Assessment of the Early Selection Efficiency in *Eucalyptus cloeziana* F. Muell. in the Northwest of Minas Gerais State (Brazil)

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Abstract

Three hundred and seventeen half-sib progenies of *Eucalyptus cloeziana* F. Muell. of 8 different origins in the northwest of the state of Minas Gerais, Brazil were assessed for early selection efficiency. The experiment was carried out in the county of Bocaiuva in 1987, using the compact progenies block design with 10 replications and 6 plants per plot. The stem diameter at breast height (DBH) was taken at 29, 42, 56, 67 and 80 months of plant age. The estimates of the genetic and phenotypic parameters for the DBH trait were obtained for each age and for the combination of ages. The trait genetic correlations at the different ages and the correlated response to selection were also estimated. The methodologies used in the assessment of the early selection efficiency demonstrated that this strategy should be used in *Eucalyptus* breeding. The selection done at the age of 29 months proved to be more efficient, propitiating a superior gain per unit of time, compared to any other of the selection strategies.

Key words: Eucalyptus breeding, *Eucalyptus cloeziana,* early selection, half-sib families, interaction, recurrent selection, genetic gain, genetic parameters, quantitative genetic, compact family blocks.

FDC: 232.11; 232.12; 165.62; 165.4; 176.1 *Eucalyptus cloeziana;* (81).

Introduction

The majority of economically important traits in forestry breeding, such as wood volume and basic density, are controlled by many loci. The breeder has to increase the frequency of the favorable alleles in these loci to improve the phenotypic expression of the trait. As it is practically impossible to increase the frequency of the favorable alleles in a single round of selection, repeated cycles of selection, named recurrent selection, must be carried out (Hallauer, 1992).

The use of recurrent selection in forestry breeding, such as in the case of the *Eucalyptus,* is limited mainly because of the length of each selection cycle. In temperate species, each selection cycle may require about 10 years for assessment and recombination.

In Brazil, the plant life is approximately seven years, but the length of each cycle of selection is still considerable. The alternative is to carry out early selection, assessing progenies or individuals at the youngest possible stage. This strategy has been the objective of much research in several countries, which show early selection to be possible (Wakeley, 1971; Borralho, 1991; Rezende, Bertolucci and Ramalho, 1995; Franklin, 1979; Mohrdiek, 1979; Magnussen, 1988; Rehfeldt, 1992).

This study was carried out to check the efficiency of early selection in *Eucalyptus* aiming forward breeding, using the data from a series of assessments in 1 half-sib progeny trial of *E. cloeziana* carried out in northwest Minas Gerais (Brazil).

Materials and Methods

The genetic materials used in the experiment were 317 progenies coming from free pollination (half sib) of *E. cloeziana* trees from 8 different provenances in Australia and introduced by Mannesmann Fi-El Florestal Ltda.(MAFLA) (*Table 1*).

Table 1. – Geographical location in Australien of the origins and number of progenies taking part in the experiment.

Origin	Latitude	Longitude	Altitude	Number of progenies
Ravenshoe	17°40'-17°41'S	145°29'E	900	51
Cardwell	18°18'S	146°01'E	130-180	56
Blackdown	23°49'S	149°01'E	725	36
Helenvale	15°45'S	145°14'E	170-230	50
Monto	24°56'S	151°00'E	500	24
Gympie	26°10'S	152°56'E	100	50
Herberton "A"	17°33'-17°35'S	145°18'E	700	25
Herberton "B"	17°21'S	144°51'E	800-1400	25

The experiment was carried out in the northwest of the state of Minas Gerais (Brazil), region located at 17°20'S latitude, 43°20'W longitude and 850 m altitude. The annual temperature varies from 11 °C to 35 °C and the pluvial precipitation since the set up of the experiment oscillated between 562.5 mm and 1648.7 mm, averaging 1010.2 mm. The winter presents from 4 to 6 dry months, with an average water deficiency of 192 mm. The soil analysis on the sight of the experiment presented the following results: 13% sand, 11.1% silt and 75.9% clay; 0,26 meq/cm^3 Ca^{++} soil; 0.31 meq/100cm^3 Mg^{++} soil; 1.37 meq/cm^3 Al^{+++} soil; 24 ppm K; 1.0 ppm P and pH 4.3.

