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### GENETIC GAIN FROM DIFFERENT SELECTION METHODS IN *Eucalyptus macarthurii* PROGENIES IN DIFFERENT ENVIRONMENTS

**Keywords:**  
Genetic parameters  
Progeny test  
Clonal seed orchard  
REML/BLUP  
HMRPGV.

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**ABSTRACT:** The aims of this research was to estimate genetic parameters of *Eucalyptus macarthurii* progenies and to predict genetic gain for different selection methods. In order to evaluate the gains, eleven progenies tests were studied. These tests were installed in 1997, in randomized blocks design, in two sites, with 5 replicates of five plants per plot. The progenies were evaluated, from the first to the eighth year, regarding the variable diameter at breast height (DBH). The genetic parameters were estimated using the mixed model procedure (REML/BLUP). The selection of the progenies for establishing a Clonal Seed Orchard was based on the analysis by location, joint analysis and on the harmonic mean of the relative performance of genotypic values (HMRPGV) with different selection intensities among and within families: three, four, five and six individuals per progeny with the selection of the top 30 individuals, taking into consideration the effective population size ( $N_e$ ). The best age to carry out the selection was seven years old, however, early selection can be made from age two onwards. Each environment characteristics influenced progenies phenotypic expression, so the higher gains in balance with  $N_e$ , were estimated with the selection of individuals for each site, and the selection of five or six individuals per progeny.

### GANHOS GENÉTICOS POR DIFERENTES MÉTODOS DE SELEÇÃO EM PROGÊNIES DE *Eucalyptus macarthurii* EM DIFERENTES AMBIENTES

**Palavras chave:**  
Parâmetros genéticos  
Testes de progênes  
Pomar clonal de sementes  
REML/BLUP  
MHPRVG

**RESUMO:** O objetivo desta pesquisa foi estimar parâmetros genéticos de progênes de *Eucalyptus macarthurii* e estimar ganhos genéticos por diferentes métodos de seleção. Foram utilizados testes de onze progênes, instalados em 1997 em blocos ao acaso, em dois ambientes, com 5 repetições de 5 plantas por parcela. Os indivíduos foram avaliados desde o primeiro ao oitavo ano, quanto à variável diâmetro à altura do peito. Os parâmetros genéticos foram estimados pela metodologia de modelos mistos (REML/BLUP). A seleção de progênes para formação de Pomar Clonal de Sementes baseou-se na análise por local, análise conjunta e no método da média harmônica do desempenho relativo dos valores genéticos (MHPRVG) com diferentes intensidades de seleção entre e dentro de famílias: três, quatro, cinco e seis indivíduos por família, com seleção dos 30 melhores indivíduos, considerando-se o tamanho efetivo populacional ( $N_e$ ). A idade mais indicada para se realizar a seleção foi aos sete anos de idade, porém uma seleção precoce pode ser realizada a partir dos dois anos. As particularidades de cada ambiente influenciaram na expressão fenotípica das progênes, de modo que os maiores ganhos, em equilíbrio com o  $N_e$ , foram estimados com a seleção dos indivíduos para cada local, sendo a seleção entre cinco e seis indivíduos por progêne.

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## INTRODUCTION

Some species of the genus *Eucalyptus* have great genotypic plasticity in Brazil, growing satisfactorily in wide an edaphoclimatic amplitude. However, the species show fundamental differences regarding the responses to environmental stimuli and it is therefore indispensable to run tests evaluating their ability to adapt in each desired location (FERREIRA, 1992). In this context, the selection of superior genotypes for genetic improvement is fundamental to generate more productive forests which are suited to different regions, having greater resistance to adverse environmental conditions (ODA et al., 2007; ROSADO et al., 2012). *Eucalyptus macarthurii* H. Deane & Maiden is endemic to New South Wales, Australia and this species is found near the swamps and creeks, growing in damp and cold locations (BROOKER; KLEINIG, 1999). In its place of origin, the species can be found from 700 m up (BENSON; MCDOUGALL, 1998; LITTLE; GARDNER, 2003).

