

Genetic variation of wood and resin production in *Pinus caribaea* var. *hondurensis* Barret & Golfari

Wanderley dos Santos¹, Danilla Cristina Lemos Souza², Mário Luiz Teixeira de Moraes³, Ananda Virginia de Aguiar⁴

¹ Faculdade de Engenharia de Ilha Solteira / UNESP – Universidade Estadual Paulista “Júlio Mesquita Filho” – Av. Brasil Centro, 56 – Caixa Postal: 31, Ilha Solteira São Paulo (SP), Brasil, CEP 15.385-000

² Faculdade de Ciências Agronômicas / Campus de Botucatu, Rua José Barbosa de Barros, 1780-Caixa Postal 237, Botucatu, São Paulo (SP), Brasil, CEP: 18610-307, Centro de Biotecnologia, Universidade Federal da Paraíba, João Pessoa, CEP 58051-900, Paraíba, Brazil

³ Faculdade de Engenharia de Ilha Solteira / UNESP - Universidade Estadual Paulista “Júlio Mesquita Filho” - Av. Brasil Centro, 56 – Caixa Postal: 31, Ilha Solteira São Paulo (SP), Brasil, CEP 15.385-000

⁴ EMBRAPA Florestas, Estrada da Ribeira, Km 111 - Bairro Guaraituba - Caixa Postal: 319 - CEP: 83411-000 - Colombo, PR.

* **Corresponding author:** W. dos Santos, Phone: + 55 (18)3743-1077, E-mail: wanderley.dossantos@hotmail.com

Abstract

The purpose of this work was to estimate genetic parameters and selection gain of *Pinus caribaea* var. *hondurensis* progeny trial for wood and resin production as well as correlation between them. Experiment was established in complete lattice square 10 x 10 (triple), 100 treatments, 10 plants per plot, 3 m x 3 m spacing. Twelve years after planting the trial had thinned considerably leaving six plants per plot. Twenty-seven years after planting height, diameter at breast height (dbh) and resin production were measured. Deviance analysis, genetic parameter estimates, selection expected gain, genetic and phenotypic correlation were based on REML/BLUP method. Significant phenotypic differences were observed among and within families for all traits. The thinning at 12 years after planting, contributed positively to dbh increase and resin production, with an average of 30.60 cm and 4.83 kg tree⁻¹year⁻¹. The individual narrow sense heritability ranged from 0.25 to 0.38 for dbh and volume. Genetic and phenotypic correlation between growth traits were positive, and significant. Therefore, different selection strategies will be proposed separately for both traits (resin and wood). The selection gains were significant, especially with 10 % selection intensity (individual selection) for dbh (7.53 %) and resin (13.49 %). The trial has had good performance for growth, resin and genetic variability to support the next breeding generation

Keywords: *heritability, genetic breeding, pine and seed production*

Introduction

Pine forests provide two products of important economic value: wood and resin. Although more than 100 pine species exist naturally in Europe, Asia, North America and especially in Central America (Lima et al., 1988), few these species produce resin feasible amount to be exploited economically.

World pine resin production amounted 1,114.000 million tons in 2010 (Cunningham, 2012). In Brazil, over season 2013/2014 the production was estimated at 92.596 tons (Aresb, 2014). São Paulo state was the largest contributor to this production. In 2014, Brazil had around 7.74 million hectares of planted forests, 1.59 ha with pine, the Brazil maintained fourth place among countries that produce pulp of all types (Ibá, 2015). The country has been the eleventh largest lumber producer and the second largest resin producer (830 t/year⁻¹) in the world. China is the first in resin production (Cunningham, 2012; Abraf, 2013).

The pine breeding programs in Brazil were initiated in 1970's decade. More than 20 species were tested and the most productive for resin and wood were *P. taeda*, *P. elliottii*, *P. caribaea* var. *bahamensis* and *P. caribaea* var. *hondurensis*. *P. caribaea* varieties are most suitable for production in regions of subtropical and tropical climate concerning resin and wood (Aguiar et al., 2011).

Despite the increase in resin productivity over the years (Aresb, 2014), investment in breeding programs for selection of more productive families for resin is much lower comparing to those for wood production in Brazil. With lack of investment and improvement actions to resin producers have been restricted to use only mass selection in their commercial plantations.

