Early selection efficiency for recommendation of *Eucalyptus* sp.

Yanca Araujo Frias
College of Agricultural and Technological Sciences, São Paulo State University (Unesp),
Dracena, SP, Brazil.

Eliel Alves Ferreira
Minas Gerais State University
Passos, MG, Brazil

Victor Hugo Cruz
College of Agricultural and Technological Sciences, São Paulo State University (Unesp),
Dracena, SP, Brazil.

Daniel Pedrosa Alves
Empresa de Pesquisa Agropecuária e Extensão Rural de Santa Catarina - Epagri/Estação
Experimental de Ituporanga,
Ituporanga, SC, Brazil

Evandro Pereira Prado
College of Agricultural and Technological Sciences, São Paulo State University (Unesp),
Dracena, SP, Brazil.

Ronaldo Cintra Lima
College of Agricultural and Technological Sciences, São Paulo State University (Unesp),
Dracena, SP, Brazil.

Cosme Damião Cruz
Federal University of Viçosa,
Viçosa, MG, Brazil.

Rafael Simões Tomaz
College of Agricultural and Technological Sciences, São Paulo State University (Unesp),
Dracena, SP, Brazil.

Abstract

This paper aims to estimate genetic and phenotypical parameters to assess the viability of early selection in progeny tests of Eucalyptus sp. We analyzed data from experiments conducted in the state of Minas Gerais, Brazil. The evaluated traits were diameter at breast height and plant height in 482 progenies of *full sibs under randomized block design, into nine experiments: four of which were assessed at progenies mean level, and five assessed at individuals mean level. It were evaluated the predicted gains with combined selection index under 5, 10 and 20% of selection; the coincidence among selected families in juvenile and adult ages, and the efficiency of early selection. Results indicated that the procedures were efficient in most of the scenarios, and the gains comparable to the direct selection on tree harvest age.*

Keywords: eucalipt; biometry; statistics; selection method; genetic parameters.

1. Introduction

Brazil has the second largest area of *Eucalyptus* planted forests, worldwide, being consolidated as the largest producer of hardwood pulp [7]. The use of clones in commercial plantations of *Eucalyptus* is a common practice in most of forestry sector companies. Thus, the identification of superior clones has been constituted as the primary objective of breeding programs. However, the main obstacle for the process is the delay in the assessment step, in such way that the early selection constitutes an alternative for lessen this problem [10].

Concerning perennial plants, the number of years to complete a selection cycle is the major limitation for recurrent selection programs. In forestry species of temperate climates, usually rotations can reach 50 years or more, whereas for subtropical species this age ranges from 25 to 30 years. Still, in conducting a recurrent selection program with *Eucalyptus* in Brazil, the assessment step lasts about seven years, which is the harvesting age of plants in commercial plantations [1]; [10].

Thus, the contribution of the number of years to complete a selection cycle is expressive. Therefore, alternatives aiming at decreasing the necessary time to complete a selection cycle must be used in order to efficiently promote the selection as younger as possible. Some methodologies have been proposed with the goal of assessing the efficacy of early selection, such as: the study of fluctuation of genetic and phenotypical parameters throughout ages [13] and the estimation of the genetic correlation in different ages [9]; [8].

Using data of experiments conducted by CENIBRA NIPO-BRASILEIRA SA, this research was performed aiming at estimating genetic and phenotypical parameters and at assessing the viability of early selection.

2. Material and Methods

For the experiments were used 517 full sibs progenies, divided into nine experiments: four of which were assessed in level of mean progeny, and five assessed in individual level within their linear plot. Experiments considered are presented in Table 1. The experiments were installed in a randomized block design between years 1995 and 2000 in the cities of Antônio Dias, Belo Oriente, Pingo D'água, Sabinópolis and Santa Bárbara, in the State of Minas Gerais, Brazil. The number of replications varied according each experiment, as well as the size of linear plot (Table 1). The spacing used was 3.0 x 2.75 m in experiments TPH 80 and 81, and 3.00 x 2.00 m in the other experiments.

Table 1. Ratio of assessed experiments, locations, year of installation, ages, and number of assessed progeny.

