Recurring Selection Strategies in Species of *Eucalyptus maculata* and *Eucalyptus torelliana*

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Abstract

The genetic breeding of *Eucalyptus* species from the subgenus *Blakella*, especially *E. maculata* and *E. torelliana*, is on the rise in Brazil. These species stand out for the quality of their wood and the possibility of taking advantage of the heterosis between them; however, they are still at the beginning of domestication. From the above, this study aims to: estimate genetic and phenotypic parameters; use this information to compare alternatives that can improve selection efficiency in progeny tests; and verify the viability of selecting the best individuals from each progeny in several locations. For this, DBH (cm) data were used from *E. maculata* progeny evaluation experiments conducted in two sites and *E. torelliana* in three sites, at six years of age, with 40 repetitions and of single-tree-plot. It was found that, for both species, the expected gain from selection was significant in all sites. In combined selection, the intensity of selection among the progenies was very mild (a large number of progenies being selected), even considering that the heritability on mean among the progenies was much higher than that obtained among individuals. The number of individuals selected per progeny was very different. This fact can reduce the effectiveness of recurrent selection in the medium term. Using clones as common controls is viable for selecting a single improved population based on the evaluation of progenies in more than one site.

Keywords: *quantitative genetics, genus Corymbia, plant breeding, experimentation.*

Introduction

Eucalyptus genetic breeding programs in Brazil began just over fifty years ago, a relatively short time considering a perennial species. The greatest gains in productivity occurred in obtaining improved populations, especially of the species *E. grandis*, *E. urophylla* and their hybrids, together with clonal selection and improved management (Castro et al., 2016). *Eucalyptus* wood productivity increased from $10 m^3.ha^{-1}.year^{-1}$ in 1970 to $38.9 m^3.ha^{-1}.year^{-1}$ in 2021 (Ibá, 2023). However, the migration of eucalyptus cultivation to new areas, especially in agricultural frontier regions, together with the occurrence of biotic and abiotic stresses and the improvement in industrial exploitation, made it necessary to continually search for gains in productivity and wood quality, which is a huge challenge.

Recently, the genus *Eucalyptus* was reclassified, some species previously considered to be in the genus *Corymbia* now belong to the genus *Eucalyptus* (Nicolle, 2024). In this new classification, there is the subgenus *Blakella*, and in this group are the species previously called *C. maculata* and *C. torelliana*, which are currently classified as Synonyms *Eucalyptus maculata* and *Eucalyptus torelliana*.

Hybrids between *E. maculata* and *E. torelliana* are promising due to the quality of the wood and are an option to replace hybrids derived from *E. grandis* and *E. urophylla* (Assis, 2022). The selection of plants within the species *E. maculata* and *E. torelliana*, however, is fundamental for future selections of hybrids between these two species, as the performance of hybrid individuals is a function of the mean performance per se of the parents and not just the heterosis between them (Hallauer et al., 2010).

In a condition like this, conducting intrapopulacional recurrent selection (RS) cycles is essential to increase the mean of the population, especially for traits of economic importance controlled by many genes. Among them, the diameter at

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breast height (DBH) and the height (H) of the trees stand out, which directly contribute to the mean annual increase in wood (MAI). Recurrent selection has been used in Brazil for a few decades, initially with mass selection and, later, with progenies, predominantly open-pollinated progenies, which makes the selection process easier, mainly because it does not require artificial pollinations. When some self-pollination events occur mixed with cross-pollination events, there is a greater release of genetic variability among and within families, which can influence the components of genetic variance (Rezende, 2015). However, predicting the increase in genetic variance and other components is difficult, as the percentage of self-pollination is unpredictable. Thus, although a certain rate of self-pollination always occurs in open pollination, as mentioned, for practical purposes, this type of strategy has been referred to as RS with half-sib (HS) progenies, and it has been widely used over time in the cultivation of eucalyptus in Brazil and worldwide. Although there was a success with the selection, as already mentioned, there is a need to improve the efficiency of the process. As experimental data is available with the evaluation of *E. maculata* and *E. torelliana* progenies, it would be important to estimate phenotypic and genetic parameters. From these estimates, it is possible to obtain the expected genetic progress with selection and make inferences on how to improve the efficiency of the process.