In this context, this study was conducted (i) to estimate genetic parameters for *P. caribaea* var. *hondurensis* for resin and wood production, (ii) estimate genetic and phenotypic correlations and (iii) evaluate potential selection gains with different selection intensities, aiming at the selection of more productive material for resin and wood.

Materials and Methods

Genetic material

Seed from 96 open-pollinated genotypes of *P. caribaea* var. *hondurensis* were collected in a clonal seed orchard at Centro de Conservação Genética e Melhoramento de Pinheiros Tropicais - CCGMPT, located in the municipality of Aracruz, ES, Brazil, (latitude 19°49'S, longitude 40°16'W, 50 m of altitude). Furthermore, seed lots from four commercial controls were included in trial from municipality of Agudos, SP, Brazil, (latitude 22°22'S, longitude 48°52'W and 550 m of altitude).

Progeny test

A progeny test was established June, 1986 in the municipality of Selvíria, MS, Brazil (latitude 20°20'S, longitude 51°23'W and altitude of 370 m) with the 96 OP-families and four controls. The climate is Aw, by Köppen classification, with an average annual temperature of 24.5 °C, annual rainfall of 1.200 mm, annual humidity of 64.8 %, insolation of 7.3 hours.day⁻¹ (Hernandez et al., 1995). Site soil is Red Latosol and clayey (Embrapa, 2006).

The experiment was established in lattice design 10 x 10 (triple) (Resende, 2007a). Each family plot consisted at the time of establishment of ten plants in a row (Moraes, 2001). The spacing was of 3.0 x 3.0 m. Twelve years after planting, a selective thinning within families based on dbh, height, stem form, foxtail and survival was performed. At each plot remained only six trees per plot.

Traits measured and assessed

Resin production (kg.tree⁻¹year⁻¹), after thinning, was assessed from April 2011 to May 2012. The resin extraction was performed every 15 days cutting surface tool to open the scoring (Scribing). To extract the resin was used American type method based on a chemical pulp stimulant containing sulfuric acid (20 %) and CEPA (2-chloroethyl acid) (3.5-4.0 %) (Aresb, 2016). The formulation was placed on the surface of sapwood after cutting. In addition to the total amount of resin, after completion of the last ribs (20), total area of panel was also measured. The cutting was performed with tool to exudation of resin gum until the depth close to the heart.

Growth traits evaluated after thinning were: diameter at breast height (dbh - cm), height (m) and survival (%). Based on the total height and dbh were estimated cylindrical volume (m³.tree⁻¹) and the average annual increment in height (m). Survival was assessed for presence (1) and absence (0) of plant.

Statistical analysis

Estimates of variance components, genetic parameters and standard errors were analyzed by REML/BLUP (restricted

maximum likelihood/best linear unbiased prediction), using genetic-statistical software SELEGEN (Resende, 2007b). Progeny test was assumed to be open pollinated (half-sib). Half-sib progenies test was analyzed considering as complete randomized block design, several plants per plot, one place and one single population. The linear model used was:

$$y = \mathbf{Xb} + \mathbf{Za} + \mathbf{Wc} + \mathcal{E};$$

where: y = data vector; b = vector of repetition effect (fixed); a = vector of additive genetic effects (random); c = vector of plot effect (random); \mathcal{E} = vector of random error effect. X, Z e W = incidence matrices for b, a , and c , respectively.

Distributions and average structures and variances to obtain the BLUP:

$$y|b, V \sim N(\mathbf{Xb}, V)$$

$$a|A, \sigma_a^2 \sim N(0, A\hat{\sigma}_a^2)$$

$$c|\sigma_c^2 \sim N(0, I\hat{\sigma}_c^2)$$

$$e|\sigma_e^2 \sim N(0, I\hat{\sigma}_e^2)$$

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

$\hat{\sigma}_c^2$: between plots variance;

$\hat{\sigma}_e^2$: residual variance (environment within plots + non-additive).

A: additive genetic correlation matrix between individuals under evaluation.

