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Genetic control of productivity and genotypes by environments interaction for *Eucalyptus dorrigoensis* in southern Brazil

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SILVICULTURE

ABSTRACT

Background: *Eucalyptus dorrigoensis* withstands cold weather and the occurrence of frost, making it a potential species for improvement programs in Southern Brazil where such conditions occur. However, the use of the species is still uncommon and its genetic variability remains poorly understood.d.

Results: For site called Sertão Santana, the narrow sense heritability ranged from 0.46 (H) to 0.64 (MAI) and for Lavras do Sul it ranged from 0.38 (H) to 0.47 (MAI). The coefficient of genetic variation varied from 8.1% (H) to 26.1% (MAI). There is significant genetic correlation between DBH and MAI, reaching a value of 0.97. The GxE interaction was significant and mostly complex (78.7%). The best genetic materials for each environment, along with the most stable genetic materials, were identified. In addition, a thinning simulation was performed and the genetic gains for Sertão Santana and Lavras do Sul were 12.62 and 7.43%, respectively.

Conclusion: The studied populations have genetic variability that can be used in breeding programs by selecting among progenies and individuals within progenies. The GxE interaction is complex, and as such, the best genetic material should be selected independently for each site. The results of this study have practical implications for the companies and offer advances in knowledge of the species for breeding programs.

Keywords: BLUP, Genetic Correlation, GGE Biplot, Quantitative Genetics, Tree Breeding

HIGHLIGHTS

It is possible to perform recurrent selection on the *Eucalyptus dorrigoensis* population.
The indirect selection between diameter at breast height and medium annual increment is feasible.
Due to the genotype x environmental interaction, different genetic material must be selected for each site.
A thinning simulation was performed to estimate genetic gains.

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INTRODUCTION

The planting of exotic tree species has brought significant social and economic benefits to Brazil, including positive impacts on the industrial sector. Among the most common exotic genera used, *Eucalyptus* is the most important and offers advantages due to the advancement of genetic studies (Grattapaglia et al., 2012). In terms of forestry, about 7.84 million hectares in Brazil are covered by forest plantations, of which about 5.7 million are planted with *Eucalyptus* species, underscoring the importance of this genus in the national context (IBÁ, 2019). The selection of a potential species is the first step in improvement programs, which involves selecting species that are resistant to environmental conditions, such as cold and dry weather, drought, and frost, while also maintaining high levels of productivity and adequate wood properties. *Eucalyptus dorrigoensis* (Blakely) L.A.S. Johnson & K.D.Hill withstands cold weather and the occurrence of frost, making it a potential species for improvement programs, since these conditions occur in Southern Brazil (Arnold, 2015; Kronzen et al., 2017).

The pulp and paper industry is the main processor of forest products in Brazil (IBÁ, 2019), and the wood properties of *E. dorrigoensis* are favorable for pulp and paper production. The average wood density is 0.491 g.cm^{-3} at ten years of age, and *E. dorrigoensis* has similar properties to other species already used for pulp and paper production, such as *Eucalyptus dunnii*. Another benefit of *E. dorrigoensis* is the quality of its sawn wood, with low rates of defects after drying, offering a good alternative to other species used for this purpose in Southern Brazil (Müller et al., 2017). In addition, *E. dorrigoensis* presents moderate resistance to attacks of the insect *Thaumastocoris peregrinus* (bronze bug) (Smaniotto et al., 2017). As such, the species presents significant potential for hybridization.

After selecting a potential species, it is crucial to estimate the genetic parameters, since this information allows breeders to understand the species genetic variability, enabling the definition of the best selection strategy to obtain short- and long-term gains (Falconer and Mackay, 1996). Genetic correlation between traits is also an important tool in the selection process, since it allows the breeder to conduct indirect selection if the correlation between two traits is high (Falconer and Mackay, 1996). For example, breeders can select individuals for volume by analyzing diameter at breast high (DBH), which is a much easier parameter to obtain. For breeding programs, it is also necessary to understand if the individual phenotypes are influenced not only by environmental and genetic factors, but also if there is an interaction between them, called genotype x environmental (GxE) interaction (Tabery, 2007).

