

Estimates of genetic parameters and prediction of additive genetic values in *Pinus kesya* progenies

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ABSTRACT - The objective of this study was to select *Pinus kesya* progenies by the estimation of genetic parameters using the method of restricted maximum likelihood (Reml) and prediction of additive genetic values by the best linear unbiased prediction (Blup). The *Pinus kesya* progeny test was installed in randomized blocks, which consisted of 30 progenies and three replications. The twenty-year-old trees were evaluated for the traits diameter at breast height (DBH), height (HT) and stem form (FOR). The DBH, HT and FOR means were, respectively, 21.89 cm, 21.89 m and 1.56 and their respective mean heritability estimates of progenies were 0.58, 0.39 and 0.66. DBH presented the highest coefficient of additive genetic variation (17.89%). The selection of the 80 best trees which belonged to 21 progenies provided a gain of 9.62% for FOR with a mean of 3.81 trees selected per progeny, an effective population size of 30.86 and genetic divergence of 0.37.

Key words: improvement, selection, genetic gain, Reml/Blup.

INTRODUCTION

Among the successfully introduced exotic forest species in Brazil, *Pinus* and *Eucalyptus* are noteworthy genera. Among the *Pinus* species potentially apt for different regions in Brazil, in particular for the southeast, *Pinus kesya*, native of Vietnam and the Philippines, is especially promising.

According to Guldager et al. (1980) *Pinus kesya*, compared to other species of the same genus is defective in terms of international wood standards, principally in the traits stem form, thick branching and heartwood with a large quantity of young wood. The presence of juvenile heartwood is common in most *Pinus* species, but among the tropical species the inferior stem form and thick branching are most pronounced in *Pinus kesya*. According to Moraes et al. (1990), genetic improvement of *Pinus kesya* with provenances from the Philippines and Vietnam is

targeting the elimination of these flaws since 1960 in Zimbabwe, Rhodesia, South Africa, and Zambia. The objectives in Brazil are the same. Encouraging results are being obtained in the northern and central regions of the state of São Paulo, particularly at altitudes from 700 to 1000 m and under limited water stress.

The traditional methodology of analysis of variance (method of the moments) for the estimation of genetic parameters is not the most recommended for data analysis in perennial species improvement (Resende et al. 2001). In view of the frequently unbalanced data in perennial species one should rather use methods that allow a more accurate prediction of genetic values. For perennial species, the optimum estimation/prediction procedure of genetic values is Reml/Blup, that is, the estimation of the components of variance by restricted maximum likelihood (Reml) and the prediction of genetic values by the best linear unbiased prediction (Blup). Genetic parameters in *Pinus* are however

mostly estimated by the traditional methodology (Sebbenn et al. 1995, Gurgel Garrido et al. 1996, Moura and Dvorak 2001, Sampaio et al. 2002, Paludzyszyn Filho et al. 2002, Johnston et al. 2003). Still, apart from *Pinus* (Missio et al. 2004a) and eucalypt (Resende et al. 1993), the Reml/Blup procedure is being successfully applied in other perennial species such as rubber (Kalil Filho et al. 2000, Costa et al. 2000, 2002a, b), *Ilex paraguariensis* (Simeão et al. 2002), coffee (Resende et al. 2001), peach palm (Farias Neto and Resende 2001), Barbados cherry (Paiva et al. 2002), cacao (Resende and Dias 2000, Dias and Resende 2001), cupuaçu (Souza et al. 2002), and king palm (Purba et al. 2001).

This study aimed at the selection of superior *Pinus kesyia* progenies by using the mixed model methodology, by means of the estimation of genetic parameters by Reml and prediction of additive genetic and genotypic values by Blup.

MATERIAL AND METHODS

Plant material

The progenies of the trial were derived from mother trees from a clonal seed orchard of *Pinus kesyia* Royle ex Gordon established in 1975, in the township of Anhembi, state of São Paulo. In turn, the matrices of this orchard came from a *Pinus kesyia* base population implanted in São Carlos - SP, by seeds originated from Vietnam and the Philippines.

The progeny test of open pollination, supposedly half-sibs of *Pinus kesyia* was installed in January 1984 on the Fazenda de Ensino e Pesquisa of the University Estadual Paulista “Júlio de Mesquita Filho” – UNESP, in the township of Selvíria, state of MS (lat 20° 20' S, long 51° 23' W and alt 370 m asl). The experiment had a randomized block design, with 30 *Pinus kesyia* progenies in three replications. The plots arranged in rows contained five trees each in 2.0 x 2.5 m spacing.