COV (a, c) = 0; COV (a, e) = 0; COV (c, e) = 0, is the covariance between all the random effects model are void. Like this:

$$E \begin{bmatrix} y \\ a \\ c \\ e \end{bmatrix} = \begin{bmatrix} \mathbf{Xb} \\ 0 \\ 0 \\ 0 \end{bmatrix} + e \quad \text{var} \begin{bmatrix} y \\ a \\ c \\ e \end{bmatrix} = \begin{bmatrix} V & ZG & WC & R \\ GZ' & G & 0 & 0 \\ CW' & 0 & C & 0 \\ R & 0 & 0 & R \end{bmatrix}, \text{ in which:}$$

$$G = A \hat{\sigma}_a^2$$

$$R = I \hat{\sigma}_c^2$$

$$C = I \hat{\sigma}_e^2$$

$$V = ZA \hat{\sigma}_a^2 Z' + WI \hat{\sigma}_c^2 W' + I \hat{\sigma}_e^2 = ZGZ' + WCW' + R \text{ (Resende, 2002).}$$

The mixed model equations are (Resende, 2002):

$$\begin{bmatrix} \mathbf{X}'\mathbf{X} & \mathbf{X}'\mathbf{Z} & \mathbf{X}'\mathbf{W} \\ \mathbf{Z}'\mathbf{X} & \mathbf{Z}'\mathbf{Z} + \mathbf{A}^{-1}\lambda_1 & \mathbf{Z}'\mathbf{W} \\ \mathbf{W}'\mathbf{X} & \mathbf{W}'\mathbf{Z} & \mathbf{W}'\mathbf{W} + \lambda_2 \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{a} \\ \hat{c} \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{y} \\ \mathbf{Z}'\mathbf{y} \\ \mathbf{W}'\mathbf{y} \end{bmatrix}, \text{ in which:}$$

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

$\hat{h}^2 = \frac{\hat{\sigma}_a^2}{\hat{\sigma}_a^2 + \hat{\sigma}_c^2 + \hat{\sigma}_e^2}$: is the narrow sense individual heritability.

$\hat{c}_2 = \frac{\hat{\sigma}_c^2}{\hat{\sigma}_a^2 + \hat{\sigma}_c^2 + \hat{\sigma}_e^2}$: Life correlation to the common environment of the plot.

Iterative estimators of variance components by REML via EM algorithm (Expectation-Maximization) are:

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

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

$$\hat{\sigma}_c^2 = [c'c^{-1} + \hat{\sigma}_e^2 \text{tr}C^{33}] / s, \text{ in which:}$$

C^{22} e C^{33} from:

$$C^{-1} = \begin{bmatrix} C_{11} & C_{12} & C_{13} \\ C_{21} & C_{22} & C_{23} \\ C_{31} & C_{32} & C_{33} \end{bmatrix}^{-1} = \begin{bmatrix} C^{11} & C^{12} & C^{13} \\ C^{21} & C^{22} & C^{23} \\ C^{31} & C^{32} & C^{33} \end{bmatrix}$$

C = coefficient matrix of the mixed model equations.

tr = operator matrix trace.

$r(x)$ = put the matrix X .

N = total number of data;

q = number of individuals;

s = plot number.

Other estimates variances and genetic parameters processed by the program:

a) Additive genetic variance

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

b) Environmental variance among plots

$$(\hat{\sigma}_c^2): \hat{\sigma}_c^2 = [\hat{c}'\hat{c} + \hat{\sigma}_e^2 \text{tr}C^{33}] / s_1;$$

c) Residual variance (Environmental + non-additive) ($\hat{\sigma}_e^2$):

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

in which: C^{22} e C^{33} It is the inverse C ; C : coefficient matrix of the mixed model equations; tr : operator matrix trace; $r(x)$: put the matrix X ; N , q , s : Data numbers of individuals and parcels, respectively.

Estimates variances, genetic parameters processed, genetic and phenotypic correlations were obtained by REML/BLUP method (restricted maximum likelihood / best linear unbiased prediction), using genetic-statistical software SELEGEM-REML / BLUP (Resende, 2007b). Standard errors and significance for genetic and phenotypic correlations were estimated via GENES® (Cruz, 2006).