Experiment	Locations	Installation (month/year)	Evaluation ages (years)	Number of progenies	Plant row plot arrangement	Replications
Progeny mean estimates						
80	Sabinópolis	11/1995	3.7 / 4.5	56	-	5
81	Belo Oriente	12/1996	3.5 / 5	42	-	3
84	Antônio Dias	12/1996	3 / 5	43	-	3
88	Sta. Bárbara	12/1996	3.5 / 5	37	-	3
Individual plant estimates						
110	Belo Oriente	12/1997	4 / 6	10	10	4
111	Belo Oriente	12/1997	4 / 5	24	12	3
115	Sabinópolis	04/1999	2.6 / 3.7	28	6	4
123E	Pingo D'água	11/2000	2 / 3	121	5	5
123B	Pingo D'água	11/2000	2 / 3	121	6	5

Diameter at breast height (DBH), in centimeters, and plant height (PH), in meters, were collected in all experiments, assessed in several ages (Table 1). Individual variance analyses were performed per location for each age. Estimations of genetic and phenotypical parameters were obtained from mean squares expected of variance analyses. Four experiments were assessed at level of mean family following the model: $Y_{ij} = \mu + G_i + B_j + \varepsilon_{ij}$. And five experiments at individual level within the plot following the model: $Y_{ijk} = \mu + G_i + B_j + \varepsilon_{ij} + \delta_{ijk}$, where, Y_{ij} and Y_{ijk} respectively correspond to the observation of the i-th progeny of j-th block; and to the observation of the i-th progeny of the j-th block in the k-th plant. μ correspond to the general mean; G_i to the effect of the i-th progeny; B_j to the effect of the j-th block; ε_{ij} to the experimental error among progenies; and δ_{ijk} to the experimental error within progenies. Estimations of heritability for the experiment at level of progeny mean was calculated following the expression: $h_P^2 = \frac{\hat{\sigma}_g^2}{\frac{\hat{\sigma}^2}{r} + \hat{\sigma}_g^2}$ where, $\hat{\sigma}_g^2$ and $\hat{\sigma}^2$, constitute the genetic variance and environment estimators, respectively; and r , number of replications.

For experiments at individual level within the plot, heritability at progeny and individual levels was estimated, respectively given by: $h_P^2 = \frac{\hat{\sigma}_g^2}{\frac{\hat{\sigma}_d^2}{nr} + \frac{\hat{\sigma}_e^2}{r} + \hat{\sigma}_g^2}$ and $h_{Ind.}^2 = \frac{\left(\frac{1}{\theta_e}\right)\hat{\sigma}_g^2}{\frac{gn(r-1)}{gnr-1}\hat{\sigma}_b^2 + \frac{n(gr-1)}{gnr-1}\hat{\sigma}_e^2 + \frac{rn(g-1)}{gnr-1}\hat{\sigma}_g^2 + \hat{\sigma}_d^2}$

where, θ_e constitutes the genetic variance fraction explored among families; $\hat{\sigma}_g^2$, the estimator of genotypic variance among means of family; $\hat{\sigma}_d^2$, estimator of phenotypic variance among plants within the plot; $\hat{\sigma}_e^2$, estimator of environmental variance among plots; $\hat{\sigma}_b^2$, estimator of environmental variance provided by difference between blocks; g, number of families; r, number of blocks; n, number of plants within plot. The selection and estimation of genetic gains of the experiments assessed at mean level were performed according method proposed by [4]: $\Delta M_e = c.SD.h^2$ where, c is the parental control, SD is the selection differential and h^2 is the trait heritability.

In the experiments assessed at individual level within the plot, the procedure of combined selection for selection and estimation of genetic gains was considered for each characteristic. The model below was followed: $I = \beta_1(Y_{ijk} - Y_{ij.}) + \beta_2(Y_{i..} - Y_{...})$ where, Y_{ijk} corresponds to the observation of the i-th progeny of the j-th block in the k-th plant; $Y_{ij.}$ corresponds to the mean value in the i-th progeny of the j-th block, and $Y_{...}$ is the general mean. Predicted gains under the selection percentages of 5%, 10% and 20% were assessed.