At the age of 20 years data were collected for the traits diameter at breast height (DBH, in cm), height (HT, in m) and stem form (FOR). A grade scale was adopted for the latter (Missio et al. 2004b), which varies from 1 (no straight trunks) to 5 (a straight trunk of 4 meters, measured base-up).

Statistical analysis

The mixed linear model applied to open-pollinated progenies in a complete random block design, with several

tree per plot and one measurement per individual as described by Resende (2002a):

$$y = Xb + Za + Wc + e$$

where:

y, b, a, c and e are the data vectors of fixed effects (block means), of additive genetic effects (random), of plot effects (random common environment effects of the plots) and of the random errors, respectively;

X, Z and W – are known matrices of incidences, formed by the values 0 and 1 which associate the incognita b, a and c, respectively, to the data vector y.

Narrow-sense heritabilities of progeny mean (\hat{h}_m^2), within progeny (\hat{h}_{ad}^2), individual and genetic parameters were estimated as described by Resende (2002a):

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

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

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_c^2 + \sigma_e^2}$$

$c^2 = \frac{\sigma_c^2}{\sigma_a^2 + \sigma_c^2 + \sigma_e^2}$ is the correlation due to the common environment of the plot;

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

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

$\hat{\sigma}_e^2$ is the residual (environmental within plots + non-additive) variance;

The effective population size (N_e) and genetic divergence (D) were obtained based on Vencovsky (1978) and Resende (2002a):

$$N_e = \left(4 \cdot N_f \cdot \bar{k}_f \right) / \left[\bar{k}_f + 3 + \left(\sigma_{kf}^2 / \bar{k}_f \right) \right], \text{ where:}$$

\bar{k}_f is the mean number of individuals selected per progeny;

σ_{kf}^2 = variance of the number of individuals selected per progeny.

$D = N_{ef} / N_{fo}$ where $0 \leq D \leq 1$ and:

N_{fo} is the original number of progenies, 30 in the present study;

N_{ef} is the effective number of selected progenies, given by:

$$N_{ef} = (\sum k_f)^2 / \sum k_f^2, \text{ where}$$

k_f is the number of individuals selected per progeny.

The estimates of genetic parameters and predictions of genotypic and additive genetic values were obtained with software Selegen-Reml/Blup (Resende 2002b), using the EM algorithm.

RESULTS AND DISCUSSION

Estimates of genetic and phenotypic parameters

The traits DBH and HT performed well, with means of 21.89 cm and 21.89 m, respectively (Table 1). The general mean of trait FOR (1.56) however indicated that the study progenies were highly tortuous, with a lower mean than Sampaio et al. (2002) found for provenances of *Pinus oocarpa* (1.76) and Missio et al. (2004b), for *Pinus caribaea* var. *bahamensis* (1.74), though superior to those found by Moura and Dvorak (2001) in *Pinus caribaea* var. *hondurensis* provenances (1.10).

In general, a high genetic variability was verified among the progenies under study. The coefficients of

Table 1. Estimates of the parameters narrow-sense heritability (\hat{h}^2), mean progeny heritability (\hat{h}_m^2), plot-within additive heritability (\hat{h}_{ad}^2), correlation due to the common environment of the plot (\hat{c}_p^2), accuracy of progeny and parent selection (\hat{r}_{aa}), additive genetic variance ($\hat{\sigma}_a^2$), variance among plots ($\hat{\sigma}_c^2$), residual variance ($\hat{\sigma}_e^2$), phenotypic variance ($\hat{\sigma}_f^2$), coefficient of additive genetic variation (CV_g), and general mean for DBH, HT and FOR, in 20-year-old *Pinus kesya* progenies

Parameters	DBH (cm)	HT (m)	FOR
\hat{h}^2	0.36	0.23	0.53
\hat{h}_m^2	0.58	0.39	0.66
\hat{h}_{ad}^2	0.30	0.21	0.48
\hat{c}_p^2	0.01450	0.10420	0.04242
$\hat{\sigma}_a^2$	15.33757	4.61638	0.03121
$\hat{\sigma}_c^2$	0.62097	2.06391	0.00250
$\hat{\sigma}_e^2$	26.86556	13.12749	0.02525
$\hat{\sigma}_f^2$	42.82409	19.80778	0.05897
\hat{r}_{aa}	0.76	0.63	0.81
CV_g (%)	17.89	9.82	11.33
Mean ($\hat{\mu}$)	21.89	21.89	1.56