The GxE interaction is considered a challenge to improvement because it interferes with the identification of genetic material. That is, the most productive genetic material in tests might not achieve peak performance across all of a company's production sites due to variations in edaphoclimatic conditions. Understanding the GxE interaction allows the breeder to identify the best genetic materials for different locations, considering these variations (Vencovsky and Barriga, 1992).

In this context, this study aimed to analyze two *E. dorrigoensis* progeny tests and estimate the genetic parameters, including genetic correlations between traits, determine the BLUP components to rank the best genetic materials, and indicate the most suitable individuals for each/both environments considering the GxE interaction.

MATERIAL AND METHODS

Field experiments

The data were provided by CMPC Company and includes information from two *E. dorrigoensis* progeny tests, each with 98 open-pollinated progenies, of which 49 were collected from Dorrigo National Park and 49 from Tenterfield, both in Australia. Five control treatments (99, 100, 101, 102, and 103), which are highly productive commercial clones used by the company were included for comparison: 99 (*Eucalyptus saligna*), 100 (*Eucalyptus benthamii*), 101 (*Eucalyptus dunnii*), 102 (*Eucalyptus urophylla* x *Eucalyptus maidenii*) and 103 (*Eucalyptus urophylla*). Both tests were established in randomized blocks with single tree plots and 20 replications (for a total of 2060 plants in each test). The evaluated traits included diameter at breast high (DBH), total height (H) and mean annual increment in volume (MAI, m^3/hectare/year). Measurements were taken at two and a half years after installation. The edaphoclimatic information for the two environments in which are the tests were established are shown in Tab. 1.

Tab. 1 Edaphoclimatic information for two progeny tests of *Eucalyptus dorrigoensis*.

	Sertão Santana	Lavras do Sul
Latitude (Degrees)	-30.512153	-30.664261
Longitude (Degrees)	-51.527669	-54.466567
Elevation (m)	134	160
Soil	Dystrophic Red-Yellow Argisol	Arsenic Yellow Dystrophic Argisol
Soil Fertility	Medium	Low
Average Temperature (°C)	19.8	19.8
Minimum Temperature (°C)	2	-2.3
Maximum Temperature (°C)	37.3	38.3
Relative Humidity (%)	83.1	75.6
Frost Risk	Low	High
Annual Rainfall (mm)	1,735	1,678

Genetic parameters

Estimates of the variance components and genetic parameters were performed using the REML/BLUP methodology in the R software environment (R Core Team, 2018), with the package lme4 (Bates et al., 2015). Both progeny tests were analyzed individually, according to the mixed model (equation 1), where, β is the fixed effects vector associated with replication; g is the random effects vector associated with progeny; ***e*** is the residual random effects vector; and *X* and *Z* are the incidence matrices of the effects. In addition, a joint analysis was performed with the two progeny tests to verify the significance of the GxE interaction (equation 2), where, *ga* is the GxE interaction random effect vector. The GxE interaction was decomposed in order to understand its effects (Cruz and Castoldi, 1991). The estimated variance components were: σ_p^2= genetic variance (among progenies); σ_e^2 = residual variance; and σ_{ga}^2 = GxE interaction variance. The estimated parameters were: narrow-sense heritability at the individual level (equation 3); mean heritability among progeny (equation 4); coefficient of genetic variation among progeny (equation 5); coefficient of individual genetic variation (equation 6); coefficient of residual variation (equation 7); and selection accuracy (equation 8). Where, m is the mean of the traits.