One of the strategies used, aiming above all to increase the heritability for selection on the mean of the progenies, is the use of experimental plots with only one plant, making it possible to increase the number of repetitions in each experiment (Stanger et al., 2012; Souza et al., 2024). However, the adoption of single-tree-plot (STP) in progeny evaluation experiments could it be questioned regarding the procedure for estimating genetic gain among plants of the same progeny or in combined selection. This occurs because, using STP, part of the genetic variation among plants is isolated by the source of variation blocks/repetitions, depending on the design used. For example, with HS progenies, ¾ of the additive variance (σ_A^2) and all the dominance variance (σ_D^2) occur among plants (Hallauer et al., 2010; Resende, 2015). This fact makes it difficult to obtain reliable of GS. Unfortunately, this information has been little explored in the literature.

Analyzes of experimental data have been carried out predominantly using mixed models due to data imbalance, caused by the death of some plants and other situations. In this condition, a selection index has been obtained that considers the merit of progenies and individuals within progenies, as already mentioned, called combined selection (Resende, 2015), replacing selection among progenies and, later, selection within progenies, as originally proposed, especially for corn crops (Hallauer et al., 2010). Combined selection has been considered the best option in the case of eucalyptus (Martins et al., 2005; Resende, 2015). However, a more careful analysis of your employment requires more intense reflection.

Progeny evaluation experiments are conducted in different environments. However, what is normally intended is to obtain only an improved population for a wider region. In this case, how to identify superior individuals, remembering that each individual is unique to each site, to obtain only an improved population after recombination? Unfortunately, there are few reports addressing this issue in eucalyptus cultivation in Brazil.

In recent decades, as already mentioned, there has been a predominance of the use of HS progenies in eucalyptus cultivation. Although this type of progeny is easy to obtain, it presents problems, especially at the time of recombination, which can reduce its efficiency (Ramalho et al., 2023). Especially with species that are at the beginning of breeding in Brazil, efforts should be made to discuss progeny alternatives that can be used and that enable the application of a greater selection intensity and more efficient recombination.

From the above, using data from experiments evaluating HS progenies of the species *E. maculata* and *E. torelliana*, conducted in some sites, this research was carried out with the following objectives: estimate genetic and phenotypic parameters; use this information to obtain alternatives that enable estimates of SG selection within the progenies when experiments are conducted using single-tree-plot; verify the viability of selecting a single improved population, for a wide region, based on the selection of the best individuals from each progeny evaluated in different sites; and discuss alternatives to increase the efficiency of RS using the species mentioned.

Material and Methods

The data used refers to the evaluation of progenies of *E. maculata* and *E. torelliana* and commercial clones of other eucalyptus species, by the company Suzano S.A. Five experiments were implemented in 2014, in Brazil, in the states of Bahia and Espírito Santo, differing in environmental characteristics, with a varied number of progenies and check clones (common clones) (Table 1).

The experiments were implemented in an alpha-lattice design. Each plot consisted of a single-tree-plot (STP) with 40 repetitions. The diameter at breast height (DBH) was measured in centimeters, six years after planting. DBH data were subjected to analysis using linear mixed models. As the lattice efficiency was low, it was decided to carry out the analyses in randomized blocks. The statistical model used was: $y = Xb + Zp + e$; where: y is a vector of observations for individual trees, b is a vector of fixed effects (mean + repetition), p is a vector of random effects related to progenies and clones, and e is a vector of random residuals. X and Z are incidence matrices that relate observations in y with effects in b and p, respectively.

Joint analyses of experiments of the same species involving common progenies and checks were carried out, using the same model already mentioned, adding the effect of sites and the interaction of progenies *x* sites. The variance components estimation method via REML (Restricted Maximum Likelihood) was used (Resende, 2015).

To carry out selection to obtain only one improved population for all sites and not one population for each site, the DBHs of

Table 1
Characterization of environments, spacing, number of treatments (NT), progenies (NP), and species at each site.

Trial	PMA (mm)	Altitude (m)	Soil type	Spacing (m)	NT	NP	Species
EM1	1187	72	Argisol	3x3	68	62	*E. maculata*
ET1	1188	73	Argisol	3x3	62	57	*E. torelliana*
ET2	944	82	Argisol	3x2.5	62	57	*E. torelliana*
ET3	1159	25	Latosol	3x2	62	57	*E. torelliana*
EM2	1159	24	Latosol	3x2	68	62	*E. maculata*

EM1 and EM2 are *E. maculata* experiments conducted in two sites (Bahia and Espírito Santo); ET1, ET2, and ET3 are E. torelliana experiments conducted at three sites (ET1 in Bahia and ET2 and ET3 in Espírito Santo) and PMA is the mean annual precipitation in millimeters.