Estimates of effective population size and expected gain selection

Selection strategies considered the results of genetic testing statistics. The variable considered to selection was dbh, which is highly correlated with volume and resin production. The selection strategy would be through genotypic values predicted by individual BLUP that would use simultaneously

information on family and individual for selection (Resende, 2002). The optimal method of selection is the individual BLUP which uses all the effects of the statistical model, contemplates the imbalance, uses the genetic relatedness between individuals under evaluation, considers the coincidence of selection and recombination unit (Resende, 2007a). Selection strategies were: (i) intensity of 2.6 %, 5.3 % and 10 % according to individual BLUP.

Effective population size (N_e) was obtained based on formula deduced by Resende (2002): $N_e = (4.N_f.\bar{k}_f) / [\bar{k}_f + 3 + (\sigma_{kf}^2 / \bar{k}_f)]$ where: N_f is number of selected families; \bar{k}_f is average number of individuals selected per family; σ_{kf}^2 is estimate of variance number of individuals selected per family.

Genetic diversity (D), after selection, was quantified by Wei and Lindgren (1996), cited by Resende (2002): $D = N_{ef} / N_{fo}$, where: $0 < D \leq 1$; N_{fo} is original number of families, N_{ef} is effective number of selected families, and is given by:

$$N_{ef} = (\sum k_f)^2 / \sum k_f^2.$$

Results

Genetic parameters and deviance analysis

Progenies trial was composed by 3.000 plants. However, selective thinning adopted at age 12 selected 60 % of tree within progenies. Thinning was performed similarly within each progeny, so significant differences between and within progenies for the trait survival were not observed. Currently the progeny test plants consists of 1.484, corresponding to 82.44 % survival rate whereas a total of 1.800 plants remaining after selective thinning.

Dbh, height, volume, total resin production, resin production per panel area, annual increment and survival mean at age 27 were 30.60 cm, 30.22 m, 1.48 m³.tree⁻¹, 4,83 kg.tree⁻¹.ano⁻¹, 68.63 g.tree⁻¹.cm⁻², 1.12 m and 82.44 %, respectively (Table 1). Coefficients of experimental variation and plot effect determination (\widehat{C}_p^2) were low, indicating that the experiment has a high precision and low environmental variation experimental and between plots within blocks. The highest \widehat{C}_p^2 was observed for average annual increment.

Coefficients of genetic variation among progenies (CV_{gp}) were low to high ranging from 4.14 % (height) to 14.15 % (volume), while coefficients of Individual genetic variation (CV_{gi}) were 8.27 % (annual increment height mean) to 28.31 % (volume). Accuracy values for selection progenies assuming complete survival were classified based on scale made by Resende (2002), as high for dbh, volume, total resin production, resin production per panel area and annual increment, and low for survival (11 %). Narrow-sense individual heritability ranged from 0.26 % to 0.39 % for dbh and volume, respectively.

In general, estimates of family mean heritability (\hat{h}_m^2), where the number of repetitions and plants per plot minimize environmental effects, were relatively high. This result may estimate high genetic gains for selected traits, due to favorable conditions for progenies selection. In the current work, total resin production (0.62) and resin production per panel area (0.65) showed the highest values.

Table 1. Estimate of genetic parameters for silvicultural traits in *Pinus caribaea* var. *hondurensis* progênies in Selvíria, Brazil (dbh = diameter at breast height; TR = total resin production; PR = resin production per panel area; AIH = Annual increment height mean; SUR = survival)

Parameters	dbh (cm)	Height (m)	Volume m ³ tree ⁻¹	TR g tree ⁻¹ ano ⁻¹	PR g tree ⁻¹ cm ⁻²	AIH (cm)	SUR (%)
\hat{h}_a^2	0.26±(0.07)	0.29±(0.08)	0.39±(0.09)	0.25±(0.07)	0.28±(0.07)	0.29±(0.08)	0.001±(0.004)
\hat{C}_p^2	0.05	0.31	0.10	0.02	0.02	0.31	0.001
\hat{h}_m^2	0.59	0.37	0.62	0.62	0.65	0.37	0.013
r_{aa}	0.77	0.61	0.79	0.79	0.81	0.61	0.11
CV _{gi} (%)	9.17	8.28	28.31	23.72	25.61	8.27	4.18
CV _{gp} (%)	4.59	4.14	14.15	11.86	12.80	4.14	2.09
CV _e (%)	6.62	9.27	19.06	15.92	16.14	9.27	32.08
CV _r	0.69	0.45	0.74	0.76	0.79	0.45	0.07
\hat{m}	30.60	30.22	1.48	4.83	68.63	1.12	82.44
LRT prog	13.47**	5.32**	336.39**	16.47**	18.29**	5.31*	43.83**
LRT plot	5.54*	165.36**	22.08**	1.92 ns	1.28 ns	165.41**	46.83**