In the South of Brazil, in higher altitude regions, this species has shown rapid growth and high tolerance to adverse climatic conditions, being a promising species for breeding programs aiming at its potential usage, as timber for sawmills, pulp, biomass source and properties for medicinal oil production (PIRRAGLIA et al., 2012), with an average volume over bark of 182.44 m<sup>3</sup>/ha and average annual increment of 36.49m<sup>3</sup>/ha/year for 5 years old plantations in the municipality of Lages, SC, Brazil (FONSECA et al., 1979). However, today, there is a need for studies about its productivity, behavior and quality of wood in Brazil.

To grow eucalyptus forests, which are more productive and adapted to different regions as well as meeting market requirements, it is important to consider the genetic aspects, once the forest is the result of actions and interactions of their genotypes with the environment (MARTINS et al., 2005). Therefore, it is advisable to evaluate its performance in more than one location so that the effect of interaction can be estimated and attenuated (SILVA et al., 2011). Estimates of genetic parameters and prediction of gains from progenies tests in several locations have been a great help in defining strategies to improve with the selection and/or recombination of individuals and progenies for a new selection cycle.

For forest species genetic improvement programs, time is a critical factor, because the exploitation involves long time consuming and expensive cycles (BELTRAME et al., 2012). Thus, the practice of selecting superior genotypes based on the first years of production, also

known as early selection, is an advantageous alternative because it aims at decreasing the time needed to complete an improved generation (FONSECA et al., 2010).

In addition to these strategies, which aim at the genetic gain with greater accuracy and more precociously, studies of the parameters of adaptability and phenotypic stability of the genotypes have been a great contribution to this aspect. These provide information about the behavior of each genotype in several environmental conditions with the identification of genotypes which are more responsive to environmental variations (CRUZ et al., 2012). Thus, several methods of selection have been employed in *Eucalyptus*, with emphasis to the procedure REML/BLUP effects (restricted maximum likelihood/best linear unbiased prediction) (ROCHA et al., 2006, 2007), as being the best procedure for generating estimates of variance components, with the maximization of selective accuracy (FARIAS NETO et al., 2009).

The major objective for the selection of individuals and progenies is to generate populations that focus on producing improved seeds with greater genetic gains. One of the strategies for the production of improved seed is the clonal seeds orchard - CSO, which presents the advantage of producing seeds earlier, allowing high selection intensity and low possibility of inbreeding.

Based on these statements, this study has as objective to indicate the most appropriate age and determine the best method for progenies selection of *Eucalyptus macarthurii* individuals, as well as to estimate the genetic gains for the formation of a production population (CSO-clonal seed orchard) for Três Barras and Timbó Grande, SC.

## MATERIAL AND METHODS

In total, eleven progenies of *Eucalyptus macarthurii* open-pollinated progenies were used, with seeds from Pietermaritzburg, South Africa provenance, imported from the Institute for Commercial Forestry Research (ICFR). The tests were implemented in October 1997, in two locations in the north of Santa Catarina: Três Barras and Timbó Grande, in randomized blocks design, with 5 replicates and 5 plants per plot, in a spacing of 2.5m x 3.0m. Seeds of the species *E. dunnii* and *E. nitens* were added as witnesses. The silvicultural practices were performed according to the characteristics required for each environment.

The geographical location, altitude and edaphoclimatic conditions of the two sites, are presented in Table I. The climate for the two regions is classified according to Köppen as Cfb, humid mesothermic, with

mild summer and uniformly distributed rainfall, without a dry season and with average air temperature in the cooler months between  $-3^{\circ}\text{C}$  and  $18^{\circ}\text{C}$  and average air temperature in the warmest month of about  $22^{\circ}\text{C}$  (ALVARES et al., 2013).

**TABLE I** Geographical location, altitude, edaphoclimatic conditions and soil types (according to the Brazilian System of Soil Classification) of the progenies test sites.