$$y = X\beta + Zg + e \tag{1}$$

$$y = X\beta + Zg + Zga + e \tag{2}$$

$$h_i^2 = \frac{4\sigma_p^2}{\sigma_p^2 + \sigma_e^2} \tag{3}$$

$$h_m^2 = \frac{\sigma_p^2}{\sigma_p^2 + \frac{\sigma_e^2}{rep}} \tag{4}$$

$$CV_g(\%) = \frac{\sqrt{\sigma_p^2}}{\bar{m}}.100 \tag{5}$$

$$CV_{gi}(\%) = \frac{\sqrt{4\sigma_p^2}}{\bar{m}}.100 \tag{6}$$

$$CV_e(\%) = \frac{\sqrt{\sigma_e^2}}{\bar{m}}.100 \tag{7}$$

$$Ac = \sqrt{h_i^2} \tag{8}$$

Adaptability, stability, and productivity

The GxE analysis for adaptability, stability, and productivity were performed in R using the GGE Biplots package (Dumble, 2017), which creates graphical representations that indicate the best genetic materials for each environment as well as the most stable materials, or those that perform well in both sites.

Genetic correlation

The genetic correlation between traits was performed according to the methodology described by Vencovsky and Barriga (1992), which consists of obtaining the mean product through three ANOVA sum of squares for Trait *x*, Trait *y*, and *x+y* (equation 9), Where SS is the sum of squares, and Df is the degrees of freedom. The genetic covariance was estimated using the mean product, according to the equation 10, where, PM_{trait} is the trait mean product; PM_{res} is the residual mean product; and rep is the number of replications. Subsequently, the genetic correlation between the two analyzed traits was estimated by the equation (11), where, COV_g is the genetic covariance; σ_{gx}^2 is the genetic variance of trait *x*; and σ_{gy}^2 is the genetic variance of trait *y*.

$$Pm = \frac{0.5\,(SS_{x+y} - SS_x - SS_y)}{Df} \tag{9}$$

$$COV_g = \frac{(PM_{trait} - PM_{res})}{rep} \tag{10}$$

$$r_{g(x,y)} = \frac{COV_g}{\sqrt{\sigma_{gx}^2\sigma_{gy}^2}} \tag{11}$$

Simulated thinning and genetic gains

In order to inform intrapopulation recurrent selection, a simulated thinning was performed, leaving only the progenies that achieved positive BLUP values (those that may aggregate positive values for subsequent generations) for mean annual increment in volume (MAI). Based on this requirement, both tests had a selection intensity of about 50%, excluding the controls.

The effective number was estimated before and after simulated thinning, according to the following equation (12), where, N_e is the effective number; N_f is the number of families; $\bar{K}_f$ is the average number of individuals selected per family; σ_{kf}^2 is the variance of the number of individuals selected per family.

The genetic gains from selection were estimated for both tests, based on the equation (13), where, $GS(\%)$ is the genetic gain (%); $\bar{x}_s$ is the mean of the selected population; $\bar{x}_0$ is the mean of the trait for original population; h_i^2 is the narrow-sense heritability.

$$N_e = \frac{4N_f\bar{K}_f}{\bar{K}_f + 3 + (\frac{\sigma_{kf}^2}{\bar{K}_f})} \tag{12}$$

$$GS\,(\%) = \frac{(\bar{x}_s - \bar{x}_0)\,.\,h_i^2}{\bar{x}_0}.100 \tag{13}$$

RESULTS

The Sertão Santana site showed greater heritability than Lavras do Sul, which suggests better selection accuracy (Tab. 2). The $CV_e(\%)$ for all traits was inferior in Sertão Santana, showing less influence of environmental factors for this site. In addition, the $CV_g(\%)$ and $CV_{gi}(\%)$ were also generally high in Sertão Santana.

The GxE interaction was tested using ANOVA (Tab. 3) of the joint database. The results show that the interaction is significant and must be considered in the improvement program. Also, the GxE was decomposed into percentage of simple and complex interaction, resulting in 21.3% simple and 78.7% complex.