each individual were adjusted independently for each species using the mean of the checks (common clones).
The adjusted data were again analyzed, using the same model previously considered for the unadjusted data. All analyses were performed using R Core Team software (2023). From the variances obtained, the following genetic or phenotypic parameters were estimated for each of the species studied:

a) Phenotypic variance among plants within progenies (σ^2_{dk}). In this case, for each site (k), the variance among plants of the same progeny was estimated. The mean of the variances of the evaluated progenies constitutes σ^2_{dk}.

b) Additive genetic variance by site (σ^2_{Ak}). This estimate was obtained from the genetic variance among progenies (σ^2_{pk}) multiplied by four, as progenies of half-sibs were evaluated, which exploits of the additive variance.

c) Accuracy $r_{\hat{g}g}$:

$$r_{\hat{g}g} = \sqrt{1 - \frac{\text{PEV}}{\sigma^2_{pk}}}$$

Where PEV is the variance of the prediction error of genetic values.

d) The heritability for selection on the mean of HS progenies for each site (h^2_{mk});

$$h^2_{mk} = r^2_{\hat{g}g}$$

e) Heritability for selection among individuals within progenies by site (h^2_{dk});

$$h^2_{dk} = \frac{(3/4)\sigma^2_{Ak}}{\sigma^2_{dk}}$$

f) Heritability for selection in the mean of progenies involving all sites (h^2_{m*});

$$h^2_{m*} = \frac{(1/4)\sigma^2_{A*}}{\sigma^2_{F*}}$$

Where: σ^2_{A*} is the additive genetic variance obtained in the joint analysis of sites and; σ^2_{F*} is the phenotypic variance among means of the progenies obtained from the joint analysis of the sites;

g) Gain from combined selection - Selection of individuals from different progenies, considering recombination at the experiment site (SG_{ck}). The procedure adopted was similar to that presented by Pires et al. (2011) e Resende (2015). In principle, the SG with selection is obtained by: SG= sd $x\ h^2$ where: sd is the selection differential and h2 is the heritability of the trait in the selective unit carried out. For combined selection, by site, the selection differential among progenies j (sdp) was obtained by: sdp = ($Y_{ij} - \bar{Y}_{..}$), where: Y_{ij} is the DBH value of individual *i* progeny *j*. In the literature, in some cases, to estimate the sdi, the mean of each progeny is used as a reference and not the general mean as was carried out in this study.

h) Selection considering the involvement of site information, obtaining only one improved population at the end, and cloning the selected individuals from each site (SG_{cre}). Thus, the procedure is like the one previously mentioned except that the estimates involve the indices of all sites for each species, that is:

$$I_{ijk} = \left[h^2_{m*}(\bar{Y}_{.j.} - \bar{Y}_{...})\right] + \left[h^2_{d*}(Y_{ijk} - \bar{Y}_{...})\right]$$

Where: I_{ijk} is the index of plant i of progeny j at site k, h^2_{m*} is the heritability for selection on the mean of the progenies in the joint analysis, $\bar{Y}_{.j.}$ is the mean of the progeny considering all sites, h^2_{d*} is the individual heritability in joint analysis, Y_{ijk} is the observation of plant *i* in progeny *j* at site *k* and $\bar{Y}_{...}$ is the general mean.

Results

The results of the estimates of genetic and phenotypic variances obtained from the individual and joint analyses for DBH, with the adjusted data from the evaluations of *E. maculata* and *E. torelliana* progenies, are presented in Table 2. The accuracy estimates were high magnitude, especially for the progenies of the *E. maculata* (EM) experiments. Another important of information is that the progenies x sites interaction was practically null for both species. In this condition, part of the results will focus on the mean of the environments.

Estimates of additive genetic variance components had a substantial difference in magnitude between the two species. For the progenies from the EM experiments, the estimates of

Table 2
Estimates of genetic and phenotypic variance components of the diameter at breast height (DBH, cm) with adjusted data (according to the mean of control clones common to the sites). It was obtained in evaluating the progenies of *E. maculata* (EM) and *E. torelliana* (ET), at six years of age, by site and joint.