Site	Latitude (°S)	Longitude (°O)	Altitude (m)	Soil type	Average Temperature (°C)
Timbó Grande, SC	26°36'	51° 06'	1120 m	Humic Cambisol	15.8
Três Barras, SC	26°04'	50°14'	770 m	Fluvic Neosol	17.1

The individuals were evaluated every year, from one to eight years old, with measurements of total height (H, m), except in the first year, and diameter at breast height (DBH, cm). The individual volume was estimated by the equation 1, where, VOL = individual volume with bark and ff is the form factor of k 0.45.

$$\text{VOL} = \frac{\pi \text{DBH}^2}{40000} \cdot H \cdot \text{ff} \quad [1]$$

The estimation of genetic parameters and the correlation between the variables of measured growth was performed by location and for each age, using the software SELEGEN (RESENDE, 2007), which uses the best linear unbiased prediction (BLUP effects) and restricted maximum likelihood (REML). We also carried out genetic correlation between the variable DBH for ages two to seven years old, for possible early selection of individuals. The mixed linear model employed was the following (equation 2), where y is the vector of fixed effects data (averages of blocks through the locations, r), individual genetic additive effects (random, a) and errors or residuals (random, p); and X, Z and W are the matrixes of incidence for r, G and P, respectively.

$$y = Xr + Za + Wp + \varepsilon \quad [2]$$

For the study of the interaction between Genotype versus environment the following model was used equation 3, where: i is the vector of the genotype versus environment interaction effects and T its respective matrix of incidence.

$$y = Xr + Za + Wp + Ti + \varepsilon \quad [3]$$

Therefore, for the selection of the progenies considering simultaneously productivity, stability and

adaptability, the harmonic mean relative performance of genetic values (HMRPGV) predicted by BLUP method was used based on the work by Resende (2004; 2007). The stability corresponds to the Harmonic Means of Genotypic Values (HMGV) through the locations; adaptability, could then be said as the relative performance of the genotypic values in relation to the average of each site (RPGV) and the stability and adaptability simultaneously (Productivity, represented by the character DBH) corresponds to the harmonic mean of the relative performance of genotypic values (HMRPGV). In this way, the statistical model used (equation 4) was, where: g is the vector of random individual genotypic effects.

$$y = Xr + Zg + Wp + \varepsilon \quad [4]$$

The genetic parameters between the different ages were compared to check which age is the most indicated to perform the selection, assuring greater genetic gain. This way, the selection of individuals to be recombined into a production population (CSO-clonal seed orchard), was estimated for the best age. For this, individual selection simulations were made using different methods, through different intensities of selection, with the selection of the best 30 individuals: Method 1 - selection of best three individuals within families; Method 2 - Selection of the four best individuals within families; Method 3 - Selection of the best five individuals within families; and Method 4 - selection of six best individuals within families.

The selection genetic gain in percentage (g%) and the effective population size were estimated according to Resende and Bertolucci (1995), where:  $K_f$  = average number of individuals selected by progeny;  $\sigma_{kf}^2$  = variance of the number of individuals selected by progeny;  $N_f^2$  = number of selected progeny; where: SG is the selection gain;  $\bar{x}_s$  is the average of the 30 selected plants;  $\bar{x}_0$  is the average of the evaluated plants; and  $h_a^2$  is the individual heritability in the narrow sense.

$$N_e = \frac{4N_f K_f}{K_f + 3 + (\sigma_{kf}^2 \cdot k_f^2)} \quad [5]$$

$$G_s = (\bar{x}_s - \bar{x}_0) \cdot h_a^2 \quad [6]$$

## RESULTS AND DISCUSSION

Both variables (diameter and total height) were highly genetically correlated to volume, over 84%. The diameter, in all analyses and at different ages, presented the greatest genetic correlation to volume (between 90%

and 96%). Silva (2008), found similar results in progeny tests of *E. benthamii*. And a great number of studies of this genetic association in arboreal species have shown high genetic correlation between diameter and volume (SEBBENN, 2009; FREITAS et al., 2008). Rocha et al. (2007) concluded that diameter is the most used variable due to its easy evaluation and accuracy. Thus, this was the variable used to estimate the genetic parameters, as well as the selection gains of the progenies test.

The genetic parameters analyzed for the variable diameter, for each site and for the joint analysis, in every age, are presented in Tables 2, 3 and 4. For the analysis of the progenies in Três Barras (Table 2), the heritability ranged from 32% to 78%, increasing with the age, with a slight decrease at age 8.