The best linear unbiased prediction (BLUP) components were also estimated to rank the best genotypes (Tab. 4) by genetic factors in both environments. The fifteen best individuals included not only the controls, which are known to be highly productive, but also progenies that have potential for further use. The top-ranking progenies in each environment were different, supporting the result that

Tab. 2 Genetic parameters of *Eucalyptus dorrigoensis* progeny tests established in Sertão Santana and Lavras do Sul for DBH (cm), H (m) and mean annual increment in volume (MAI) ($m^3 \cdot hectare^{-1} \cdot year^{-1}$) at 2.5 years of age.

	Sertão Santana					
Parameters	DBH	H	MAI	DBH	H	MAI
h_i^2	0.612	0.465	0.644	0.402	0.380	0.478
h_m^2	0.783	0.725	0.793	0.691	0.677	0.730
Ac	0.885	0.851	0.891	0.831	0.820	0.854
$CV_g(\%)$	12.2	8.1	26.1	10.0	8.3	22.2
$CV_{gi}(\%)$	24.5	16.2	52.1	20.0	16.5	44.4
$CV_e(\%)$	28.8	22.4	59.5	28.9	25.5	60.2
Mean	11.64	11.22	24.73	10.35	9.87	18.70

h_i^2: narrow-sense heritability; h_m^2: progeny mean heritability; Ac: selection accuracy; $CV_g(\%)$: coefficient of genetic variation; $CV_{gi}(\%)$: coefficient of individual genetic variation; $CV_e(\%)$: coefficient of residual variation.

Tab. 3 Joint ANOVA for both *E. dorrigoensis* progeny tests implemented in Sertão Santana and Lavras do Sul for mean annual increment in volume (MAI, $m^3 \cdot hectare^{-1} \cdot year^{-1}$) at 2.5 years of age.

Factors	Df	Sum Sq	Mean Sq	F Value
Replications	19	10278	540.95	3.20***
Progenies	102	61772	605.61	3.58***
Environment	1	25543	25543.00	150.98***
G x E Interaction	102	46493	455.81	2.69***
Residual	2566	434118	169.18	

***: Significant at 0.1%; Df: Degrees of freedom; Sum Sq: Sum of squares; Mean Sq: Square mean.

78.7% of the GxE interaction is complex, meaning that the influence of the environment will most likely affect the rank of the best progenies between the environments.

The biplot analysis (Fig. 1) indicates the best genetic materials for each environment. In this graph, the closer the genotype is to the environment region, the better its performance at that site. Consequently, the further away the genotype, the poorer its performance in that environment. The size of the vector indicates how productive the genetic material is. In this case, control 103 occurs between both environments and with a large vector, meaning that it is a highly productive genetic material. This also corroborates its selection by BLUP (Tab. 4), where it is ranked in the top 15 for both environments. For Lavras do Sul, progenies 18, 3, and the control 99 achieved the greatest means for MAI (Volume). For Sertão Santana, progenies 89, 56, and the control 102 were the most productive. The larger vectors that are opposite to the plotted environments were the least productive genetic materials, including progenies 6, 54, 47, and 83.

In addition, the most stable genetic material, or those that perform equally (good or poor) in all environments were also analyzed (Fig. 2). In this graph, the closer the genotype is to the centerline, the more stable it is, with the most productive genotypes occurring in the direction of the arrow. Again, control 103 was the most productive in both environments, making it the most stable and most productive genetic material. The most productive and stable progenies are 95 and 70.

The genetic correlation between traits was estimated (Tab. 5) and shows high correlation in both environments, above 0.80 for all traits.

The thinning simulation (Tab. 6) showed 12.62 and 7.43% genetic gains for Sertão Santana and Lavras do Sul, respectively. The original effective number for both cases were 340, decreasing more than 50% after thinning.