Estimates	EM		ET		
	EM1	EM2	ET1	ET2	ET3
σ^2_{Ak}	19.66	10.81	1.62	0.94	2.38
σ^2_e	24.60	21.72	6.54	8.33	11.45
σ^2_{dk}	24.07	21.17	6.98	8.76	11.77
$r_{\hat{g}g}$	0.94	0.91	0.84	0.72	0.82
h^2_{mk}	0.89	0.83	0.71	0.53	0.68
h^2_{dk}	0.61	0.38	0.17	0.08	0.15
Progenies mean	16.03	14.75	11.57	14.49	10.06
Check mean[1]	22.30	21.99	21.91	17.22	22.28

Joint	EM	ET
σ^2_{A*}	16.41	1.58
σ^2_e	23.49	8.76
σ^2_d	23.21	21.44
h^2_{m*}	0.94	0.83
h^2_{d*}	0.57	0.12
Progenies x Sites	0.67[NS]	0.00 [NS]
Progenies mean	15.46	11.97
Checks mean	22.14	20.47

1Mean data of checks. σ^2_{Ak} e σ^2_A is the additive genetic variance by site and joint. σ^2_{dk} e σ^2_d is the phenotypic variance within progenies e joint. σ^2_e e σ^2_{e*} is the variance of the error of individual and joint analyses. $r_{\hat{g}g}$ is the experimental accuracy. h^2_{dk} is the heritability for selection among individuals of the same progeny in each site and in the joint. h^2_{mk} e h^2_{m*} is the heritability for selection among progeny means at each site and in the joint. [NS] not significant.

σ^2_{Ak} per site were much higher. These results reflect the difference in the estimates of the DBH means, which were also higher for EM. It is worth noting that plant survival in the *E. maculata* experiments was much lower than in the *E. torelliana* (ET) experiments, as will be emphasized later. Therefore, the trees had less competition and, thus, better conditions to express their growth in diameter. These results, as expected, were reflected in the estimates of heritability among plants of the progenies, which were also much higher for EM.

It should be noted that the mean number of eucalyptus clones used as checks varied between sites, especially in the experiments involving *E. torelliana*. In all situations, the mean of clones was higher than that of progenies. For example, in experiments with EM the mean of the checks was 22.1 cm, which is 43.2 % higher than the mean of the progenies. A similar observation was made in experiments where ET progenies were evaluated (Table 2).

Remember that σ^2_d corresponds to the mean phenotypic variance among plants of the same progeny, while σ^2_e corresponds to the variance of the experimental error considering the design used, in this case, randomized blocks. The similar magnitudes, between σ^2_d and σ^2_e, indicate that the variation isolated by the experimental blocks was negligible.

The heritability estimates for selection among individuals by site (h^2_{dk}) proved lower than the heritabilities for selection among progeny means (h^2_{mk}). It is worth noting that h^2_{dk} was also different between species. It is observed that the heritability for selection among plants within progenies, involving all sites (h^2_{d*}) for *E. maculata* was much higher than that for *E. torelliana* (Table 2).

The frequency distribution of the combined selection index (I_{ijk}) per site is shown in Figures 1a and 1b for EM and in Figures 2a, 2b, and 2c for ET. As expected, considering the estimates of phenotypic and genetic variances, the indices for EM were higher than for ET. This is coincident with the variance components estimates and the means obtained at each site for the two species (Table 3). All these results show that the estimates of expected gains from selection, however, should be significant, for both species, as will be discussed later.

Estimates of genetic gain with selection as a percentage (SG %) in progeny means varied among sites and species. Considering 100 selected plants and the recombination performed being carried out in the experiment itself to obtain HS progenies, SG % was 53.2 % for EM1 and 30.3 % for EM2, which still was high. Due to lower plant survival rates in the EM experiments, the population subjected to selection comprised only 992 plants for EM1 and 797 for EM2. Thus, the selection intensity applied, relative to the number of plants evaluated, was 10.1% for EM1 and 12.6% for EM2. It is worth noting that to achieve the 100 selected plants, many progenies were involved in the selectioni.e, 24 out of 62 (38.7 %) for EM1 and 32 out of 62 (51.6 %) for EM2. In other words, the proportion of selected progenies is very high (Table 3).