With the purpose of assessing the efficiency of selection, the following methodologies were used: a) correlated response with the selection between early and mature age [6]; b) percentage of coincidence among selected families in juvenile and adult ages [15]; and c) efficiency of early selection quantified by the expression: $E = \dfrac{R_j / T_j}{R_m / T_m}$ where, R_j is the response of the mature trait after juvenile selection, and R_m is the direct response on selection in the adult age; T_j and T_m are the juvenile and mature ages, respectively [5]. The program GENES [2]; [3] was used for statistics analysis.

3. Results and Discussion

In the variance analysis, it was noticed that the progeny effect was significant ($p<0.05$) for characteristics of DBH and PH, in juvenile and adult ages, excepting for the PH in the experiment 111 (Table 2-3).

The coefficients of experimental variation (CV_E) were ranging from 7.51% and 17.21% (Tables 2 and 3), agreeing with the findings of other authors for the eucalyptus crop — [18]; [17]; [16] —, indicating a good experimental accuracy. [14] and [11], evaluating experiments of *E. camaldulensis* and *E. grandis*, respectively, obtained results that corroborate this information. In the results found, despite only the experiments 80, 84, 110 and 115 provided estimates of CVg/CVe higher than 1.0, all the experiments provided genetic gains with the selective process. Moreover, in all experiments, both early and mature selection were efficient.

An increase in estimations of genetic ($\hat{\sigma}_G^2$) and environmental variance ($\hat{\sigma}_E^2$) was seen with increase of age in the experiments in mean progeny level. In principle, one can infer that a greater release of genetic variability over the years has occurred. However, estimations of heritability, which is a relative measure, practically do not change among different ages (Tables 2-3). Thus, it can be argued that the genetic variability released among clones was the same in the different ages, because CV_E was maintained in similar levels. These results allow us to infer that, at least in principle, selection in juvenile ages is viable. Such results are confirmed by [16] and [15].

In experiments at individual level, within the plot, generally, variances increased throughout the years, but there were estimations of variances that decreased: $\hat{\sigma}_G^2$ and $\hat{\sigma}_E^2$ of experiment 110 (in PH); $\hat{\sigma}_E^2$ of experiment 111 (DBH); $\hat{\sigma}_E^2$ of experiment 123B (in DBH and PH); $\hat{\sigma}_E^2$ of experiment 123E (in DBH and PH). These results are showed in Table 2. There were also situations where the variance was negative: TPH 111 (PH at 5 years); TPH 123E (DBH at 2 and 3 years; and PH at 3 years). These results, unlike what was expected, might be explained by the effect of competition between plants, which is common in the eucalyptus crop [20]; [14]. It should be stressed that heritabilities ($\hat{h}_P^2$ or $\hat{h}_{Ind.}^2$) were similar in the different ages. Thus, along with good experimental accuracy, it might be said (at least a priori) that selection in early ages is viable.

Table 2. Summary of variance analysis of experiments assessed at mean level of plot. Mean Squares (MS), coefficient of experimental (CV_E) and genetic (CV_G) variation, corrected mean, estimations of genetic and environmental variance, and estimation of heritability at progeny level were presented.

DBH								
Experiment	80		81		84		88	
	3.7 year	4.5 year	3.7 year	4.5 year	3 year	5 year	3.5 year	5 year
	MS	MS	MS	MS	MS	MS	MS	MS
Blocks	0.98	0.69	1.02	0.52	5.16	5.94	3.22	2.90
Progeny	12.80**	17.05**	5.32**	6.79**	6.53**	10.51**	3.40*	5.50*
Residual	1.31	1.74	1.88	2.28	1.43	2.11	1.96	2.96
CV_E (%)	9.46	10.26	10.96	11.26	9.08	9.76	12.87	12.72
Mean	12.09	12.86	12.51	13.40	13.16	14.57	10.88	13.52
CV_G (%)	12.54	13.61	8.56	9.16	9.90	11.25	6.37	6.82
$\hat{\sigma}_G^2$	2.2980	3.0619	1.1467	1.1561	1.7014	2.8004	0.4803	0.8496
$\hat{\sigma}_E^2$	0.2618	0.3480	0.6269	0.7588	0.4762	0.7022	0.6535	0.9853
$\hat{h}_P^2$ (%)	89.77	89.79	64.65	66.50	78.13	79.75	42.34	46.30