DISCUSSION

Genetic variation higher than 8% was detected among progeny ($CV_g\%$) and for individual genotypes ($CV_{gi}(\%)$) for all traits, indicating that both trials have potential for improvement by selection among progeny and at the individual level, respectively. This result is essential for breeding programs since the higher the genetic diversity the longer the program will last, enabling genetic gains in the short and long term (Pereira and Vencovsky, 1988). According to Sebbenn et al. (2008), values of $CV_{gi}(\%)$ above 7% are considered high. It is noteworthy that the higher the $CV_{gi}(\%)$, the greater the chances of genetic gain throughout the breeding program. The highest genetic variation was observed for MAI in both progeny tests. The coefficient of residual variation ($CV_e\%$) was higher for all traits in Lavras do Sul, suggesting that the environmental control of the trial was lower, and the progenies are more likely to be suffering environmental effects. For DBH and H, the $CV_e(\%)$ was lower in both trials (ranged from 22.4 to 20.9%), than MAI (59.5-60.2%). These values are considered acceptable in field experiments, due to the difficulty in controlling the effects of environmental variation (Pimentel-Gomes and Garcia, 2002). For MAI, the values are considered high, but also expected due to the fact that the trait is estimated from DBH and H, accumulating the experimental variation of both traits (Rocha et al., 2007; Moraes et al., 2015). High $CV_e\%$ value means that the model could not capture all the variance effects, indicating that environmental conditions are affecting plant development.

For Sertão Santana, the narrow-sense heritability (varied among traits from 0.465 to 0.644) was generally higher for the traits than in Lavras do Sul (0.380 to 0.478). The values between 0.380 to 0.478 are classified as medium magnitude and higher than 0.5 as high magnitude (Resende, 1995). The fact that Lavras do Sul had lower heritability can be explained by the higher residual $CV_e(\%)$ values, which indicates greater environmental effects that directly influence the calculation of heritability.

Average heritability among progeny was estimated in order to determine selection accuracy and verify the reliability of the selection. As expected, Sertão Santana presents higher accuracy values, since it had lower residual effects and captured more genetic variance due to greater environmental control (lower $CV_e(\%)$). The Ac values ranged from 0.851 (H) to 0.891 (MAI). Although Lavras do

Tab. 4 Ranking of the best individuals according to the BLUPs component from two *E. dorrigoensis* progeny tests implemented in Sertão Santana and Lavras do Sul for mean annual increment in volume (MAI, m^3·hectare^{-1}·year^{-1}) at 2.5 years of age.

	Sertão Santana				Lavras do Sul			
Rank	Progeny	Replication	MAI	Control	Progeny	Replication	MAI	Control
1	65	16	78.81	No	103	5	51.72	Yes
2	76	6	72.47	No	94	5	67.06	No
3	94	6	69.86	No	103	12	47.85	Yes
4	103	17	62.18	Yes	4	4	67.46	No
5	93	17	71.45	No	103	7	47.18	Yes
6	86	3	71.26	No	103	9	45.88	Yes
7	98	16	70.62	No	103	6	45.38	Yes
8	103	11	60.16	Yes	103	2	44.10	Yes
9	76	10	65.52	No	103	10	42.88	Yes
10	94	8	64.49	No	103	19	41.42	Yes
11	72	14	73.07	No	56	3	55.79	No
12	102	1	61.77	Yes	81	2	55.85	No
13	103	13	56.88	Yes	3	2	55.81	No
14	67	3	64.85	No	103	15	37.28	Yes
15	67	5	64.41	No	103	8	38.49	No