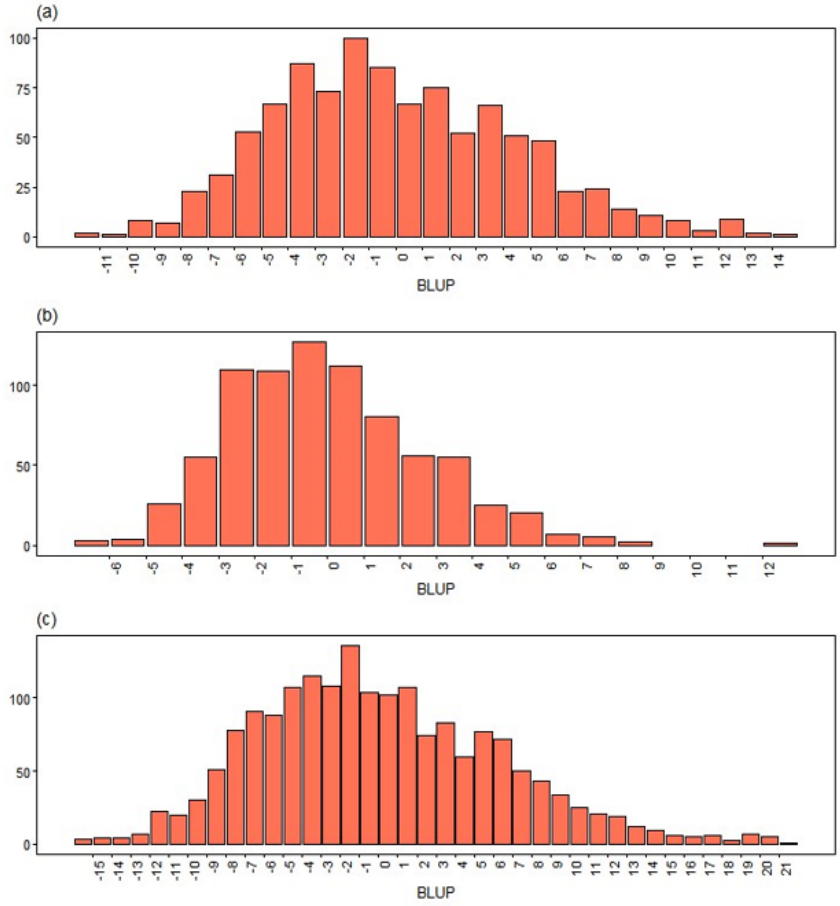

Figure 1
Frequency distributions of the BLUP obtained in progenies evaluation of the *Eucalyptus maculata* (EM) at each site (EM1 and EM2) and the in joint, for diameter at breast height (DBH, cm), at six years of age. (a) EM1; (b) EM2, and (c) joint.

Considering the ET experiments, the SG% estimates were lower than those obtained with EM. One reason for this is the lower heritability among ET progenies compared to EM (Table 3). However, this species had more survival, a higher number of plants evaluated, and greater selection intensity, factors that could potentially compensate for the lower heritability. This compensation, however, did not occur. For instance, in ET1, there were 2170 plants, and the selected proportion amounted to 4.6 % [(100/2170) /100].

Estimates of the expected gain from selection aimed at obtaining a unique population, considering selection involving sites, are presented in Table 3. In this case, one of the recombination alternatives is to obtain clones of selected individuals. Thus, it is possible to obtain the gain considering obtaining a single recombination population, utilizing information from the joint analysis. It is noted that the estimates of the combined gain, involving the two sites for EM and the three for ET, reflect the previously discussed results of the analyses by site. In other words, the SG% was higher for EM compared to ET, the expected gain from the selection was also substantial.

Again, attention is drawn to the number of progenies that would be selected if a single recombination were carried out involving information from all sites per species. For example, if 100 individuals were selected for recombination in EM, 25 progenies would be involved among the 62 that were evaluated, thus , the selected proportion would be 40.3 %. In the case of ET, it would be 43 out of 57, a selected proportion of 75.4 % (Table 3). As already mentioned, the heritability in the joint analysis for selection among the mean of progenies with TE, for example, was 83 %, and among individuals in the same condition, it was 12 % (Table 2). That the greater the heritability, the greater the selection intensity used by breeders. However, the use of combined selection in the joint analysis of sites did not reflect this fact. The number of progenies involved in each selection process was substantial, indicanting high proportion of selected progenies, compared to the intensity of selection among individuals, which had lower heritability. An important part of information is the contribution of the number of individuals of each progeny considering the combined selection. For EM (results not shown), among the 25 selected progenies, it was found that progeny 40 had 39 individuals out of the 100 selected. The second progeny with the largest number of individuals was progeny 11, with 14 selected. Of the remaining 28 progenies, the contribution was five or fewer individuals per progeny. Another relevant fact is that still considering EM, of the 100 individuals selected, 73 were from EM1.