PH								
Experiment	80		81		84		88	
	3.7 year	4.5 year	3.7 year	4.5 year	3 year	5 year	3.5 year	5 year
	MS	MS	MS	MS	MS	MS	MS	MS

Blocks	4.95	22.66	26.47	1.27	12.03	8.16	3.64	16.99
Progeny	16.88**	32.88**	7.74**	13.43**	10.62**	24.49**	4.20*	7.78*
Residual	1.84	3.43	2.73	4.98	2.24	4.01	2.67	4.41
CV$_E$ (%)	7.79	8.96	8.37	9.85	7.51	8.23	10.09	9.47
Mean	17.40	20.67	19.73	22.64	19.93	24.36	16.21	22.16
CV$_G$ (%)	9.97	11.58	6.55	7.42	8.38	10.72	4.40	4.79
$\hat{\sigma}_G^2$	3.0079	5.7298	1.6697	2.8185	2.7922	6.8238	0.5086	1.1260
$\hat{\sigma}_E^2$	0.3676	0.6856	0.9095	1.6585	0.7467	1.3394	0.8908	1.4686
$\hat{h}_P^2$ (%)	89.11	89.31	64.74	62.96	78.90	83.59	36.34	43.40

* $p < 0.05$; ** $p < 0.01$

TABLE 3. Summary of variance analysis of experiments assessed at individual level of plot. There are showed Mean Squares for Variation Sources, experimental coefficient (CV$_E$) and genetic coefficient (CV$_G$) of variation, estimation of mean ($\hat{\mu}$), estimations of genetic and environmental variance between-plots, and estimation of heritability at progeny and individual levels in the experiment.

DBH										
Experiment	110		111		115		123B		123E	
	4 years	6 years	4 years	5 years	2.6 years	33.7 years	2 years	3 years	2 years	3 years
Blocks	27.42	23.87	57.39	71.74	1.89	2.85	2.84	10.24	5.07	30.73
Progeny	54.81**	69.89**	26.98**	36.49**	19.24**	58.91**	9.79**	24.98**	7.36**	18.84**
Between Plot	10.94	12.99	11.23	12.27	3.13	8.25	5.41	11.68	2.48	6.72
Within Plot	10.70	12.51	10.41	14.01	2.90	7.78	3.74	10.72	2.99	7.66
CV$_E$ (%)	10.14	10.19	9.18	8.60	8.22	9.90	14.35	17.21	9.71	13.33
$\hat{\mu}$	12.25	13.33	11.93	13.31	9.67	13.19	8.52	10.31	8.57	10.12
CV$_G$ (%)	10.16	10.66	6.28	6.97	9.32	12.26	5.78	8.21	6.09	8.01
$\hat{\sigma}_G^2$	1.5469	2.0203	0.5620	0.8628	0.8141	2.6176	0.2431	0.7172	0.2729	0.6562
$\hat{\sigma}_E^2$	0.0346	0.0679	0.0879	-0.186	0.0465	0.0985	0.4609	0.2585	-0.1415	-0.2561
$\hat{h}_P^2$ (%)	80.04	81.41	58.37	66.36	8374	85.99	44.79	53.25	66.26	64.34
$\hat{h}_{Ind}^2$ (%)	25.09	27.61	9.98	11.54	43.41	50.07	10.95	12.27	17.47	16.17

PH										
Experiment	110		111		115		123B		123E	
	4 years	6 years	4 years	5 years	2.6 years	33.7 years	2 years	3 years	2 years	3 years
Blocks	20.20	87.76	540.05	263.15	2.12	2.29	77.92	97.76	15.50	197.39
Progeny	111.81**	105.78**	52.49^{ns}	53.53^{ns}	26.93**	56.50**	23.80**	38.73**	12**	35.32**

