Correspondence between performance of *Eucalyptus* spp trees selected from family and clonal tests

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ABSTRACT. We examined the correspondence in performance between trees selected from a family test and their respective clones from a clonal test of *Eucalyptus*. Full-sib families were obtained from controlled pollination among individuals of *Eucalyptus grandis* and between *E. grandis* and *E. urophylla*. The hybridizations did not follow a factorial scheme. The family tests were carried out at three locations in Eunápolis and Itabela counties, in Bahia, Brazil, in 2003. Four hundred and ninety-seven high-performance trees were selected, by the individual BLUP procedure, in the family tests at two years of age, based on wood volume. The clones from these trees and 14 checks were evaluated in clonal tests carried out in the same region in 2006. The wood volume of the clones was evaluated at two years of age. Trait correlation between the trees selected from the family and clonal tests was low. The estimate of the coincidence between the best trees and the best clones using an average of the different intensities of selection was only 27%. These results demonstrate that the selection of trees in the family test should not

be too drastic; otherwise the chance plus clones may be overlooked.

Key words: Forest breeding; Clonal selection; Genetic correlation; Individual BLUP procedure; Genotypes by years interaction

INTRODUCTION

One of the greatest genetic advances known in Brazil occurred in the breeding of the genus *Eucalyptus*. It was based on mass selection followed by the vegetative propagation of plus individuals. This procedure not only allowed a marked increase in wood yield but also yielded more homogeneous cultures, which made the production of cellulose and other products much more efficient and profitable in this country (Silva and Barrichelo, 2006).

The genetic progress with clonal selection was spectacular in the beginning, mainly because the companies had at their disposal millions of plants that originated from sexual propagation and evidently had applied a strong intensity of selection. During the two subsequent decades, some strategies aimed at improving the efficacy of the process, such as extensive evaluation of new clones, were adopted, since resampling of the population had not proven to promote additional gains (Gonçalves et al., 2001). Thus, clonal selection strategies were intensified. In this context, interspecific hybridization has become the fastest and most efficient strategy to obtain genetic gain, with direct and significant reflections on the industrial process (Assis and Mafia, 2007). Several authors, such as Bison et al. (2006) and Volker et al. (2008), have reported the results of interspecific hybridization. Plus individuals are chosen out of a family test to be used in clonal tests. Some articles in the literature have reported the performance of clones compared to their families obtained through open and controlled pollination, all evaluated in the same experiment. Gaspar et al. (2005) showed that there were no significant differences between the two types of plant material (cuttings versus seedlings) for the traits examined in the study. However, an important information that is not found in the breeding programs in Brazil is the correlation in performance between the plus tree and the clone derived from it. That is because they are evaluated in different environments, mainly years. Such information is essential to guide the strategies used by breeders to improve the success rate of selection.

The objective of this study was to determine the correlation between the trees selected from a family test and their respective clones in clonal tests.

MATERIAL AND METHODS

The experimental material was provided by the Veracel S.A. Forest Company and the experiments were conducted in two phases. The first phase involved a family test implemented at three locations, and the second phase consisted of clonal tests of trees selected from the family test.

Family test

The family test was evaluated at three Veracel S.A. locations in Eunápolis and Itabela, State of Bahia, Brazil, in 2003 (Table 1). The 45 full-sib families used were obtained from controlled pollination among individuals of *Eucalyptus grandis* and between individuals of *E. grandis* and *E. urophylla*. The hybridizations did not follow the factorial scheme.

Table 1. Geographic characterization of the locations of full-sib family test and clonal tests established by the Veracel S.A. Forest Company situated in Eunápolis and Itabela counties, BA, Brazil.

Location	Latitude (S)	Longitude (W)	Precipitation (mm)	Soil texture	Relief
Family test					
A	16°20'50"	39°35'57"	1200	Medium/clay	Flatland
B	16°16'19"	39°45'45"	1000	Medium	Flatland/wavy
C	16°40'02"	39°34'55"	1300	Medium	Flatland
Clonal tests					
A'	16°41'12"	39°19'47"	1300	Sandy/medium/clay	Flatland
B'	16°45'04"	39°15'49"	1300	Sandy/clay	Flatland
C'	16°45'04"	39°15'49"	1300	Sandy/clay	Flatland

The experiments were carried out using a randomized complete block design with four replications, six plants per plot, and spacing of 3 x 3 m. Three commercial clones of the company were used as controls. The silvicultural management used was the same as that followed in the commercial stands.