\hat{h}_a^2 narrow-sense individual heritability; \hat{C}_p^2 coefficient of plot effect determination; \hat{h}_m^2 family heritability mean; r_{aa} accuracy; \hat{h}_{ad}^2 additive heritability within plot; CV_{gi} coefficient of individual additive genetic variation; CV_{gp} coefficient of genotypic variation among progenies; CV_e coefficient of experimental variation; CV_r coefficient of relative variation; \hat{m} general mean; LRT: Likelihood ratio test; χ^2 chi-squared deviance; ** significant at 1% (6.63), * significant at 5% (3.84), with 1 degree of freedom ns not significant.

Genetic and phenotypic correlations between traits

Genetic and phenotypic correlations between growth traits varied low to high magnitude and were significant for all correlations ($p < 0.01$) (Table 2).

Table 2. Estimates of genetic correlations (r_g above the diagonal) and phenotypic correlations (r_f below the diagonal) between growth and resin production traits in *Pinus caribaea* var. *hondurensis* progenies, at 27 years old, in Selvíria, Brazil

	Dbh	Height	Volume	TR	PR
Dbh	-	0.60**	0.92**	0.24**	0.22**
Height	0.52**	-	0.75**	0.12**	0.10**
Volume	0.93**	0.69**	-	0.20**	0.19**
TR	0.41**	0.23**	0.36**	-	0.98**
PR	0.39**	0.22**	0.35**	0.96**	-

Significance levels for correlation coefficients: *** $P < 0.001$; ** $P < 0.01$; and * $P < 0.05$. - denote the value of correlation coefficient over 1. dbh = diameter at breast height; TR = total resin production; PR = resin production per panel area.

Trait with the highest relation to volume was dbh. For volume indirect selection this trait might to be considered. Genetic correlations for almost all traits were lower than the corresponding phenotypic correlation, which indicates that the use of phenotypic correlations to evaluate traits will result potential gain overestimation for indirect selection, rather than genetic ones. High correlation was observed between dbh and volume ($r_g = 0.92$), while between volume and height is medium ($r_g = 0.60$). In additional, phenotypic correlations were high for total resin production and resin production per panel area ($r_f = 0.96$) and low for resin production per panel area in relation to height ($r_f = 0.10$).

Expected genetic gain and effective population size

Expected genetic gain was estimated based on dbh and resin production (Table 3).

Table 3. Estimates of selection gain for individual selection (SI) for dbh and resin in *P. caribaea* var. *hondurensis* progeny test in Selvíria, Brazil

Parameters	Dbh			Resin		
	S ₁ 2,6	S ₁ 5,3 %	S ₁ 10 %	S ₁ 2,6 %	S ₁ 5,3 %	S ₁ 10 %
N	40	80	143	40	80	147
N _{fo}	96	96	96	96	96	96
N _e	17.73	38.73	63.15	23.89	40.37	68.61
GS(%)	9.31	8.27	7.39	17.01	15.81	14.5
\hat{D}	0.08	0.16	0.24	0.11	0.19	0.27

N: number of selected individuals; N_{fo}: number of original families; N_e: effective size or status number; GS: Gain from selection; \hat{D} : Genetic diversity.

Individual selection strategies with intensity of 2.6% (40 individuals), 5.3% (80 individuals) and 10% (152 individuals) were adopted in order to select materials to compose clonal and commercial plantations. Although providing decrease N_e around the 80% and genetic divergence (\hat{D}) around 50% (Table 2), genetic gains were higher for resin (17.01%, 15.81% and 14.50%) and dbh (9.31%, 8.27% and 7.39%).