The experimental design used was the compact family blocks with 10 replications. The plots consisted of one line with 6 plants. The spacing adopted were 2.0 m between plants in one line, and 3.0 m between lines. The fertilization used was 100 g of 08-28-06 formula NPK per plant and 150 kg/ha of natural phosphate.

The measurements of the diameter at breast height (DBH) were taken using a measuring tape at the following ages: 29 months (May of 1990); 42 months (June of 1991); 56 months (August of 1992); 67 months (July of 1993) and 80 months (August of 1994).

Without considering the provenances variance analysis of the diameter at breast height (DBH) were done for each age considering only the general average as fixed effect and adopting the following statistical model:

$$Y_{ijk} = m + b_j + f_i + e_{(ij)} + d_{(ijk)}$$

in which Y_{ijk} is the observation of the k plant in the i family in the j block; m is the general average; b_j is the block effect; f_i is the i family effect; $e_{(ij)}$ is the experimental error; $d_{(ijk)}$ is the average effect among plants within the plots associated to the k individual of the i family in the j block.

The estimates of the genetic and phenotypic parameters for each age were obtained from the expected mean squares of the variance analysis using a procedure similar to the one presented by Hallauer and Miranda Filho (1983). For the estimation

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of the narrow sense heritability at individual level (h^2_w) the following expression was used:

$$h^2_w = \frac{4\sigma^2_{pw}}{\sigma^2_{dw} + \sigma^2_{ew} + \sigma^2_{pw}},$$

in which σ^2_{pw} is the half sib progeny variance at w age; σ^2_{dw} is the phenotypic variance within the plots at w age; and σ^2_{ew} is the environmental variance among the plots at w age.

For the variance analysis involving the different ages, the following statistical model was adopted, considering every effect as random except for the average and age:

$$Y_{ijkw} = m + b_j + f_i + (fb)_{ij} + a_w + (ab)_{jw} + (fa)_{iw} + e_{(ijw)} + d_{(ijkw)},$$

in which Y_{ijkw} is the observation of the k plant in the i family at w age in the j block; m is the general average; b_j is the j block effect; f_i is the i family effect; $(fb)_{ij}$ is the effect of the interaction of i family with j block; a_w is the w age effect; $(ab)_{jw}$ is the effect of the interaction of w age with j block; $(fa)_{iw}$ is the effect of the interaction of i family with w age; $e_{(ijw)}$ is the effect of the experimental error associated with the i family at w age in the j block; and $d_{(ijkw)}$ is the average effect among plants within the plots, associated with the k individual in the i family at w age in the j block.

The genetic correlation ($r_{ww'}$) among the average performance of the materials at different evaluation ages was estimated by the expression:

$$r_{ww'} = \frac{COV_{ww'}}{\sqrt{\sigma^2_{pw}\sigma^2_{pw'}}};$$

in which $COV_{ww'}$ is the genetic family averages at ages w and w'; σ^2_{pw} $\sigma^2_{pw'}$ is the genetic variance among the half sib progenies at ages w and w', respectively.

The breakdown of the component of the progeny x age interaction(σ^2_{pa}) into simple and complex parts was based on the expression proposed by ROBERTSON (1959) and adapted by CRUZ and CASTOLDI (1991) for the cases in which the genetic correlation is superior to 0.8, as it happened in this work, by the expression:

$$\sigma^2_{pa_{ww'}} = 0{,}5(\sigma_{P_w} - \sigma_{P_{w'}})^2 + q\sigma_{P_w}\sigma_{P_{w'}} + [(1 - r_{ww'})^3\sigma^2_{P_w}\sigma^2_{P_{w'}}]^{1/2},$$

in which $q = 1 - r_{ww'} - [(1 - r_{ww'})^3]^{1/2}$. The first part of the interaction component, $0{,}5(\sigma_{Pw} - \sigma_{Pw'})^2 + q\sigma_{Pw}\sigma_{Pw'}$, corresponds to the simple part which does not cause great problems in the selection. The remainder is denominated complex, occurring due to the lack of correlation.