additive genetic variation were 17.89%, 9.82% and 11.33 for DBH, HT and FOR, respectively, reinforcing the importance of these progenies for the improvement program of the species. The estimates of individual heritability in the narrow sense (\hat{h}^2) were 0.36, 0.23 and 0.53 for DBH, HT and FOR, respectively. The mean progeny heritability estimates (\hat{h}_m^2) on the other hand where the environmental effects are minimized by the number of replications and plants per plots were 0.58, 0.39 and 0.66, respectively. Moraes et al. (1990) studied *Pinus kesya* progenies and observed a mean plant height of 9.38 m at the age of 6 years, with a genetic variation coefficient of 6.23% and mean progeny heritability of 0.36; these values were lower than those found in the present study. In our study the mean heritability estimates of progenies for trait FOR were lower than those observed by Sampaio et al. (2002) for *Pinus oocarpa*, and superior to those reported by Otegbeye (1988) for *Pinus caribaea* var. *hondurensis*, Missio et al. (2004b) for *Pinus caribaea* var. *bahamensis*, Matziris (2000) for *Pinus halapensis*, and Schermann et al. (1997) and StClair (1994) for *Pseudotsuga menziesii*.

The accuracy or correlation between the predicted and the true genetic values ranged from 0.63 for HT to 0.81 for FOR (Table 1). According to Resende (2002a), accuracy is a measure that is associated to selection precision and is the principal component in genetic progress that the breeder can change in order to maximize the genetic gain. The accuracy can be increased by more adequate experimentation, maintaining the same experiment size but altering the number of plots and replications (Resende et al. 2001). The accuracy values observed in this study were higher than those found by Sampaio et al. (2002) in *Pinus oocarpa* (for all studied traits) by Resende et al. (2001) in coffee (for height and diameter) and by Costa et al. (2000) in rubber (for rubber yield).

Predicted genetic values

Tables 2 and 3 present the additive genetic (\hat{a}) and genotypic effects (\hat{g}), assuming a mean dominance degree of 1 in a population with an intermediate improvement level), genotypic values ($\hat{\mu} + \hat{g}$) and additive genetic values ($\hat{\mu} + \hat{a}$) predicted for the 20 best *Pinus kesya* trees, for the traits FOR and DBH, respectively.

Among the selected trees, considering asexual propagation (ranked by) for FOR (Table 2), 18 (90%)

Table 2. Genotypic effects (\hat{g}), genotypic values ($\hat{\mu} + \hat{g}$), additive effects (\hat{a}) and predicted additive genetic values ($\hat{\mu} + \hat{a}$) for the 20 best individuals of *Pinus kesya*, 20 years old, for FOR

Order	Asexual propagation					Sexual propagation				
	Block	Progeny	Tree	\hat{g}	$\hat{\mu} + \hat{g}$	Block	Progeny	Tree	\hat{a}	$\hat{\mu} + \hat{a}$
1	1	27	3	0.52	2.08	1	27	3	0.52	2.08
2	2	26	3	0.37	1.93	2	26	3	0.37	1.93
3	3	27	4	0.35	1.91	3	27	4	0.35	1.91
4	1	21	2	0.35	1.91	1	21	2	0.35	1.91
5	3	21	3	0.34	1.90	3	21	3	0.34	1.90
6	3	21	5	0.34	1.90	3	21	5	0.34	1.90
7	1	27	2	0.33	1.89	1	27	2	0.33	1.89
8	3	24	2	0.33	1.89	3	24	2	0.33	1.89
9	1	9	2	0.32	1.88	1	9	2	0.32	1.88
10	1	9	5	0.32	1.88	1	9	5	0.32	1.88
11	3	8	4	0.32	1.88	3	8	4	0.32	1.88
12	1	30	5	0.32	1.88	1	30	5	0.32	1.88
13	1	17	2	0.32	1.88	1	17	2	0.32	1.88
14	3	23	3	0.31	1.87	3	23	3	0.31	1.87
15	3	23	5	0.31	1.87	3	23	5	0.31	1.87
16	1	19	4	0.31	1.87	1	19	4	0.31	1.87
17	1	10	4	0.31	1.87	1	10	4	0.31	1.87
18	2	27	1	0.21	1.77	2	27	1	0.21	1.77
19	2	27	3	0.21	1.77	2	27	3	0.21	1.77
20	2	27	4	0.21	1.77	2	27	4	0.21	1.77

$\hat{\mu} = 1.56$. Numbers in italic represent the common trees for asexual propagation and numbers in bold common trees for FOR and DBH

matches were observed with the best trees for sexual propagation (ranked by). Furthermore the sequence of the trees (individuals) was altered by the considered propagation type, in agreement with observations of Resende and Dias (2000) for the trait number of fruits per plant in full-sib cacao progenies. For trait DBH, 16 (80%) progenies were common to both propagation systems (Table 3). The selection of the best individuals based on the propagation system (asexual or sexual) is therefore closely linked to the objectives of the improvement program of the species. If one aims at the

transformation of the progeny test into a seedling seed orchard, the trees must be selected based on . When the objective is the supply of material to set up a clonal seed orchard, then the individuals should be selected based on to maximize the genetic gain.

