et al., 2000	Dry rubber content	0.10	0.42	-	-	2.1429	12.232	-	-	20.9149	6.5396
		Cetonic Extract	0.00	0.06	-	-	0.00	0.2559	-	-	0.2711	0.0151
		Wallace plasticity	0.00	0.00	-	-	0.00	225.84	-	-	225.84	0.00
		Plasticity after 30 min.	0.00	0.64	-	-	0.00	43.493	-	-	119.40	75.9003
		Plast. retention index	0.00	0.11	-	-	0.00	145.09	-	-	162.96	17.8658
Rubber	Costa et al., 2002a	Rubber yield	-	0.22	0.84	-	-	-	6.235	-	414.351	-
		Plant height	0.03	0.05	-	0.554	-	-	183.404	130.698	331.107	-
Coffee	Resende et al., 2001	Trunk diameter	0.06	0.12	-	0.288	-	-	4.460	9.223	15.512	-
		Plagiotropic branch fruits	0.00	0.01	-	0.024	-	-	2.522	100.614	103.263	-
Cupuaçu	Souza et al., 2002	Yield of fruits/plant	0.26	-	0.72	0.002	-	-	-	-	-	-
		Nr of fruits per plant	0.24	-	0.70	0.002	-	-	-	-	-	-
<i>Pinus*</i>	Resende et al., 1996b	Volume	0.67	-	-	-	0.000533	-	-	0.000259	-	-
		Mean	0.19	0.22	-	-	-	-	-	-	-	-

$h^2$ : narrow-sense heritability;  $h_a^2$ : broad-sense heritability;  $\hat{\rho}$ : repeatability;  $c^2$ : correlation due to the common environment;  $\hat{\sigma}_a^2$ : additive genetic variance;  $\hat{\sigma}_p^2$ : permanent environment variance;  $\hat{\sigma}_c^2$ : variance among plots;  $\hat{\sigma}_e^2$ : residual variance;  $\hat{\sigma}_f^2$ : phenotypic variance;  $\hat{\sigma}_d^2$ : variance of the dominance effects; \**Pinus maximinoi*

Resende (2002a), an adequate value for the estimate of  $\hat{g}$  would be lower than or equal to 15%, that is, 15% of the total phenotypic variation is caused by the environmental variation among the plots.

### Predicted genetic values

Tables 3, 4 and 5 present additive ( $\hat{a}$ ) and genotypic effects ( $\hat{g}$ ), assuming a average dominance degree equal to 1 in a population with intermediate improvement level), genotypic values ( $\hat{\mu} + \hat{a}$ ) and additive genetic values ( $\hat{\mu} + \hat{a}$ ) predicted for the 20 best trees of *Pinus caribaea* var. *bahamensis* for height, DBH and volume, respectively, are presented in the Tables 3, 4 and 5. Among the selected trees of asexual reproduction (trees arranged according to  $\hat{g}$ ) for height (Table 3), only 13 trees coincide with the best of sexual reproduction (trees arranged according to  $\hat{a}$ ). For DBH and volume, 15 individuals are concordant in both reproduction systems (Table 4 and 5). For the selection process of trees to be used in improvement programs the reproduction type of the species should therefore be taken into consideration, since the best trees for sexual reproduction (by seeds) may not be the best for asexual reproduction (vegetative or clonal) and

vice-versa. This fact was also observed by Resende and Dias (2000) for the trait number of fruits per plant in full-sib progenies of cacao. However, the selection of the best trees based on the reproduction system (asexual or sexual) is intimately linked to the objectives of the improvement program of the species. When the objective is the transformation of the progeny test in a seedling seed orchard, the trees must be selected based on  $\hat{a}$ , and when the objective is the achievement of material to install a clone seed orchard, then the trees should be selected based on  $\hat{g}$ , so there is a maximization of the genetic gain.

A selection aiming at the volume ( $m^3 tree^{-1}$ ) provided genetic gains of up to 73.19%, depending on the number of selected trees (Table 6). The selection of 250 trees focusing on this trait provided a greater gain (27.72%) than the selection of 5 trees based on the DBH (26.65%). However, in the realization of the selection process the manageability of obtaining the data must be taken into account. According to Sampaio et al. (2000), besides the facility and precision in the achievement of DBH compared to height, the same presented a high genetic correlation with the volume. DBH-based selection is therefore recommendable in spite of achieving lower genetic gains.