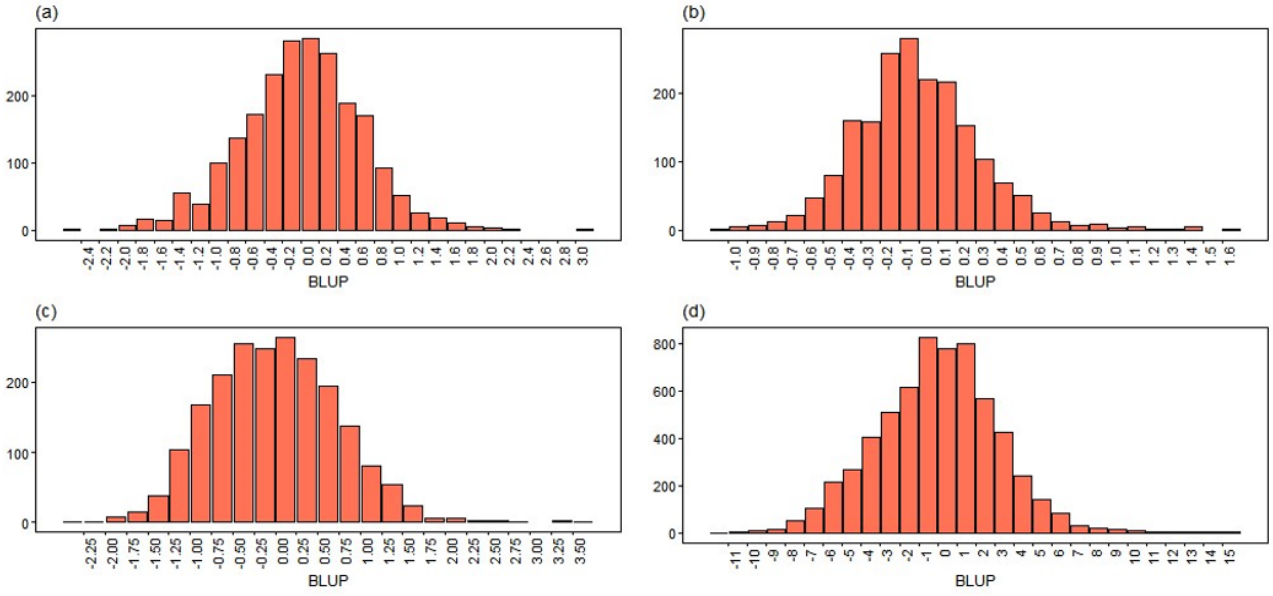

Figure 2
Frequency distributions of the estimates BLUP obtained in progenies evaluation the *Eucalyptus torelliana* at each site (ET1, ET2, and ET3) and the in joint, for diameter at breast height (DBH, cm), at six years of age. (a) ET1; (b) ET2, (c) ET3 and (d) joint.

Discussion

The experiments were carried out in five sites, involving the states of Bahia and Espírito Santo, which are responsible for significant wood production in Brazil. The choice of these sites had as its main focus the occurrence in recent years of physiological disturbances in these states, which caused serious damage to the eucalyptus crop. Available information indicates that the species *E. maculata* and *E. torelliana* are tolerant to this anomaly (Reis et al., 2011; Araujo et al., 2021; Silva et al., 2022). The aim of these experiments was also to confirm these reports. However, the occurrence of the phenomenon in these experiments was not significant, even among checks from commercial eucalyptus clones that are not tolerant.

When evaluating clones in STP, the variation among experimental blocks (repetitions/plants) is entirely environmental. However, in progeny evaluation experiments, the block effect is not just environmental. It also involves part of the genetic variation among plants of the same progeny. In terms of evaluating the mean performance of progenies, this fact has no major implications. However, when considering selection among and within progenies, or combined selection, clearly this genetic variation among plants of the same progeny, which is isolated by the source of variation, is important. Evaluating half-sib progenies, for example, the genetic variance among plants contains ¾ of the additive variance and all of the dominance variance. Therefore, this part of the variation is challenging to isolate to obtain estimates of the gains arising from genetic variation within the progenies. In this study, to obtain this information, estimates of phenotypic variance among plants of the same progeny were used. The mean of these variances at each site gave rise to the phenotypic variance within the progenies per site (σ^2_{dk}). This σ^2_{dk} contains the genetic variance among plants and the environmental

Table 3
Estimate of expected gain for diameter at breast height (DBH, cm), at six years of age, for progenies the *Eucalyptus maculata* (EM) and *Eucalyptus torelliana* (ET), considering 100 individuals selected at each site and joint.