Between Plot	20.51	18.74	54.72	42.29	5.10	9.90	10.60	17.77	5.67	13.27
Within Plot	17.31	17.52	21.26	22.64	2.84	7.5	5.43	13.71	4.58	24.87
CV_E (%)	8.01	8.16	11.73	10.13	8.36	7.73	13.71	15.53	9.75	12.22
$\hat{\mu}$	21.24	19.98	20.62	20.98	12.57	18.50	12.49	14.09	12.91	15.51
CV_G (%)	8.45	8.80	-	-	8.36	8.39	6.84	7.55	4.61	7.04
$\hat{\sigma}_G^2$	3.2197	3.0909	-	-	1.1029	2.4084	0.7313	1.1297	0.3548	1.1934
$\hat{\sigma}_E^2$	0.4506	0.1734	-	-	0.4544	0.4948	1.4341	1.0944	0.3045	-0.4324
$\hat{h}_P^2$ (%)	81.66	82.29	-	-	81.08	82.48	55.45	54.11	52.79	62.42
$\hat{h}_{Ind}^2$ (%)	30.69	29.44	-	-	50.38	46.54	18.88	14.02	13.49	14.88

$^{*}p < 0.05$; $^{**}p < 0.01$

Three percentages of selection were assessed; 5%, 10% and 20% (Table 4-6). The use of higher intensities of selection conducted to predicted gains of higher magnitude; what was expected. However, despite the genetic gains being higher in short term, such strategy is not efficient when associated to procedures of recurrent selection which tends to deplete genetic variability more rapidly [15]; [11].

Aiming at clearing what occurs with the genetic gain when early selection is performed, scenarios where selection was performed in a juvenile age with measurement of the genetic gain in the adult age of the tree were assessed. In all scenarios evaluated, early selection proved to be efficient due to $\hat{E}$ >1.0 ou $\hat{E}$ (%) > 100%. However, this does not necessarily imply that the gain from early selection is necessarily higher than the genetic gain with selection being performed in mature age. This is because direct comparison does not take into account into account how long the genetic material is at the field until it is evaluated, and consequently its breeding cycle, which in the case of perennials species such as eucalypt can be considerably large.

The percentage of coincidence of selected individuals quantified by the percentage of genotypes that had the best performance in early age, and that presented in mature age, was always superior to 57.00%, a scenario obtained for experiment 115 for DBH (Table 4) with selection intensity of 5%. For the other intensities of selection, the percentage of coincidence was similar; 59.93 for selection intensity of 10% (Table 5), and 62.50 for 20% (Table 6). Another indicator of the early selection viability was provided by the analysis of correlation between genetic values of family/individual means for DBH in early and mature ages (data not shown). The existence of high genetic correlation (≥0.78) suggests that selection in early age will also conduct to selection of individuals that will also present significant performance in mature age.

In forestry breeding, early selection has been shown as viable for presenting advantages in relation to selection only in the mature age of the tree. The main one is the decrease of interval of progenies generation, and consequently in the decrease of the breeding cycle [9]; [12]. In this sense, early selection must be desirable when allowing an expressive genetic gain, associated to significant decrease of generation time. Theoretical studies developed by [19] indicate that both genetic information obtained by selection of the tree in early ages and molecular information – genealogy, and data of markers linked to characteristics of interest – might be used to increase the efficiency of selection in mature age.

Table 4. Gain with selection in early and mature ages with selection intensity of 5%, and efficiency of early selection in relation to the selection in mature age. I_i corresponds to the age of measurement of the trait, and I_j is the age in which the individuals classified as the best were selected. Values prior to parenthesis in Genetic gain indicate the value of gain with selection in the measurement of the trait, and values within parentheses are the percentage gain.