**Table 3.** Genotypic effects ( $\hat{g}$ ), genotypic values ( $\hat{\mu} + \hat{g}$ ), additive effects ( $\hat{a}$ ) and additive genetic values ( $\hat{\mu} + \hat{a}$ ) predicted for the 20 best 13-year-old trees of *Pinus caribaea* var. *bahamensis* for height (in m)

Order	Asexual reproduction					Sexual reproduction				
	Progeny	Block	Tree	$\hat{g}$	$\hat{\mu} + \hat{g}$	Progeny	Block	Tree	$\hat{a}$	$\hat{\mu} + \hat{a}$
1	26	1	6	1.18	20.01	106	2	6	0.90	19.72
2	108	3	6	1.15	19.98	108	3	6	0.87	19.70
3	106	2	6	1.12	19.95	106	2	2	0.86	19.68
4	49	1	4	1.12	19.95	106	2	3	0.84	19.67
5	106	2	2	1.05	19.88	26	1	6	0.81	19.64
6	106	2	3	1.02	19.85	74	5	4	0.78	19.61
7	20	6	6	0.98	19.81	49	1	4	0.77	19.60
8	49	2	2	0.98	19.81	74	4	1	0.77	19.60
9	74	5	4	0.95	19.78	20	6	6	0.76	19.59
10	19	6	6	0.94	19.77	74	5	3	0.74	19.57
11	74	4	1	0.92	19.75	74	1	6	0.73	19.56
12	8	2	4	0.91	19.74	19	6	6	0.72	19.55
13	74	5	3	0.88	19.71	74	1	5	0.72	19.55
14	20	5	2	0.88	19.71	106	4	2	0.72	19.55
15	75	1	5	0.87	19.70	74	2	2	0.72	19.54
16	74	1	6	0.86	19.69	74	2	3	0.71	19.54
17	108	5	3	0.86	19.69	106	5	3	0.71	19.54
18	96	1	1	0.85	19.68	106	3	3	0.71	19.54
19	74	1	5	0.84	19.67	106	4	6	0.71	19.54
20	74	2	2	0.84	19.67	106	1	1	0.71	19.53

$\hat{\mu} = 18.83$  m

Another important factor in the selection process is the mean number of trees selected per progeny ( $K_f$ ). Missio et al. (2003), simulating three selection types ( $K_f$  variable;  $K_f$  fixed = 6;  $K_f$  maximum = 5) based on the multi-effect index in *Pinus caribaea* var. *bahamensis* progenies demonstrated that the

maximum  $K_f = 5$  allows a raise of the effective population size, the selection of a larger number of progenies and the maintenance of a high genetic divergence. These are ideal conditions for the transformation of the progeny test in a seedling seed orchard or to provide material for the installation of a clonal seed orchard.

**Table 4.** Genotypic effects ( $\hat{g}$ ), genotypic values ( $\hat{\mu} + \hat{g}$ ), additive effects ( $\hat{a}$ ), and additive genetic values ( $\hat{\mu} + \hat{a}$ ) predicted for the 20 best 13-year-old individuals of *Pinus caribaea* var. *bahamensis* for DBH (in cm)

Order	Asexual reproduction					Sexual reproduction				
	Progeny	Block	Tree	$\hat{g}$	$\hat{\mu} + \hat{g}$	Progeny	Block	Tree	$\hat{a}$	$\hat{\mu} + \hat{a}$
1	98	6	6	7.61	28.41	98	6	6	5.91	26.71
2	98	6	1	6.76	27.56	98	6	1	5.40	26.20
3	98	1	3	6.47	27.27	98	1	3	5.23	26.03
4	98	1	6	6.14	29.94	98	1	6	5.03	25.83
5	46	5	6	5.81	26.61	98	3	5	4.65	25.45
6	111	2	3	5.64	26.44	98	5	5	4.59	25.39
7	98	3	5	5.50	26.30	98	5	6	4.59	25.38
8	98	5	5	5.41	26.21	98	4	4	4.26	25.06
9	98	5	6	5.41	26.21	98	4	6	4.22	25.02
10	70	1	1	5.21	26.01	98	3	3	3.99	24.78
11	96	1	1	4.98	25.78	70	1	1	3.91	24.71
12	98	4	4	4.86	25.66	46	5	6	3.88	24.67
13	96	1	6	4.81	25.61	96	1	1	3.87	24.66
14	98	4	6	4.79	25.59	98	4	5	3.86	24.65
15	19	1	1	4.61	25.41	98	4	3	3.83	24.62
16	92	2	5	4.57	25.37	96	1	6	3.77	24.56
17	70	6	1	4.52	25.32	98	4	2	3.65	24.44
18	23	2	3	4.52	25.32	111	2	3	3.62	24.41
19	96	3	4	4.45	25.25	96	3	4	3.56	24.35
20	70	2	1	4.44	25.24	70	6	1	3.50	24.29

$\hat{\mu} = 20.80$  cm

**Table 5.** Genotypic effects ( $\hat{g}$ ), genotypic values ( $\hat{\mu} + \hat{g}$ ), additive effects ( $\hat{a}$ ), and additive genetic values ( $\hat{\mu} + \hat{a}$ ) predicted for the 20 best 13-year-old individuals of *Pinus caribaea* var. *bahamensis* for volume ( $\text{m}^3 \text{ tree}^{-1}$ )