	Mean	NIS	NPE	NPS	SG	SG %
EM1	16.03	992	62	24	8.52	53.15
EM2	14.75	797	62	32	4.47	30.30
Joint EM1 e EM2	15.39	1827	62	25	14.21	92.33
ET1	11.57	2170	57	40	1.31	11.32
ET2	14.48	1915	57	49	0.80	5.52
ET3	10.06	2053	57	35	1.61	16.00
Joint ET1, ET2 e ET3	12.04	6138	57	43	9.06	75.25

NIS is the number of individuals evaluated, NPE is the number of progenies evaluated, NPS is the number of progenies selected considering the application of the selection index, SG is the expected gain and SG % is the genetic gain in percentage.

variance. In a situation like this, Resende (2007) suggested using a completely randomized design, which was basically the strategy used in this research.

To carry out a combined selection among, and within progenies for each species, involving all sites, the strategy used was to obtain the DBH of each plant adjusted through the mean of common controls evaluated at the sites. As the variation among individuals within the same clone is environmental, the difference among the means of clones in different sites is also environmental. This occurs mainly when the interaction of clones x environments is not significant, as occurred. However, the adjusted general means of the progenies of the same species, mainly *E. maculata*, were different between sites (Table 2). The reasons for this difference are likely primarily attributable to the sampling effect. The 40 plants selected from each progeny may not have an accurate genetic representation of the progenies. This issue is compounded by the differences in survival rates of plants from the same progeny across various sites. For instance, in the case of *E. maculata*, the number of plants varied between sites, 992 (EM1) and 797 (EM2). This variation in plant number may account for the differences observed in this study . It is noteworthy that the adjustment made contributes, at least in part, to the combined selection of sites, thereby mitigating the impact of plants numbers.

With the advent of intensive use of mixed models in plant data analysis, some changes occurred in the case of perennial plants, especially *Eucalyptus* (Resende, 2015). In this context, it is clear that one of the great advantages of mixed models is their ability to mitigate the damage caused by imbalance due to loss of plants and treatments, which can occur in the field or during data analysis. However, using mixed models in data analysis, the selection among the best progenies and the best individuals within the progenies is replaced by the combined selection, in which the merit of the progenies and the individual. Thus, selection is no longer referred to as among and within progenies and is now called combined selection.

This selection strategy was adopted in this study. It was found that, for both species, the expected gain from selection can be considered significant in all sites (Table 4). This fact occurred due to the variation observed among the progenies and between individuals evaluated. Additionally, the heritability/accuracy estimates were of great magnitude, especially among *E. maculata* progenies, which were greater than 90 %. In contrast, the h^2 for selection among individuals, h^2_{d*} was smaller magnitude, the noted was of smaller magnitude, especially for *E. toreliana*, where it was less than 20 % (Table 2). The estimates of genetic and phenotypic parameters are similar in magnitude to those obtained in Brazil with *Eucalyptus* species (Araujo et al., 2021; Silva et al., 2022). It should be emphasized that, even so, the estimates of expected gains from selection concerning the population mean were significant (Table 3).

However, a fact that drew attention to the use of combined selection was the large number of progenies involved in the selection process. For example, in the EM1 experiment, of the 62 progenies evaluated, individuals from 24 progenies were selected, and in EM2, individuals from 32 progenies. In the latter case, the proportion of selected progenies was greater than 51 %. With *E torelliana*, this number of progenies involved would be even greater. For example, at site ET2, there were 49 progenies out of a total of 57.

Comparing selection among and within progenies concerning combined selection based on evaluation data from HS progenies of *Eucalyptus grandis*, Martins et al. (2005) concluded that the combined selection process proved to be superior to selection among and within, due to higher estimates of expected genetic gains and to the fact of selecting a greater number of progenies for recombination. As already mentioned, the same fact was observed in this study.

However, the combined selection strategy, which considers a recurring selection program, requires some considerations. The primary advantage first is that using progenies is greater precision with evaluations. Under these conditions, the selection intensity, is defined as, a smaller proportion of selected progenies, can and should be increased due to greater, reliability in the selection of a smaller number of progenies. With combined selection, this fact is normally not observed, as occurred in the present study. The argument for having the best genetic representation by selecting a greater number of progenies, as commented by Martins et al. (2005), must be questioned. Does selecting a greater number of progenies with lower selection intensity justify the use of progenies? This question could be asked another way: is it justifiable to invest in an experiment evaluating progenies for six or more years and then apply a low selection intensity among the progenies?