In 2005, when the plants were two years old, the wood volume in cubic meters of all individuals from the three locations was estimated by the expression:

$$V = 0.42 \frac{\pi DBH^2}{40,000} H \qquad \text{(Equation 1)}$$

where V is the wood volume in cubic meters; DBH is the breast height diameter in centimeters; H is the height in meters, and 0.42 is the average shape factor of the tree, which converts the cylindrical volume into real volume.

The genetic evaluation of the family test was performed by using the mixed model methodology: REML/BLUP - restricted maximum likelihood/best linear unbiased prediction (Patterson and Thompson, 1971; Henderson, 1975). For this purpose, the SELEGEN software, a computer program for genetic selection in the breeding of perennial species (Resende, 2007), was used. The analyses were performed according to the following statistical model: $y = Xr + Zg + Wp + e$, where y is a vector of data, r is a vector of fixed effects of repetition added to the general average; g is a vector of random effects of individual genotypic $g \sim N(0, \sigma^2_g)$; p is a vector of random effects of plot $p \sim N(0, \sigma^2_p)$, and e is a vector of random effects of errors or residues. The capital letters represent the matrix of incidence for the referred effects.

In the joint analysis the statistical pattern was: $y = Xr' + Zg + Wp + Ti + e$, in which r' is a vector of fixed effects of combination repetition-local added to the general average, and i is a vector of random effects of genotypes by interaction of locations. The letter T represents the matrix of incidence for the referred effect. The other components are identical to the previous model.

Through these analyses, the components of variance for site by site and across sites were estimated and the genotypic values of the individuals were predicted. Using the individual BLUP procedure, 497 best performing trees in the family test were selected, where 105 trees were selected at location A of the family test, 204 trees at location B, and 188 trees at location C.

Clonal tests

The three clonal tests were carried out in the same counties as the family test, in 2006

(Table 1). A randomized complete block design was used, with 20 replications, single tree plot, each plant occupying an area of 7.5 m². Fourteen commercial clones from the company were used as controls. The silvicultural management used was identical to that used in commercial stands.

The wood volume, in cubic meters, was evaluated at the age of two years in the clonal tests. The evaluations were also performed using the SELEGEN computational program (Resende, 2007). The analyses were carried out considering the following statistical model: $y = Xr + Zg + e$, where y is a vector of data; r is a vector of fixed data of repetition added to general average; g is a vector of random genotypic effects, and e is a vector of random effects of errors or residues. The capital letters represent the matrix of incidence for the referred effects.

Correspondence between performance of selected trees from family and clonal tests

The correspondence between performance of selected trees from family and clonal tests was evaluated by two strategies:

a) Estimate of the genetic correlation between performance of selected trees from the family test and their respective clones in the clonal tests, according to an estimator presented by Bernardo (2002):

$$ r_{g_{tc}} = \frac{COV_{g_{tc}}}{\sqrt{\sigma^2_{g_t} \sigma^2_{g_c}}} \qquad \text{(Equation 2)} $$

where $COV_{g_{tc}}$ is the genetic covariance between performances of selected trees from the family test and their respective clones; $\sigma^2_{g_t}$ is the genetic variance obtained from REML/BLUP of trees selected in the family test, and $\sigma^2_{g_c}$ is the genetic variance obtained from REML/BLUP of the clones in the clonal test, without checks.

Estimate of the genetic correlation between performance of selected trees from the family test and their respective clones in the clonal tests, according to an estimator presented by Notter and Diaz (1993):

$$ r_{g_{ND}} = \frac{r_{g_{tc}}}{a_t . a_c} \qquad \text{(Equation 3)} $$

where $r_{g_{tc}}$ is the genetic correlation between performance of selected trees from the family test and their respective clones in the clonal tests, according to an estimator presented by Bernardo (2002); a_t is the accuracy of trees selected from the family test obtained from REML/BLUP, and a_c is the accuracy of the clones in the clonal test obtained from REML/BLUP, without checks.

b) Estimates of the coincidence index, that is, the proportion of superior and inferior trees in the family test with the same behavior in the clonal test, disregarding the chance of effect. The selection intensities of 5, 10, 15, 20, and 25% were considered for the analyses. For this purpose, the Hamblin and Zimmermann (1986) expression was used:

$$CI = \frac{X - Y}{Z - Y} * 100 \qquad \text{(Equation 4)}$$

where X is the number of selected trees or clones, common to both environments; Y is the number of randomly selected trees or clones in both environments, estimates considering selection intensity of the value X (Hamblin and Zimmermann, 1986), and Z is the number of selected trees and clones in one of the environments.