In Timbó Grande (Table 3), the values of heritability ( $h^2a$ ) ranged from 9% to 43.8% of from lower to higher age. These results were considered high in the older ages, according to Simeon et al. (2002) classification for the variable diameter, except for values found in the joint analysis (Table 4), which varied from 5%, for the age of 2 years, to 15.8% for 8 years. Garcia and Nogueira

(2005) affirm that the estimates of heritability coefficient, high and positive, show good genetic control in the expression of the characters and show great potential for selection within the experiment, with good prospects for genetic progress. Similar results of high heritability for the variable diameter were found for *E. resinifera* (Sato et al. 2007), *E. pellita* (Zanata et al., 2010) and *E. grandis* (Miranda et al., 2015).

The accuracy values increase with the age of the individuals, being considered high (over 70%) from the first year of age onwards, except for the joint analysis. In older ages these values were higher (over 90%). In a genetic variation study of *E. camaldulensis*, the accuracy found was high for diameter, height and taper with values ranging from 85% to 89% (Moraes, et al., 2007). The accuracy of selection indicates the likelihood and reliability to reach the expected results (Pires et al., 2011).

The genetic correlation between the performance of the progenies in the different sites, as shown in Table 4 for joint analysis, had results below 27%, except in the first year, which indicates low performance of the progenies considering a single

**TABLE 2** Genetic parameters of variable DBH at each age, from 1 to 8 years old, for *E. macarthurii* progeny test in the municipality of Três Barras, SC.

Variance	Year							
	1	2	3	4	5	6	7	8
Va	0.578	3.266	5.158	12.193	15.215	18.321	25.455	25.824
Vparc	0.208	0.602	1.075	1.538	1.493	1.584	1.576	1.552
Ve	0.979	3.700	5.008	4.696	5.278	5.071	5.566	8.638
Vf	1.765	7.568	11.241	18.427	21.986	24.976	32.596	36.014
h <sup>2</sup> a	0.327	0.431	0.458	0.6616	0.692	0.733	0.780	0.717
	+ - 0.215	+ - 0.255	+ - 0.269	+ - 0.330	+ - 0.343	+ - 0.361	+ - 0.374	+ - 0.359
h <sup>2</sup> aj	0.371	0.469	0.507	0.722	0.742	0.783	0.821	0.749
c <sup>2</sup> parc	0.118	0.080	0.096	0.083	0.068	0.063	0.048	0.043
h <sup>2</sup> mp	0.596	0.690	0.693	0.780	0.797	0.811	0.830	0.819
Acprog	0.772	0.831	0.833	0.883	0.893	0.900	0.911	0.905
h <sup>2</sup> ad	0.307	0.398	0.436	0.661	0.684	0.730	0.774	0.692
CVgi%	18.920	23.134	22.353	28.662	29.469	29.873	32.375	31.475
CVgp%	9.460	11.567	11.177	14.331	14.734	14.937	16.187	15.737
CVe%	17.427	17.329	16.615	17.033	16.605	16.138	16.369	16.566
CVr	0.543	0.667	0.673	0.841	0.887	0.926	0.989	0.950
PEV	0.058	0.253	0.395	0.671	0.770	0.867	1.080	1.171
SEP	0.242	0.503	0.629	0.819	0.878	0.931	1.039	1.082
Overall average	4.017	7.811	10.161	12.183	13.237	14.328	15.584	16.145

Where : Vg: additive genetic variance; Vparc: environmental variance between plots; Vf: individual phenotypic variance; h<sup>2</sup>a = h<sup>2</sup>: individual heritability in the narrow sense, i.e. of additive effects; h<sup>2</sup>aj: individual heritability in the narrow sense, adjusted for the effects of plots; c<sup>2</sup>parc = c<sup>2</sup>: coefficient of determination of the plots effects; h<sup>2</sup>mp: heritability of average of progenies, assuming full survival; Acprog: Accuracy of selection, assuming full survival; h<sup>2</sup>ad: additive heritability within the plot; CVgi%: individual additive genetic coefficient of variation; CVgp%: coefficient of genotypic variation between progenies; CVe%: coefficient of variation; CVr = CVgp/CVe = coefficient of variation concerning residuals; ENP: variance of the genotypic values of progenies error of prediction, assuming full survival; SEP: standard deviation of the genotypic value of progenies predicted, assuming full survival.

**TABLE 3** Genetic parameters of variable DBH at each age, from 1 to 8 years old, for *E. macarthurii* progeny test in the municipality of Timbó Grande, SC.