Discussion

The present study shows the important genetic variation in resin and dbh yield among *P. caribaea* var. *hondurensis* families. The family heritabilities for resin and dbh yield were moderately high. Narrow-sense individual heritabilities (h_a^2) for resin

production and dbh were moderate according to scale deduced by Resende (2002), where $h_a^2 < 0.15$ is low, $0.15 < h_a^2 < 0.50$ is moderated and $h_a^2 > 0.50$ is high. Selections within progeny tests can be further carried out to develop high-yielding resin genotypes. dbh h_a^2 was estimated by other authors for many pine species, such as *P. caribaea* var. *hondurensis* (0.20 at age 5) (Sampaio et al., 2000); *P. caribaea* var. *bahamensis* (0.35 at age 21 and 0.56 at age 13, respectively) (Missio et al., 2004 and Pires et al., 2013) and *P. caribaea* var. *hondurensis* (0.28 at age 14) (Moraes, 2001). For height estimated h_a^2 were 0.44 at age 14 for *P. caribaea* var. *hondurensis* (Moraes, 2001) and 0.41 for *P. caribaea* var. *bahamensis* at age 13 (Missio et al., 2004). This result will estimate moderate genetic gains for growth and resin traits due to favorable conditions for the selection of progeny. The narrow-sense heritabilities for resin and dbh yield were high in the present study, and selections within the progeny tests can be further carried out to develop high-yielding resin genotypes. High coefficients of genetic variation values indicate possibility high-expected genetic gains. These estimates were higher than the values CV_{gp} obtained for all traits, mainly resin. These should to superior individuals of some families that if it was selected will provide significant gains. *P. caribaea* var. *bahamensis*, estimated coefficients of genetic variation among progenies of 6.56 % and 3.70 % for dbh and height, respectively (Gurgel Garrido et al., 1997). Sebbenn et al. (1994) estimated lower CV_{gp} in *P. caribaea* var. *bahamensis* progenies of 2.43 % and 1.85 % at age 2 and 1.86 % and 1.06 % at age 5 for the same traits.

Freitas et al. (2005) and Sebbenn et al. (2008) also observed significant genetic variation between *P. caribaea* var. *bahamensis* progenies for growth traits, indicating the possibility of promising genetic gains in the first generations of breeding. On the other hand, variety *caribaea* have showed low genetic variation for quantitative traits in the same site (Silva et al., 2012).

Accuracy values of this study were higher than *P. oocarpa* observed by Sampaio et al. (2002), who found average accuracy of 35 %. These estimates confirm with high probability that the genetic material maximize the genetic progress possibilities with selection. According to Aguiar et al. (2011), these values indicate possibilities of genetic gains in all selection levels. We propose to select individuals based on dbh, because this trait had the highest heritability and has less measurement errors, and reflects the wood production volume.

Genetic correlations between growth traits were high and positive, however, it between dbh and resin production was positive and low. Rossmann (2001) reported that for pine species positive genetic correlation between growth traits (height and dbh) are expected, but these must be estimated in each population to confirm the efficiency of indirect selection. Several studies suggested that the correlation genetic between growth and resin production is positive and significant ($r > 0.77$) (Roberds et al., 2003; Romanelli and Sebbenn, 2004). Blanche et al. (1992) have also observed high and moderate genetic correlations between resin production and growth traits in loblolly pine (*P. taeda* L.). This indicates that genetic factors act concurrently to increase resin production and growth. On the other hand, this study few genes may have contributed

to increase both, dbh and resin. Then, this tend to cause a positive and low correlation.

Resin exploitation starts at seven or eight years after planting. An alternative to speed up the breeding process would be the early selection. However, this alternative would only be possible if there was significant positive genetic correlation between traits in early and adult ages. One positive aspect is the selection for volume as early as possible will not affect the resin production, in view of the direction of the relationship between these traits. Sampaio et al. (2000) consider that the selection of *P. caribaea* var. *hondurensis* trees based on diameter may reflect high genetic gain estimates in volume and with good accuracy, since they have high correlations and low standard deviations. High and positive genetic correlations between growth traits for *P. caribaea* var. *bahamensis* were also observed by Missio et al. (2004).