***: Significant at 0.1%; Df: Degrees of freedom; Sum Sq: Sum of squares; Mean Sq: Square mean.

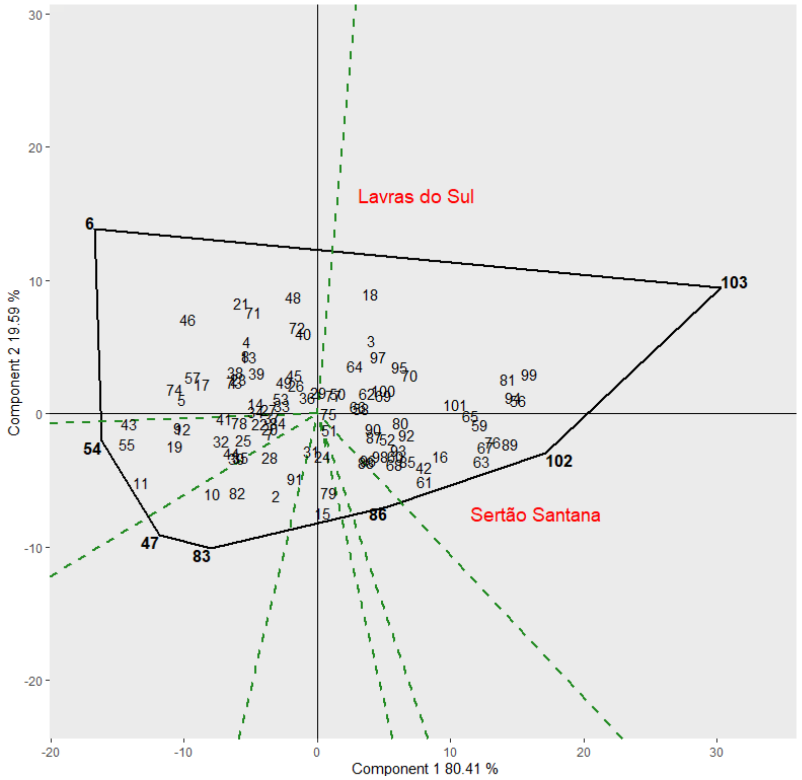

Fig. 1 Which-won-where GGE biplot indicating the performance of 98 progenies of *E. dorrigoensis* and 5 controls in Sertão Santana and Lavras do Sul, Rio Grande do Sul State, Brazil, for mean annual increment in volume (MAI, m^3·hectare^{-1}.year^{-1}) at 2.5 years of age.