Variance	Year							
	1	2	3	4	5	6	7	8
Va	0.124	0.638	2.329	4.459	5.896	8.474	14.460	14.460
Vparc	0.002	0.059	0.100	0.393	0.593	0.756	0.306	0.306
Ve	1.219	3.375	5.860	8.012	10.205	12.809	18.187	18.187
Vf	1.345	4.072	8.289	12.863	16.694	22.039	32.952	32.952
h2a	0.092	0.156	0.280	0.346	0.353	0.384	0.438	0.438
	+ - 0.108	+ - 0.142	+ - 0.198	+ - 0.224	+ - 0.231	+ - 0.243	+ - 0.261	+ - 0.261
h2aj	0.092	0.159	0.284	0.358	0.366	0.398	0.443	0.443
c2parc	0.001	0.015	0.012	0.031	0.036	0.034	0.009	0.009
h2mp	0.370	0.490	0.642	0.677	0.677	0.698	0.747	0.747
Acprog	0.608	0.700	0.801	0.823	0.823	0.835	0.864	0.864
h2ad	0.071	0.124	0.230	0.294	0.302	0.332	0.374	0.374
CVgi%	7.955	10.996	14.211	16.728	16.969	19.175	22.767	22.767
CVgp%	3.978	5.498	7.106	8.364	8.484	9.588	11.384	11.384
CVe%	11.602	12.536	11.859	12.930	13.108	14.110	14.802	14.802
CVr	0.343	0.439	0.599	0.647	0.647	0.679	0.769	0.769
PEV	0.020	0.081	0.208	0.360	0.476	0.640	0.914	0.914
SEP	0.140	0.285	0.456	0.600	0.690	0.800	0.956	0.956
Overall average	4.431	7.266	10.738	12.623	14.309	15.181	16.702	16.702

Where : Vg: additive genetic variance; Vparc: environmental variance between plots; Vf: individual phenotypic variance; h2a = h2: individual heritability in the narrow sense, i.e. of additive effects; h2aj: individual heritability in the narrow sense, adjusted for the effects of plots; c2parc = c2: coefficient of determination of the plots effects; h2mp: heritability of average of progenies, assuming full survival; Acprog: Accuracy of selection, assuming full survival; h2ad: additive heritability within the plot; CVgi%: individual additive genetic coefficient of variation; CVgp%: coefficient of genotypic variation between progenies; CVe%: coefficient of variation; CVr = CVgp/CVe = coefficient of variation concerning residuals; ENP: variance of the genotypic values of progenies error of prediction, assuming full survival; SEP: standard deviation of the genotypic value of progenies predicted, assuming full survival.

population for both locations. Similar results were found in the work by Santos et al. (2015), for *Eucalyptus* clones in Rio Grande do Sul. According to Resende (2002), only when the genetic correlation value between locations is over 70% it is possible to carry out a single improvement population. The low genotypic performance correlation (27%) indicates complex type genotype x environment interaction. Therefore, the performance of the progenies is differentiated based on the variations of the environment, because when subjected to different environments, the performance of one progeny compared to other varies, so that progeny which are superior in one environment may not be in another (PIRES et al., 2011). This result also indicates the importance of studying the ability of stability and adaptability of the progenies in different places of this research and for each location where genetic testing of the species is warranted.

It was found that the variable diameter at ages two, four, five and six years is highly correlated with the diameter at 7 years old (over 0.70), for both locations, except for the age two years in Timbó Grande (Table 5). Thus, it is possible to perform early selection from two to

three years of age for *E. macarthurii*. In a study conducted by Sato et al. (2010), with progenies of *Corymbia maculata*, correlations between growth traits at ages 4 and 21 years were also significant, positive and high, suggesting that early selection at age 4 could be made. This is possible because of the variables DBH, height and volume present significant correlations among themselves, in different ages, which enables the efficiency in the early selection of genetic material (MASSARO et al., 2010). Therefore, for each location analyzed separately, the best age to perform the selection of progenies test would be at seven years old, for presenting high values of heritability and accuracy of selection, however with the possibility of early selection from two years of age.