RESULTS

The average performance of the families, in volume, varied between the field trials. Location C showed the best performance, with 63.60% higher average volume than in location B, which recorded the lowest growth (Table 2). Significant effect of the families in the site by site as well as in the multi-site analyses was observed (data not shown). The estimates of the selective accuracy were all higher than 86%, indicating a good experimental precision in the evaluation of the experiments.

Table 2. Estimates of genetic parameters for wood volume (m³/plant x 10⁶) per experiment and for the joint analysis, obtained from the evaluation of full-sib families.

Parameter	Locations			Joint analysis
	A	B	C	
Genetic variance between full-sib families	204.00	79.00	351.00	190.00
Phenotypic variance within the plot	1,197.00	496.00	1,383.00	1,032.00
Genetic variance within the plot	833.00	339.00	1,113.00	768.00
Environment variance within the plot	364.00	157.00	270.00	264.00
Heritability of the family average	77.63	75.65	82.81	-
	(61.92-85.97)*	(58.34-85.03)*	(69.90-89.47)*	
Variance of the interaction between families and locations	-	-	-	25.00
Accuracy (%)	88.10	86.97	91.00	91.19
Average	0.0743	0.0492	0.0805	0.0672

*Confidence interval of heritability of the family average estimated according to Knapp et al. (1985).

The estimates of the variance components in the family test are presented in Table 2. It can be noticed that the highest estimate of genetic variance between families was obtained at location C and the lowest at location B. The estimate of the variance component within families was superior to the genetic variance obtained between the families (Table 2). The estimate of variance for the interaction families x locations was of low magnitude, corresponding to only 14% of the genetic variance between families (Table 2). The estimates of genetic correlations between performances in families from several locations, two by two, had a higher magnitude. The genetic correlation between locations A and B was 1.00, between locations A and C, 0.97, and between B and C, 0.83. The estimated heritability for selection based on means of full-sib families varied from 75.65 to 82.81%, and the estimates of the confidence intervals showed that they are different from zero, at 95% probability (Table 2).

In the clonal evaluation of the trees selected from the previous stage, it was observed that the average performance of the clones was similar in the experiments (Table 3). Significant effects of clones were observed (data not shown) according to the likelihood ratio test ($P \leq 0.01$). The estimates of mean of clonal heritability were greater than 74%, all being different from zero, at 95% probability. These results are concordant with the high magnitudes of accuracy.

Table 3. Estimates of genetic parameters for wood volume (m^3/plant x 10^6) per location, obtained in the evaluation of clonal tests.

Parameter	Locations		
	A'	B'	C'
Genetic variance between clones	429.00	395.00	390.00
Residual variance	340.00	265.00	270.00
Heritability for the clonal selection	96.18	74.90	74.27
	(94.88-97.06)*	(69.15-79.18)*	(68.16-78.83)*
Accuracy (%)	98.07	86.54	86.18
Average	0.0711	0.0609	0.0626

*Confidence interval of heritability for the clonal selection estimated according to Knapp et al. (1985).

The estimate of genetic correlation between the value of the tree in the family test and the average of the clone originating from it were low and varied from test to test (Table 4). In clonal test A, where 105 clones were evaluated, the estimate of correlation was zero. The estimates of genetic correlation obtained from the expression of Notter and Diaz (1993) were higher, as expected, although still of low magnitude.

Table 4. Estimates of genetic parameters for volume (m^3/plant x 10^6).