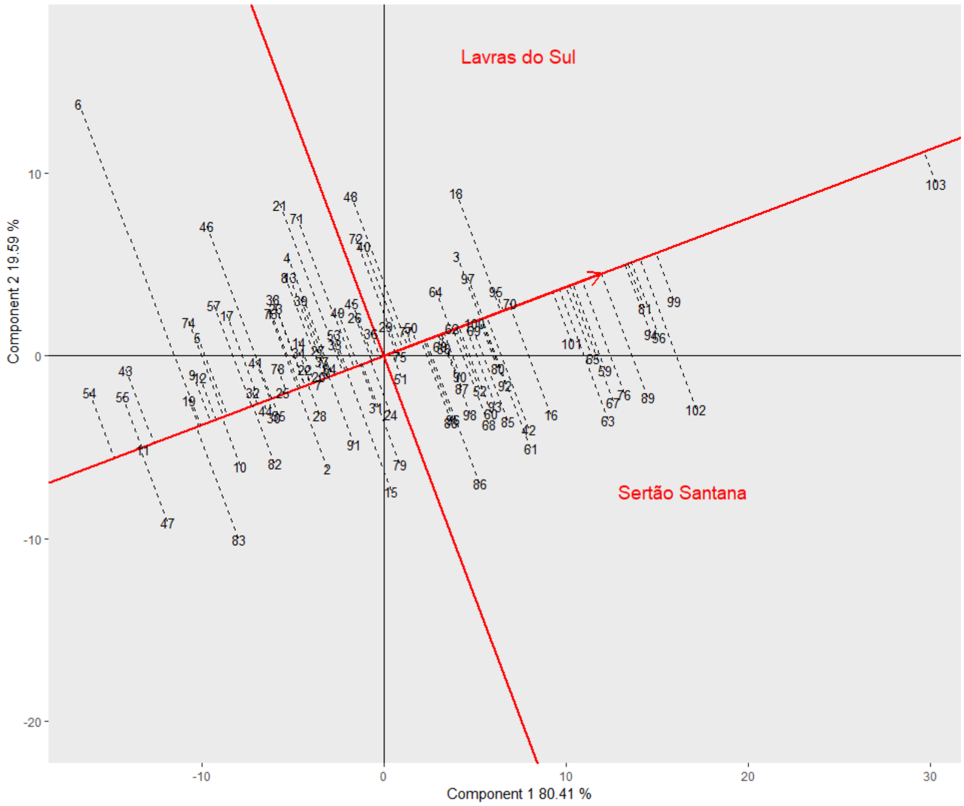

Fig. 2 Mean vs. Stability GGE biplot indicating the stability of 98 progenies of *E. dorrigoensis* and 5 controls in Sertão Santana and Lavras do Sul for mean annual increment in volume (MAI, $m^3 \cdot hectare^{-1} \cdot year^{-1}$) at 2.5 years of age.

Tab. 5 Genetic (upper diagonal) and phenotypic (lower diagonal) correlation between traits for two *E. dorrigoensis* progeny tests established in Sertão Santana and Lavras do Sul at 2.5 years of age.

	Sertão Santana			Lavras do Sul		
	DBH	H	MAI	DBH	H	MAI
DBH	1	0.9*	0.97*	1	0.84*	0.94*
H	0.97*	1	0.95*	0.94*	1	0.89*
MAI	0.94*	0.86*	1	0.92*	0.86*	1

*Significant at 5% ($P < 0.05$); DBH: diameter at breast high; H: total height; MAI: mean annual increment in volume..

Tab. 6 Thinning simulation based on medium annual increment in volume (MAI) for two *E. dorrigoensis* progeny tests established in Sertão Santana and Lavras do Sul at 2.5 years of age.

	Sertão Santana			Lavras do Sul		
	Mean	Ne	GS%	Mean	Ne	GS%
Original	27.73	340.00	-	18.70	340.00	-
After Thinning	30.16	146.08	12.62	21.63	156.50	7.43

Sul had lower accuracy values, they still reached around 0.7, which can be considered reliable for selection and implies increases in genetic gains (Resende, 1995).

The best genotypes were ranked in each environment by its BLUP components, and we can see a notable difference between those selected in both environments. This result is reasonable since the GxE interaction is significant at 0.01%, meaning that the interaction is highly complex and requires further analysis to indicate the most stable materials or those with the best performance for each location (Cruz et al., 2004). When the GxE interaction is strong, it is crucial to conduct an environmental stratification in order to select the most suitable genetic materials for the different locations. The complex interaction found in the current study may be related to the differences between the two environments, including soil type, fertility level, and occurrence of frost. In addition, it is important to note that many *E. dorrigoensis* individuals performed better than the controls according to the BLUP component, indicating high-productivity genetic materials.

GGE Biplot graphs (Fig. 1 and 2) offer information for breeders to understand the best genetic materials for each location, while also showing the most stable materials that can be planted in any location for good productivity. The GGE Biplot also substantiate the individual BLUPs (Tab. 3).

In both sites, the greatest genetic correlation was found between DBH and MAI (0.94 and 0.97). This indicates that DHB can be used in selection to improve MAI, considering that DBH is easy to measure. For DBH/MAI and H/MAI the genetic correlation was superior than the phenotypic correlation, the same phenomenon was reported by Andrade et al. (2018), which may be attributed to the minimum square analysis.

The thinning simulation showed higher genetic gains for Sertão Santana (12.62%) compared to Lavras do Sul (7.43%). This result is reasonable since Sertão Santana achieved greater levels of productivity and higher narrow-sense heritability than Lavras do Sul. The selected progenies include those that are the most productive and the most stable for each site.