The different selection strategies of progenies were carried out based on the performance analysis of the progenies in two separate locations and joint analysis, considering the results of the genetic gain with the yield, stability and adaptability of progenies. The average performance in both locations selected the best seven families with genotypic values free of interaction (Table 6).



There was coincidence of 100% for the ordering of the seven most productive progenies by criteria of simultaneous adaptability and stability (HMRPGV) and average productivity (Table 6 and 7). The value of HMRPGV x general average value is the genotypic progenies average in the studied locations, considering the instability as a negative factor and the adaptability as a positive one (CARBONELL et al., 2007, MAIA et al., 2009). Therefore, these seven progenies might be recommended for planting in both areas, following the interaction pattern of the experimental network, contemplating three attributes: production, stability and adaptability.

This way, it is necessary to compare the prediction of genetic gains between analysis for each site, by joint analysis and by yield, stability and adaptability (HMRPGV) (Table 8). The genetic gain, with the average of the harmonic mean relative performance of genetic values (HMRPGV), was larger than only by joint analysis. However, the genetic gain obtained with the selection was even greater in the analysis by location, between 36.2% and 43.9% for Três Barras and 18.8% to 24.4% for Timbó Grande.

The genetic gain increases with the reduction of the selection intensity within progenies, consequently

reducing the number of families selected. It is important to determine the number of individuals for recombination of the production population, the appropriate effective population size to ensure safety in the selection considering the inbreeding in the generation of planting. Therefore, the intensity of selection that ensures a balance between the genetic gain and the effective population size ( $N_e$ ) is between five and six individuals per family in the selection of 30 individuals with higher genetic value in the population, with  $N_e$  ranging from 15.9 to 17.8 for the two sites. In the studies by Rocha et al. (2006a), with *E. urophylla* progeny test, similar results were found, twenty one progenies were selected with genetic gain of 21.22% and a  $N_e$  of 18.3.

**TABLE 5** Genetic correlations of the variable DBH between the age of seven years and other ages, from two to six years old, for both locations, Timbó Grande and Três Barras, SC.

Age	Location	
	Três Barras - SC	Timbó Grande - SC
2 years	0.63	0.70
3 years	0.77	0.81
4 years	0.87	0.91
5 years	0.91	0.97
6 years	0.98	0.99

**TABLE 4** Genetic parameters of variable DBH at ages 1 to 8 years old, *E. macarthurii* progenies test for the joint analysis of both sites Três Barras and Timbó Grande, SC.

Variance	Year							
	1	2	3	4	5	6	7	8
Va	0.239	0.029	0.285	1.846	3.071	3.336	4.803	6.111
Vparc	0.011	0.094	0.102	0.168	0.077	0.163	0.051	0.062
Vint	0.001	0.553	0.906	1.565	2.062	2.716	4.124	4.286
Ve	1.086	5.190	8.511	12.063	14.513	17.792	24.609	27.758
Vf	1.337	5.865	9.804	15.641	19.723	24.008	33.586	38.218
h2a	0.178	0.005	0.029	0.118	0.155	0.138	0.143	0.159
	+ - 0.106	+ - 0.019	+ - 0.046	+ - 0.095	+ - 0.112	+ - 0.107	+ - 0.109	+ - 0.115
c2parc	0.008	0.016	0.010	0.011	0.004	0.007	0.002	0.002
c2int	0.001	0.094	0.092	0.100	0.105	0.113	0.123	0.112
h2mp	0.529	0.014	0.080	0.254	0.309	0.275	0.273	0.307
Acprog	0.727	0.120	0.282	0.504	0.556	0.524	0.522	0.554
h2ad	0.142	0.004	0.024	0.103	0.137	0.123	0.128	0.142
rgloc	0.986	0.013	0.073	0.228	0.271	0.235	0.226	0.263
PEV	0.028	0.007	0.066	0.344	0.531	0.605	0.873	1.059
SEP	0.168	0.085	0.256	0.587	0.729	0.778	0.934	1.029
Overall average	4.428	7.547	10.462	12.398	13.770	14.763	16.175	16.753

Where : Vg: additive genetic variance; Vparc: environmental variance between plots; Vf: individual phenotypic variance; h2a = h2: individual heritability in the narrow sense, i.e. of additive effects; h2aj: individual heritability in the narrow sense, adjusted for the effects of plots; c2parc = c2: coefficient of determination of the plots effects; h2mp: heritability of average of progenies, assuming full survival; Acprog: Accuracy of selection, assuming full survival; h2ad: additive heritability within the plot; CVgi%: individual additive genetic coefficient of variation; CVgp%: coefficient of genotypic variation between progenies; CVe%: coefficient of variation; CVr = CVgp/CVe = coefficient of variation concerning residuals; ENP: variance of the genotypic values of progenies error of prediction, assuming full survival; SEP: standard deviation of the genotypic value of progenies predicted, assuming full survival.