Order	Asexual reproduction					Sexual reproduction				
	Progeny	Block	Tree	$\hat{g}$	$\hat{\mu} + \hat{g}$	Progeny	Block	Tree	$\hat{a}$	$\hat{\mu} + \hat{a}$
1	98	6	6	0.50	0.96	98	6	6	0.38	0.84
2	98	1	3	0.43	0.89	98	1	3	0.34	0.81
3	98	6	1	0.43	0.89	98	6	1	0.34	0.80
4	98	1	6	0.40	0.86	98	1	6	0.32	0.79
5	19	1	1	0.38	0.84	98	2	3	0.29	0.76
6	111	2	1	0.37	0.83	98	3	4	0.29	0.75
7	23	2	3	0.37	0.83	98	5	6	0.27	0.73
8	98	2	3	0.35	0.81	98	5	5	0.27	0.73
9	98	3	4	0.34	0.80	98	4	4	0.26	0.72
10	26	1	6	0.33	0.79	98	4	6	0.26	0.72
11	98	5	6	0.32	0.78	19	1	1	0.25	0.72
12	96	1	1	0.32	0.78	96	1	1	0.24	0.70
13	98	5	5	0.31	0.77	111	2	1	0.24	0.70
14	70	1	1	0.31	0.77	98	3	2	0.23	0.70
15	46	5	6	0.31	0.77	23	2	3	0.23	0.69
16	98	4	4	0.29	0.75	98	4	5	0.23	0.69
17	98	4	6	0.29	0.75	98	4	3	0.23	0.69
18	108	3	6	0.29	0.75	70	1	1	0.23	0.69
19	96	1	6	0.28	0.74	98	1	1	0.21	0.67
20	3	4	4	0.28	0.74	96	1	6	0.21	0.67

$\hat{\mu} = 0.462 \text{ m}^3 \text{ tree}^{-1}$

**Table 6.** Genetic gains ( $G_s$ ), mean of the improved population ( $M$ ), number of selected progenies ( $N_f$ ), mean number of selected trees per progeny ( $K_f$ ), and effective population size ( $N_e$ ) in function of the number of selected trees ( $N$ )

Trait	N	$G_s$	$G_s \%$	M	$N_f$	$K_f$	$N_e$
DBH cm	5	5.54	26.65	26.34	01	5.00	2.50
	10	5.25	25.25	26.05	01	10.00	3.08
	50	4.26	20.49	25.06	11	4.55	11.83
	100	3.74	18.00	24.54	30	3.33	29.15
	150	3.42	16.45	24.22	41	3.66	45.41
	200	3.19	15.35	23.99	48	4.17	58.76
	250	3.02	14.50	23.81	56	4.46	72.72
Volume $\text{m}^3 \text{ tree}^{-1}$	5	0.34	73.19	0.80	01	5.00	2.50
	10	0.30	64.53	0.76	01	5.00	3.08
	50	0.22	47.21	0.68	16	3.13	14.36
	100	0.18	38.55	0.64	37	2.70	33.36
	150	0.16	34.23	0.62	47	3.19	50.62
	200	0.14	29.89	0.60	55	3.64	65.40
	250	0.13	27.72	0.59	64	3.91	78.70

## CONCLUSIONS

- Results of this study revealed an expressive genetic variability in the *Pinus caribaea* var. *bahamensis* progenies, in particular for volume and DBH, which is of top importance for the continuation of the improvement program for this population.
- Selection using the vegetative reproduction can lead to greater genetic gains than the seed reproduction, owing to the superiority of the predicted genotypic values.

- The procedure for the prediction of genotypic values (BLUP) proved adequate for the selection of genetically superior individuals.

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# Seleção em progênes de *Pinus caribaea* var. *bahamensis* com base no valor genético predito

**RESUMO** - Progênes de *Pinus caribaea* var. *bahamensis* foram selecionadas com emprego de modelos mistos, através da estimação dos parâmetros genéticos por REML e seu uso na predição de valores genéticos aditivos por BLUP. O delineamento experimental utilizado foi o látice quadrado 11 x 11, parcialmente balanceado, contendo 119 progênes e duas testemunhas comerciais. Aos 13 anos foram avaliados o diâmetro à altura do peito (DAP), a altura e o volume. As progênes apresentaram boa performance média (18,83 m, 20,80 cm e 0,462 m<sup>3</sup> árvore<sup>-1</sup>), e estimativas de herdabilidade de 0,12, 0,20 e 0,21 para altura, DAP e volume, respectivamente. O caráter de maior variabilidade foi o volume, com um coeficiente de variação genética de 22,60%, ao passo que a altura apresentou menor variação genética (3,73%). Obteve-se um ganho genético de 14,5% para DAP, com a seleção de 250 árvores de 56 progênes, com média de 4,46 árvores selecionadas por progêne e tamanho efetivo populacional de 72.

**Palavras-chave:** REML/BLUP, *Pinus*, melhoramento de plantas perenes, parâmetros genéticos, seleção.

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