The predicted genotypic (\hat{g}) and additive genetic values (\hat{a}) for the 20 best trees varied from 2.08 to 1.77 and 1.93 to 1.74, respectively for FOR (Table 2). For the trait DBH (Table 3) the values ranged from 32.50 to 27.54 and 29.35 to 26.08, respectively. In general, the predicted genotypic (\hat{g}) were superior to the additive

Table 3. Genotypic effects (\hat{g}), genotypic values ($\hat{\mu} + \hat{g}$), additive effects (\hat{a}) and predicted additive genetic values ($\hat{\mu} + \hat{a}$) for the 20 best individuals of *Pinus kesya*, 20 years old, for DBH (cm)

Order	Asexual propagation					Sexual propagation				
	Block	Progeny	Tree	\hat{g}	$\hat{\mu} + \hat{g}$	Block	Progeny	Tree	\hat{a}	$\hat{\mu} + \hat{a}$
1	1	30	5	10.61	32.50	1	27	5	7.46	29.35
2	1	29	5	8.89	30.78	1	26	5	6.19	28.08
3	1	19	1	8.22	30.11	1	27	1	5.84	27.73
4	2	24	5	8.10	29.99	2	21	1	5.20	27.09
5	3	8	1	7.87	29.76	3	21	1	5.09	26.98
6	1	16	5	7.81	29.70	2	21	5	5.08	26.97
7	3	5	3	7.33	29.22	2	27	5	5.01	26.90
8	2	29	1	7.24	29.13	1	24	3	4.94	26.82
9	1	22	3	7.12	29.01	2	9	4	4.66	26.55
10	2	29	5	7.04	28.93	2	9	3	4.61	26.49
11	2	9	3	6.40	28.29	1	8	3	4.51	26.40
12	2	29	4	6.34	28.23	2	30	5	4.49	26.38
13	2	19	3	6.16	28.05	2	17	3	4.47	26.36
14	1	29	3	6.09	27.98	1	23	5	4.43	26.32
15	1	10	4	6.05	27.94	3	23	3	4.42	26.30
16	1	9	2	5.98	27.87	2	19	1	4.31	26.20
17	2	5	3	5.98	27.87	2	10	4	4.28	26.17
18	3	23	5	5.81	27.70	3	27	1	4.28	26.17
19	2	19	1	5.66	27.55	1	27	2	4.22	26.10
20	2	30	5	5.65	27.54	2	27	3	4.19	26.08

$\hat{\mu} = 21.89$ cm. Numbers in italic represent the common trees for asexual propagation and numbers in bold common trees for FOR and DBH

genetic values (\hat{g}), for FOR as well as for DBH (Tables 2 and 3), which could indicate greater possibilities of gains with the implantation of clonal seed orchards. This will of course depend on the selection accuracy of the genotypic values, on the selection intensity and the genotypic variance.

The additive effects (\hat{a}) and the genetic gain of the 12 bests parents corresponded to a selection intensity of 40% among parents (Table 4). The genetic gains with selection of the best parents varied from 25.09% to 12.48% and 18.59% to 8.33% for the traits DBH and FOR, respectively, according to the selection

intensity. In this case it is noteworthy that if the progenies and not the parents were recombined (mother plants), half the gain mentioned would be obtained. Of the 12 best parents selected for FOR (Table 4), eight participated or were represented by some individual (tree) in the individual selection (Table 2) and seven parents were common to both FOR and DBH (Table 4).

The selection predicted based on DBH provided predicted genetic gains of up to 27.26%, depending on the number of selected individuals (Table 5). Selection for DBH with the 80 best trees would select individuals belonging to

Table 4. Additive effects (\hat{a}), genetic gains (G_s) and new mean of the 12 best parents of *Pinus kesya*, 20 years old, for DBH and FOR