## CONCLUSION

There is high genetic correlation between the variables diameter at breast height total height and volume over bark. The ideal age for performing the selection in *E. macarthurii* stands is at seven years old, with higher value of heritability and genetic gain, being possible however to perform early selection starting at two years of age, assuring high selection reliability.

**TABLE 6** Estimates of genetic gain predicted for the DBH in *E. macarthurii*, progenies at age 7 years, considering the average performance in both location Três Barras and Timbó Grande, SC.

Order	Progenie	G	u + g	Gain	New Average	u+g+gem
1	4	0.7453	16.9062	0.7453	16.9062	18.3675
2	11	0.4271	16.5879	0.5862	16.7471	17.4253
3	5	0.3865	16.5474	0.5196	16.6805	17.3053
4	2	0.3053	16.4662	0.466	16.6269	17.0647
5	1	0.2651	16.426	0.4258	16.5867	16.9458
6	8	0.1332	16.294	0.3771	16.538	16.5551
7	3	0.1137	16.2746	0.3394	16.5003	16.4975

Where: g: genotypic effect; u + g: genotypic predicted value; u + g + gem: average genotypic value in the environments.

**TABLE 7** Stability and adaptability (MHRPGV and MHRPGV\*MG) of genotypic values of *E. macarthurii* families for the variable DBH at 7 years old.

Order	Progenies	HMRPGV	HMRPGV*MG
1	4	1.1367	18.3694
2	11	1.0780	17.4209
3	5	1.0688	17.2726
4	2	1.0497	16.9643
5	1	1.0462	16.9068
6	8	1.0244	16.5544
7	3	1.0007	16.1715
8	7	0.9482	15.3240
9	9	0.8997	14.5393
10	6	0.8731	14.1108
11	10	0.8173	13.2080

In that: HMRPGV: harmonic means of the relative performance of the genotypic values; HMRPGV\*MG: refers to the general average HMRPGV multiplied in all environments.

**TABLE 8** The genetic gain predicted for the variable diameter and effective population size by different selection methods, analysis by location, joint analysis and HMRPGV interaction analysis for *E. macarthurii*, at 7 years old.

Selection Intensity		Três Barras, SC	Timbó Grande, SC	Joint Analysis	HMRPGV Interaction
Best 30 individuals with the selection of three individuals per progenies	G %	36.2101	18.8684	7.7816	9.6994
	New average	21.2268	19.8535	17.4341	17.7443
	Ne	20.8456	19.6215	20	14.0000
Best 30 individuals with the selection of four individuals per progenies	G %	41.8322	21.4656	9.107	9.3481
	New average	22.1029	20.2873	17.6485	17.6875
	Ne	17.2612	17.6846	17.6846	16
Best 30 individuals with the selection of five individuals per progenies	G %	43.6746	23.1114	9.4946	9.5859
	New average	22.39	20.5621	17.7112	17.7259
	Ne	17.8682	17.3725	17.1705	15.9185
Best 30 individuals with the selection of six individuals per progenies	G %	43.9805	24.3632	9.6372	9.5859
	New average	22.4377	20.7712	17.7342	17.7259
	Ne	17.7493	15.9265	16.0815	15.9185

where: G%: genetic gain in percentage; Nf: number of families selected; Kf: average number of individuals selected per family; Ne: effective population size.

The genetic correlation between the performance of the progenies in the different environments was low, thus, the genetic gain obtained with the selection is greater when raising a production population (CSO) in each location.

The intensity of selection for the formation of a CSO, which ensures balance between the genetic gain and the Ne, lies between five and six individuals per family in the selection of the 30 individuals with higher genetic value in the population.

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