Combined selection has as its main argument that individuals with excellent performance may occur in progenies with a lower mean that must selected. The argument is valid. However, for individual selection within progenies, heritability (h^2_{dk}) is normally low. In certain situations, as observed in this research, h^2_{dk} was, on mean, three times smaller than h^2_{mk} (Table 2). Thus, the security in selecting an individual with excellent performance in progeny with a mean DBH of small magnitude is low. This fact, at least partially, may contribute to the low performance of individuals selected in progeny tests and the clone derived from them, as reported in some situations (Reis et al., 2011).

Another fact that must be considered, given the large variation observed in the number of individuals selected per progeny, is its effect on the medium-term RS result. Of course, this has consequences for recombination. It is easy to imagine that the imbalance in the number of individuals per progeny power causes consequences for the recombination of selected individuals. In the selection carried out with *E. maculata*, considering the two sites and recombination for HS selection, of the 100 selected individuals, 39 were from a single progeny.

In the case of eucalyptus breeding, the recombination of individuals occurs in the experiment itself after the elimination of those not selected. This recombination option has the advantage of reducing the time needed to complete each selection cycle. However, there are disadvantages, such as the difference between the distances among the trees to be recombined, forming gaps, and the lack of coincidence in the flowering of plants, which reduces the probability of recombination being entirely random. Another option is to clone the

selected plants. Using available technologies that make artificial hybridizations viable (Assis et al., 2005; Castro et al., 2021) improves recombination efficiency.

When progeny evaluation experiments are conducted across multiple sites, two primary objectives emerge: i) to increase the number of repetitions in progeny evaluation, and ii) to estimate progeny interaction across different sites. However, the objective is not always to obtain a specific population for each site. The focus is to obtain a single improved population, involving individuals most adapted to the conditions of a wider region, in which the evaluation sites represent. In this scenario, how to proceed? If the recombination is carried out in the experiment itself, which is very common in perennial plants, the only alternative is to keep the best progenies/individuals for recombination. Later, after the production of the seeds in each experiment, they are mixed, preferably in equal proportions, to constitute a single improved population.

An additional approach for establishing a single population based on the evaluation of progenies in some sites would be to select, for example, 10 % progenies on mean across different sites. The remaining seeds of these progenies saved in the germplasm bank would be used for planting in an isolated field in a single site (recombination field). In this field, 100 plants of each progeny, for example, must be planted in a row. Before flowering, selection would be carried out, for example on ten plants from each progeny. Under this condition, the process came to be called selection among and within progenies. The additional advantage is that the progeny test will only use information referring to the mean of the progenies, which, as already mentioned, is much more accurate.

Another approach is to identify the best individuals in each site, which will be cloned. All selected clones will be planted in the same site, recombining to obtain HS progenies. The challenge in this situation is to develop a strategy to identify the individuals to be recombined, considering the sites together. The alternative used in this study was to obtain the performance of each individual through adjustments involving common checks (clones) evaluated in different sites. In this way, differences in environmental conditions can be mitigated. As mentioned previously, this methodology is especially recommended when the checks x sites interaction is not significant, how it happened in this study. No reports on this matter were found in the literature evaluating progenies of species of the *Eucalyptus* genus.

The efficiency of recurrent selection programs, especially in perennial plants, must be evaluated by genetic progress per unit of time. Therefore, methodologies must be applied that make it possible to achieve maximum efficiency per unit of time. Among the possibilities in this regard is to employ other types of progenies that exploit a greater proportion of the additive variance of population (σ_A^2). For example, employing full-sib (FS) instead of half-sib. This is because, with FS, ½ of the σ_A^2 is explored for selection among progenies, while with HS only ¼. Another advantage of using FS is the possibility of applying a greater selection intensity than with HS.

Therefore, in recombination, the number of individuals participating in the process, maintaining the same number of progenies to be evaluated in the next cycle, may be smaller. Instead of using 100 individuals to recombine with HS, it could be just 15 with FS. This is because by crossing 15 clones in pairs, it is possible to obtain 105 FS progenies [(15X 14)/2]. In other words, the selection intensity with FS is 6.7 times higher than that with HS, resulting in, in the end, the same number of progenies being evaluated in the following cycle. Genetic progress per year is expected to be much greater with FS than with HS.

Conclusions

For the species *E. maculata* and *E. torelliana*, the expected gain from selection was significant in all sites.

The intensity of selection among progenies was very mild (large number of progenies being selected), even considering that the heritability in the mean of the progenies was much higher than that obtained among individuals.

The number of individuals selected by progeny was very different. This fact can reduce the effectiveness of recurrent selection in the medium term.

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