Results and Discussions

Highly significant differences ($P \leq 0.01$) occurred among the families at all evaluated ages (*Table 2*). The estimates of the genetic variance (σ^2_{pw}) stand out, in which a substantial increase in the values along the ages is verified. At first, it could be inferred an increase in the genetic variability with age. However, when the estimates of the genetic variation coefficient (CV_g) are used, it is apparent that, in relation to the average, the variation even tended to reduce with age. That way, it is evident that the σ^2_{pw} estimate values should be looked at with reservation since they are influenced by the magnitude of the data.

This last observation is corroborated by the heritability estimates (h^2_w). It is noticed that the values at different ages are very similar and the small existing variation could be attributed to the error associated to these estimates. Both the σ^2_{pw} and h^2_w values allow to foresee success with the selection.

Table 2. – Summary of analysis of variance at individual level and estimates of the genetic and phenotypic parameters for diameter.

Age	Mean(s.d)	MS prog	MS error	σ^2_{Pw}	CV_g(%)	h^2_w(%)
29	5.3	28.72**	3.22	0.54	14.0	40.85
42	7.4	42.61**	5.02	0.77	12.0	35.69
56	9.2	51.48**	6.75	0.93	10.0	31.32
67	10.1	57.22**	7.71	1.04	10.0	30.52
80	11.3	64.27**	8.16	1.24	10.0	33.73

**) Significant at the 1% level of probability by the F test.

Table 3. – Summary of the variance analysis involving the different ages from evaluation of the trees.

Source of Variation	MS	F	Prob.
Progenies	49.12	9.13	< 0.01
Age	17651.87	5191.73	< 0.01
Progenies x Age	0.98	3.38	< 0.01
Residual	0.29		

Table 4. – Partitioning the variance component family x age interaction obtained from the analysis of the 2 age sets.

Estimates	Age (months)			
	29/80	42/80	56/80	67/80
σ^2_p	0.7215	0.9253	1.0303	1.1110
σ^2_{pa}	0.1691	0.0826	0.0554	0.0306
σ^2_{pa}/σ^2_p(%)	23.44	8.93	5.38	2.75
Simple interaction (S)	0.1361	0.0697	0.0465	0.0266
Complex interaction (C)	0.0330	0.0129	0.0089	0.0040
C/σ^2_{pa}(%)	19.52	15.62	16.06	13.07
$r_{ww'}$	0.88	0.94	0.96	0.98

$r_{ww'}$: genetic correlation

Significant differences ($P \leq 0.01$) were detected for every variation source in the variance analysis involving the different ages (*Table 3*). Considering the fact that the greatest interest is the possible interaction between the families precociously evaluated and families evaluated at harvest time, joint analysis of variance were done, considering in each the harvest age (80 months) and one of the other ages (*Table 4*). It is observed that the σ^2_{pw} tended to increase when the analysis considered ages closer to the rotation ages, while the component of the families x ages (σ^2_{pa}) interaction presented an inverse behavior. However, the σ^2_{pa}/σ^2_p relation always presented little expressive values and, when σ^2_{pa} was broken down, the simple part of the interaction was always responsible for more than 80% of the σ^2_{pa}. This fact indicates that the interaction occurred due to a difference in the genetic manifestation of the families along the ages and not to different ranking of the

Table 5. – Estimates of the expected gain from selection at 80 months and correlated responses.

Selection (months)	Estimated gain(%)	Selection cycle(years)	Yearly gain(%)	Early selection relative efficiency
29/80	11.5(14.4)[1]	4.5	2.6(3.2)	168 (168)
42/80	12.3(15.4)	5.5	2.2(2.8)	147 (147)
56/80	12.4(15.5)	6.5	1.9(2.4)	126 (125)
67/80	12.6(15.8)	7.5	1.7(2.1)	111 (110)
80/80	13.0(16.2)	8.5	1.5(1.9)	100 (100)

1) Values inside and outside the parenthesis correspond to selection pressures of 10% and 20%, respectively.

materials. This observation was reinforced by high and positive values of the genetic correlation ($r_{ww'}$) of the average performance of the progenies at juvenile age and at the harvest time.