Genetic correlations of growth vary between different species of *Pinus*, and these variations, according to Rezende and Ferraz (1992), can be attributed to several factors, including the sampling standards, age of trees, competition degree, availability of water and nutrients and influence of canopy traits in the sampling period. The main cause of genetic correlation between growth traits is pleiotropism effect. This is attributed when a gene affects two or more traits. Another cause of correlation between traits is the gene linkage disequilibrium observed in most populations originating from different mating; it may be larger when closer the genes on chromosome, but it is transient (Falconer, 1981). The results suggest that a small number of genes affect positively dbh and resin production. So response selection for dbh on the resin production, one must calculate the genetic value of the regression coefficient of resin on the genetic value of dbh.

Furthermore, the genetic correlation is due to genetic linkage to any extent, it is likely the decrease in magnitude value in subsequent breeding cycles, through recombination, and thereby decrease the correlated response (Falconer, 1981). On the other hand, if there were a significant positive correlation, it would be expected that indirect resin production selection should be superior to direct for this trait that have a heritability coefficient slightly higher than the dbh. This would be advantageous because of the difficulty of measuring the trait resin accurately. For a correlated response must apply the direct and indirect selection and results obtained in the next generation. Thus, dbh is believed to be the optimum assisted trait for indirectly selecting high yielding resin trees. Were obtained gains meaning with the selection of dbh and resin using variants of information and genetic correlations.

P. caribaea var. *hondurensis* population has provide genetic gains above other populations studied by other authors. The selection by MEI Index was 12.8 % more efficient than selection among and within families in *P. caribaea* var. *hondurensis* (Moraes, 2001). *P. caribaea* var. *bahamensis* progenies determined that the MEI was 36.9 % more efficient than selection among and within families (Missio et al., 2004). Sampaio et al. (2002) verified genetic gain of 15 % in *P. oocarpa*. Paludzyszyn-Filho et al. (2002) obtained gain of 8 % in *P. taeda*. Leonardez Neto (1998) estimated genetic gain of 15.04 % and 4.25 % for volume and dbh with selection among and within

progenies of *P. patula*. Furthermore, Magnussen (1994) noted gains 6 % to 15 % for both height and volume correspond to realistic selection intensity in a forest species-breeding program.

The genetic variability is reduced in each improvement cycle. The control of this parameter in proper level is carried out from the knowledge of effective size. Resende (1999) reported the importance of maintaining an effective size (N_e) above 50 in each selection cycle, thereby preventing loss of variability and increasing the likelihood for maintaining favorable alleles in each breeding generations, and, consequently, keeping genetic improvements in continuous cycles. The artificial selection, an important component of any breeding program reduces the effective population size, and can thus reduce genetic variation and increase inbreeding (Frankham et al., 2004). For Resende (1999), the ideal is to start with a base population represented by a large number of offspring in order to allow high intensity selection as in the first generations, while maintaining the effective size compatible with the improvement in the long term. The N_e indicated as selective threshold is between 30 to 60 (Leonardcz-Neto et al., 2003). This population still has enough genetic variability for the N_e value minimum of 50 with a small percentage of individuals per family.

Breeding programs have aimed increasing production in specific populations while maintaining sufficient genetic variation for genetic gains continued throughout the reproductive cycle. The trial presented good production performance (growth and resin) and enough genetic variability to the next generation of breeding. Therefore, the genetic germplasm conservation is strategic for the forestry sector and the country, especially if we consider that most of *P. caribaea* var. *hondurensis* tests have been replaced by other species of greater commercial interest, such as the Eucalyptus genus.

Conclusion

There are significant differences between and within *P. caribaea* var. *hondurensis* progenies for growth traits (dbh, height and wood volume), and resin production.

Genetic variation and heritability coefficients for silvicultural traits show the possibility of significant gains in subsequent breeding cycles, especially for resin.

Estimates of expected selection response in different intensity selections showed the possibility of gain both dbh and resin.

The selections for wood and resin can be performed independently, due to the low relationship between the traits. However, the direct and indirect selection should be quantified to confirm this relationship in subsequent breeding generations.

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