Trait	Order	Parent	\hat{a}	G_s	G_s (%)	Mean
DBH	1	30	5.50	5.50	25.09	27.38
	2	21	4.75	5.12	23.40	27.01
	3	19	4.57	4.94	22.53	26.82
	4	29	4.27	4.77	21.80	26.66
	5	22	3.31	4.48	20.47	26.37
	6	9	3.14	4.25	19.42	26.14
	7	10	2.44	4.00	18.23	25.88
	8	8	1.83	3.73	17.00	25.61
	9	14	0.94	3.42	15.58	25.30
	10	3	0.84	3.16	14.44	25.05
	11	24	0.75	2.94	13.44	24.83
	12	23	0.41	2.73	12.48	24.62
FOR	1	27	0.29	0.29	18.59	1.85
	2	21	0.29	0.29	18.59	1.85
	3	9	0.20	0.26	16.67	1.82
	4	23	0.11	0.22	14.10	1.78
	5	1	0.10	0.20	12.82	1.76
	6	2	0.09	0.18	11.54	1.74
	7	5	0.08	0.17	10.88	1.73
	8	8	0.08	0.16	9.62	1.71
	9	24	0.08	0.15	9.62	1.71
	10	30	0.07	0.14	8.97	1.70
	11	28	0.07	0.13	8.33	1.69
	12	19	0.06	0.13	8.33	1.69

Parents in italic are common for the traits FOR and DBH

Table 5. Genetic gains (G_s), improved population mean (M), number of selected progenies (N_f), mean number of selected trees per progeny (K_p), effective population size (N_e) and genetic diversity (D) in function of the number of selected trees (N) for the traits DBH and FOR in 20-year-old *Pinus kesya* trees

Traits	N	G_s	G_s (%)	M	N_f	N_e	D	
DBH (cm)	5	5.96	27.23	27.85	4	1.25	4.49	0.12
	10	5.41	24.72	27.30	6	1.67	7.21	0.14
	50	3.97	18.14	25.86	14	3.57	23.78	0.32
	80	3.32	15.17	25.21	20	4.00	33.59	0.42
	120	2.73	12.47	24.62	23	5.22	43.14	0.50
	150	2.35	10.74	24.24	27	5.56	51.82	0.59
FOR	5	0.29	18.59	1.85	2	2.50	3.51	0.06
	10	0.26	16.67	1.82	5	2.00	7.27	0.14
	50	0.18	11.54	1.74	14	3.57	19.49	0.24
	80	0.15	9.62	1.71	21	3.81	30.86	0.37
	120	0.13	8.33	1.69	24	5.00	44.16	0.52
	150	0.12	7.05	1.67	27	5.56	57.15	0.67

20 progenies, with a predicted genetic gain of 15.17%, a mean number of 4.00 trees selected per progeny, an effective population size of 33.59, and a genetic divergence of 0.42. The selection predicted for the trait FOR provided genetic gains between 7.05% and 18.59%. With the selection simulation of the 80 best trees for FOR, we would be selecting individuals that belonged to 21 progenies, with a predicted genetic gain of 9.62%, mean number of 3.81 trees selected per progenies, an effective population size of 30.86, and a genetic divergence of 0.37 (Table 5).

CONCLUSIONS

The evaluated *Pinus kesya* progenies presented potential for improvement in view of the high genetic variability and moderate heritability estimates for the traits FOR, DBH and HT. The accuracy of predicted genotypic values of the progenies was of high magnitude, in particular for the traits FOR and DBH, confirming the reliability of the genetic gain estimates in the progeny test. Selection targeting vegetative propagation would result in greater genetic gains than seed propagation due to the superiority of the predicted genotypic values. The predicted genetic gains with FOR-based progeny selection showed that the progeny test is extremely important for the improvement of this trait in *Pinus kesya*.

Estimativas de parâmetros genéticos e predição de valores genéticos aditivos em progênies de *Pinus kesyia*

RESUMO - O objetivo deste trabalho foi selecionar progênies de *Pinus kesyia* por meio da estimação de parâmetros genéticos pelo método de máxima verossimilhança restrita e predição de valores genéticos aditivos pela melhor predição linear não viciada. O teste de progênies de *Pinus kesyia* foi instalado em blocos casualizados, composto por 30 progênies e três repetições. Aos 20 anos foram avaliados os caracteres diâmetro à altura do peito (DAP), altura (ALT) e forma do fuste (FOR). As médias para DAP, ALT e FOR foram, respectivamente, 21,89 cm, 21,89 m e 1,56 e suas respectivas estimativas de herdabilidade média de progênies de 0,58, 0,39 e 0,66. DAP apresentou o maior coeficiente de variação genético aditiva (17,89%). A seleção das 80 melhores árvores, pertencentes a 21 progênies, proporcionou ganho de 9,62% em FOR, com média de 3,81 árvores selecionadas por progênies, tamanho efetivo populacional de 30,86 e divergência genética de 0,37.

Palavras chaves: melhoramento, seleção, ganho genético, Reml/Blup.

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