Experiment	Age of selection (I_i/I_j)	Genetic gain (%)		Selection Efficiency (%)		Coincidence of selected	
		DBH	PH	DBH	PH	DBH	PH
80	3.7 / 3.7	2.42 (20.00)	2.42 (13.88)				
	4.5 / 4.5	2.96 (23.00)	3.22 (15.57)				
	3.7 / 4.5	2.66 (20.68)	3.18 (15.36)	109.30	120.11	66.67	66.67
81	3.5 / 3.5	1.71 (13.69)	1.72 (7.74)				
	5 / 5	1.83 (13.71)	1.76 (7.81)				
	3.5 / 5	1.61 (12.00)	1.75 (7.74)	125.68	142.045	100.00	100.00
84	3 / 3	1.88 (14.27)	1.01 (5.06)				
	5 / 5	2.55 (17.14)	2.23 (13.25)				
	3 / 5	2.54 (17.11)	3.23 (13.24)	166.01	241.41	100.00	100.00
88	3.5 / 3.5	0.91 (8.39)	0.86 (5.32)				
	5 / 5	1.23 (9.09)	1.19 (5.38)				
	3.5 / 5	1.23 (9.09)	1.19 (5.38)	142.86	142.86	100.00	100.00
110	4 / 4	2.47 (20.23)	3.16 (14.86)				
	6 / 6	2.89 (21.71)	3.04 (15.20)				
	4 / 6	2.81 (21.08)	2.86 (14.30)	145.85	141.12	79.54	79.54
111	4 / 4	1.02 (8.56)	-				
	5 / 5	1.44 (10.86)	-				
	4 / 5	1.39 (13.45)	-	120.66	-	75.00	-
115	2.6 / 2.6	1.66 (17.19)	1.99 (15.82)				
	3.7 / 3.7	2.69 (20.42)	2.47 (13.36)				
	2.6 / 3.7	2.40 (18.19)	2.32 (12.51)	126.97	133.67	57.00	67.86
123E	2 / 2	1.07 (12.49)	1.10 (8.53)				
	3 / 3	1.68 (16.65)	2.26 (14.55)				
	2 / 3	1.64 (16.22)	2.19 (14.13)	146.43	145.35	80.13	83.44
123B	2 / 2	0.71 (8.30)	1.39 (11.17)				
	3 / 3	1.48 (14.38)	1.95 (13.86)				
	2 / 3	1.34 (13.09)	1.74 (12.32)	135.81	133.85	66.89	60.93

Table 5. Gain with selection in early and mature ages with selection intensity of 10%, and efficiency of early selection in relation to the selection in mature age. I_i corresponds to the age of measurement of the trait, and I_j is the age in which the individuals classified as the best were selected. Values prior to parenthesis in Genetic gain indicate the value of gain with selection in the measurement of the trait, and values within parentheses are the percentage gain.

Experiment	Age of selection (I_i/I_j)	Genetic gain (%)		Selection Efficiency (%)		Coincidence of selected	
		DBH	PH	DBH	PH	DBH	PH
80	3.7 / 3.7	2.09 (17.25)	2.15 (12.38)				
	4.5 / 4.5	2.46 (19.06)	2.78 (13.43)				
	3.7 / 4.5	2.32 (18.02)	2.72 (13.16)	114.7	119.00	66.67	66.67
81	3.5 / 3.5	1.29 (10.29)	1.45 (7.27)				
	5 / 5	1.59 (11.90)	1.54 (6.85)				
	3.5 / 5	1.47 (11.00)	1.64 (7.26)	132.08	152.13	75.00	75.00
84	3 / 3	1.50 (11.38)	1.22 (6.10)				
	5 / 5	2.04 (13.71)	2.85 (11.68)				
	3 / 5	2.00 (13.43)	2.65 (10.88)	163.40	154.97	75.00	75.00
88	3.5 / 3.5	0.77 (7.08)	0.70 (4.30)				
	5 / 5	0.99 (7.30)	1.05 (4.73)				
	3.5 / 5	0.78 (5.77)	0.77 (3.46)	112.55	104.76	75.00	75.00
110	4 / 4	1.86 (15.21)	2.43 (11.46)				
	6 / 6	2.21 (16.62)	2.39 (11.95)				
	4 / 6	2.16 (16.17)	2.15 (10.76)	146.61	134.94	75.00	58.89
111	4 / 4	0.83 (6.93)	-				
	5 / 5	1.17 (8.81)	-				
	4 / 5	1.06 (8.00)	-	113.25	-	60.4651	-
115	2.6 / 2.6	1.41 (14.56)	1.64 (13.07)				
	3.7 / 3.7	2.26 (17.13)	2.05 (11.08)				
	2.6 / 3.7	2.08 (15.78)	1.86 (10.02)	130.97	129.12	65.67	67.16
123E	2 / 2	0.85 (9.88)	0.86 (6.70)				
	3 / 3	1.33 (13.20)	1.79 (11.57)				
	2 / 3	1.31 (13.02)	1.66 (10.74	147.74	139.12	81.79	75.83
123B	2 / 2	0.55 (6.45)	1.09 (8.71)				
	3 / 3	1.19 (11.58)	1.53 (10.90)				
	2 / 3	1.08 (10.49)	1.33 (9.47)	136.13	130.39	65.56	59.93