Parameter	Tests		
	A/A'	B/B'	C/C'
Genetic covariance between trees selected from the family test and their clones	0.00	29.50	66.00
Genetic variance of trees selected in family test	3.00	36.00	90.00
Genetic variance of the clones in the clonal test	429.00	395.00	390.00
Accuracy of trees selected from the family test	21.65	88.75	87.90
Accuracy of the clones in the clonal test	98.05	86.55	86.20
Genetic correlation[1]	0.0000	0.2475	0.3525
Genetic correlation[2]	0.0000	0.3220	0.4650

[1]Genetic correlation between performance of trees selected from the family test and their respective clones in the clonal tests according to an estimator presented by Bernardo (2002). [2]Genetic correlation between performance of trees selected from the family test and their respective clones in the clonal tests according to an estimator presented by Notter and Diaz (1993).

Another procedure used to evaluate the efficiency of the selection of trees was estimating the coincidence index (Table 5). It was observed that all the indices were low, especially when the worst clones were considered to be in the selection, when 5, 10, or 15% of selection intensity was applied. The coincidence index increased with increase in number of selected clones.

Table 5. Estimates of coincidence index (CI) in the classification of the best or worst trees from family test and from clonal test, using different selection intensities.

	Selection intensities					
	5%	10%	15%	20%	25%	Average
Best	22.70	23.80	22.20	31.80	34.30	27.00
Worst	0.00	9.50	14.30	17.70	29.50	14.20

Data are reported as CI in percent.

DISCUSSION

The average wood volume of the families varied between the locations (Table 2). Considering that the soil fertility did not differ between the locations, this difference probably occurred due to the differences in the average annual precipitation between them (Table 1).

The good association between the performance of the families at the different locations is a consequence of the elevated magnitude of the genetic correlation estimates between family performances in the various locations, and it proves to be the absence of the interaction between families and locations. The interaction *Eucalyptus* families x locations, in experiments conducted at experimental areas of the companies in Brazil, is not very expressive according to Mori et al. (1988), Santos et al. (1990), Pereira et al. (1997), and Nunes et al. (2002). In other countries, the contribution of the interaction families x locations seems to be more pronounced (MacDonald et al., 1997; Costa e Silva et al., 2006).

The estimated heritability for selection based on means of full-sib families was high (Table 2). The majority of the estimates of the available heritability in Brazil were mainly obtained with half-sib families that explore only ¼ additive variance ($1/4\sigma^2_A$). When full-sib families are used, as in this study, $1/2\sigma^2_A + 1/4\sigma^2_D$ is explored. At this point, it is necessary to emphasize that there are not many available estimates of the dominance variance (σ^2_D) for volume in the genus *Eucalyptus*. There are reports that it could be expressive (Bouvet et al., 2009), and there are other findings that it is not expressive as in the case of *E. globulus* in Europe. In Brazil, reports of Bison et al. (2006) show that there is dominance for wood volume, but not of great magnitude. In spite of its low significance, it will contribute to the increase in heritability estimates. Nevertheless, it should be emphasized that these estimates are more useful in recurrent selection programs. In this research, all genetic variance is explored.

Considering the trials with clonal tests, the similarity in the average performance in volume (Table 3) can be related to the fact that they were located geographically very close to each other and hence had similar climate and soil fertility conditions, as well as similar latitude, that is, similar environmental conditions (Table 1). It was observed that variability among the clones occurred, which demonstrates the possibility of gains with the selection. The high heritability estimates in clones provide a very favorable condition for selection (Table 3).

What is of great interest in this research is the degree of association between the trees selected from the family test and from their respective clones. Genetic correlations between the performance of the tree in the family test and the clone derived from it were very low. Confirming these results, the coincidence index estimate between the best trees in the family test and their clones, in the average of different selection intensity, was only 27%. As the accuracy in the experiments by local was high, the estimate of correlation by expressions from Bernardo (2002) and Notter and Diaz (1993) was similar (Table 4).

In a study carried out in Europe with *E. globulus*, Gaspar et al. (2005) noticed that the performance of clones and their family, evaluated in the same experiment, was similar. On the other hand, the simulation of Borralho and Kanowski (1994) showed that the correlation between seedlings and propagules taken from them is expected to be of low magnitude. Even though the situation of the present study is not exactly the same, it is possible to infer that the low estimate of the genetic association between the elite trees and clone performance should be attributed to the interaction of genotypes x years. By confirming the presence of a marked interaction between genotypes and years, the option would be to make a less drastic selection

of the trees in the family test to increase the chance of identifying truly plus clones.

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