Aiming to clarify what occurs with genetic gain when the selection is applied in more precocious ages, the correlated response with the selection was estimated (*Table 5*). It is verified that the differences in value of the estimates of the correlated response with the selection were small at different ages. They also differed very little from the estimate of gain at harvest time itself. If the focus is estimating the gain per unit of time, which is more expressive, the superiority of the correlated response with the selection in relation to the selection done at the rotation age is verified. This difference was more accentuated as the selection age was reduced. Under these circumstances, the selection at 29 months would be recommended. It presented a gain superior to the selection done at 80 months.

Conclusions

– The methodologies used in the assessment of the early selection efficiency show that this strategy should be used in *Eucalyptus* breeding;

– The selection taking place at the age of 29 months proved to be more efficient, resulting in gains per unit of time superior to any of the other selection strategies.

References

BORRALHO, N. M. G.: Genetic improvement of *Eucalyptus globulus* LABILL. ssp. *globulus* for pulp production. Wolfson College, Oxford. 221 p. Thesis – Doctor in – Philosophy (1991). — CRUZ, O. D. and CASTOLDI, F. L.: Decomposição da interação genótipos x ambientes em parte simples e complexa. Revista Ceres, Viçosa, **38** (219), 422–430, set./out. (1991). — FRANKLIN, E. C.: Model relating levels of genetic variance to stand development of four North America conifers. Silvae Genetica **28** (5–6), 207–212 (1979). — HALLAUER, A. R.: Recurrent selection in maize. Advance in Agronomy, 115–179 (1992). — HALLAUER, A. R. and MIRANDA FILHO, J. B.: Quantitative genetics in maize breeding. Iowa State University Press, Ames. 468 p. (1983). — MAGNUSSEN, S.: Minimum age-to-age correlations in early selections. Forest Science **34** (4), 928–938 (1988). — MOHRDIEK, D.: Juvenile-mature correlations in some Aspen and Poplar trials. Silvae Genetica **28** (2–3), 107–111 (1979). — REHFELDT, G. E.: Early selection in *Pinus ponderosa:* compromises between growth potential e growth rhythm in developing breeding strategies. Forest Science **38** (3), 661–677 (1992). — REZENDE, G. D. S. P., BERTOLUCCI, F. DE L. G. and RAMALHO, M. A. P.: Eficiência da seleção precoce na recomendação de clones de eucalipto avaliados no norte do Espírito Santo e sul da Bahia. Revista Ceres **1** (1), 1995 (in press). — ROBERTSON, A.: Experimental design on the measurement of heritabilities and genetic correlations. Pergamon Press, New York. 186 p. (1959). — WAKELEY, P. C.: Relation of thirtieth-year to earlier dimensions of southern pines. Forest Science **17** (2), 200–209 (1971).

A Multivariate Study on Genetic Variation in Teak (*Tectona grandis* (L.))

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Abstract

Genetic differentiation between populations of teak (*Tectona grandis* (L.)) was examined in 9 quantitative characters and 10 allozyme loci. Large differences between populations were revealed in the quantitative traits. Regional patterns were revealed by multivariate analysis of the data, but there were also substantial variation within ecological-geographical defined regions. The differentiation between provenances from Laos were found to be less than the variation within Thailand, West India and Indonesia. A much less pronounced differentiation between populations was found in allozyme markers. The fixation index (F_{ST}) was only 4%, and no clear geographical pattern was found in the allozyme data. However, some differences were found in the level of diversity. An assignment procedure based on allozyme markers did not prove efficient in differentiating between populations, but this was probably a result of the low F_{ST} value.

The larger differentiation between populations in morphological traits than in allozyme markers is probably a result of adaptation through natural selection and, possibly, a higher mutation rate in quantitative traits than in allozyme loci. Similar result have been found in other studies of forest trees.

Key words: Tectona grandis, provenance variation, multivariate analysis of variance, allozymes, genetic diversity.

FDC: 165.3; 165.5; 232.12; 176.1 *Tectona grandis;* (593).

1. Introduction

Teak (*Tectona grandis* (L.)) is a tree species grown in many tropical regions due to its valuable timber. It has a large natural distribution area in south east Asia, covering geographically isolated regions in India, Myanmar (formerly Burma), Thailand and Laos (KAOSA-ARD, 1981). It is found naturally in moist and dry mixed, deciduous forests below 1000 m in elevation. It grows naturalized in parts of Indonesia

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