Table 6. Gain with selection in early and mature ages with selection intensity of 20%, and efficiency of early selection in relation to the selection in mature age. I_i corresponds to the age of measurement of the trait, and I_j is the age in which the individuals classified as the best were selected. Values prior to parenthesis in Genetic gain indicate the value of gain with selection in the measurement of the trait, and values within parentheses are the percentage gain.

Experiment	Age of selection (I_i/I_j)	Genetic gain (%)		Selection Efficiency (%)		Coincidence of selected	
		DBH	PH	DBH	PH	DBH	PH
80	3.7 / 3.7	1.94 (16.01)	2.20 (12.66)				
	4.5 / 4.5	2.24 (17.47)	3.07 (14.86)				
	3.7 / 4.5	2.01 (15.68)	2.47 (11.93)	109.13	97.85	83.33	83.33
81	3.5 / 3.5	1.16 (9.14)	1.40 (6.99)				
	5 / 5	1.32 (9.77)	1.78 (7.75)				
	3.5 / 5	1.10 (8.18)	1.47 (6.49)	119.04	117.98	75.00	75.00
84	3 / 3	1.65 (12.52)	2.12 (10.65)				
	5 / 5	2.18 (14.64)	3.44 (14.13)				
	3 / 5	1.65 (11.12)	2.26 (9.28)	126.15	109.50	87.50	87.50
88	3.5 / 3.5	0.61 (5.56)	0.57 (3.49)				
	5 / 5	0.84 (6.24)	0.94 (4.24)				
	3.5 / 5	0.66 (4.87)	0.70 (3.14)	112.25	106.38	62.50	62.50
110	4 / 4	1.30 (10.62)	1.73 (8.13)				
	6 / 6	1.54 (11.58)	1.77 (8.84)				
	4 / 6	1.57 (11.78)	1.68 (8.41)	152.92	142.37	74.44	65.28
111	4 / 4	0.63 (5.30)	-				
	5 / 5	0.88 (6.65)	-				
	4 / 5	0.83 (6.26)	-	117.90	-	75.58	-
115	2.6 / 2.6	1.14 (11.83)	1.31 (10.47)				
	3.7 / 3.7	1.85 (14.01)	1.67 (9.04)				
	2.6 / 3.7	1.66 (12.60)	1.47 (7.93)	127.69	125.26	74.63	75.37
123E	2 / 2	0.60 (7.01)	0.61 (4.70)				
	3 / 3	0.97 (9.59)	1.27 (8.24)				
	2 / 3	0.96 (9.50)	1.26 (8.14)	148.45	148.82	84.63	78.18
123B	2 / 2	0.41 (4.77)	0.80 (6.42)				
	3 / 3	0.88 (8.52)	1.10 (7.84)				
	2 / 3	0.83 (8.11)	1.05 (7.42)	141.48	143.18	74.38	67.27

4. Conclusion

Traits evaluated had moderate magnitude heritability in the assessed experiments, showing good responses to selection. Early selection procedure was efficient in all of the assessed scenarios, providing similar responses to the direct selection in mature age, allowing expressive genetic gain associated to significant decrease of breeding cycle in eucalypt culture.

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