E. dorrigoensis is a poorly exploited species in breeding programs in Brazil. However, it can be considered a potential genetic resource, as its wood density is adequate for pulp production (0.491 g.cm^{-3} at ten years of age) and it is tolerant to cold, an important characteristic for Southern Brazil. The average MAI reached 24.73 m^3/ha.year at 2.5 years of age, although some individuals reached values > 78 m^3/ha.year (progeny 65, plot 16). This value is higher than that reported for *Eucalyptus grandis* of 70 m^3/ha.year at five years of age (Fernandes et al., 2012). The studied *E. dorrigoensis* progeny tests presented genetic variability, which is crucial for breeding programs and enables short- and long-term genetic gains. To advance our understanding of pure populations, the progeny tests must be evaluated again at the age of harvesting, when the best progenies and the best individuals of each progeny can be selected based on the BLUP methodology. These top-performing individuals can be used to establish clonal seed orchards to increase favorable allele frequencies, since *E. dorrigoensis* is not yet included in the company's breeding program. The results of this study must be compared to future analyses to create an early selection methodology for this species. High-productivity progenies (i.e., progeny 89 with an average MAI 38.11 m^3/ha.year) were identified within these populations, suggesting that there is potential to exploit this genetic variability, beginning with the recurrent selection of the best genetic material. Considering that the controls (average MAI of 32.44 m^3/ha.year) represent productive clones, the individuals whose performance exceeded that of the clones may provide an option for short-term gains in productivity, with the utilization of tested clones.

It is important to highlight that control 103 proved to be the most productive genetic material in both sites; however, it is a commercial clone used by the company and its superiority was expected. This fact reinforces that it is crucial to select the best *E. dorrigoensis* progenies to develop a seed orchard to advance the species' breeding program through recurrent selection. In the same region where this study was conducted, clone productivity of 37 different *Eucalyptus* species reached an average MAI of 32.84 m^3/ha.year at three years of age (Santos et al., 2015). These results underscore the potential of *E. dorrigoensis,* since several progenies (89, 56, 76, 94, 63, 67, 81, 59, 65, 16, 61, and 42) obtained a MAI greater than those reported in the previous study. It must be considered, however, that the GxE interaction is significant and mostly complex. Thus, the identification of the best genetic material is different depending on the environment.

The results obtained herein have practical implications since they can indicate either: i) the best progenies and individuals for both Sertão Santana and Lavras do Sul; or ii) the most stable progenies and individuals that perform well in both sites. In case i), we may opt to select different genetic materials for each site, cloning the best individuals for each environment to proceed with clonal tests. In this scenario, the selected individuals for Sertão Santana would be 65 (plot 16), 76 (plot 6), 94 (plot 6), 93 (plot 17), and 86 (plot 3) with progeny average MAI in this environment of 34.48, 36.84, 36.83, 30.66, and 31.67 m^3/ha.year, respectively. For Lavras do Sul, on the other hand, the selected individuals would include 94 (plot 5), 4 (plot 4), 56 (plot 3), 81 (plot 2), and 3 (plot 2) with progeny average MAI of 25.59, 21.11, 25.48, 26.59, and 24.99 m^3/ha.year, respectively. Although these progeny did not achieve the largest MAI in the population, they were the most productive *E. dorrigoensis* individuals within the tests based on their BLUP score.

In case ii), the breeder may opt to select stable genetic material to be used simultaneously in both sites. In this scenario, the selected progenies would be 70 and 95, with progeny average MAI of 26.44 and 26.07 m^3/ha.year, respectively. In addition, the genetic correlation between traits shows that breeders may select individuals for high productivity based on a larger DBH, which is much easier and cost effective to obtain, since both environments showed high genetic correlation of these traits.

CONCLUSIONS

The studied populations have genetic variability that can be used in breeding programs by selecting among progenies and individuals within progenies. The genetic correlation between traits indicates that DBH can be used in selection to increase the MAI. The GxE interaction is mostly complex, and as such, the best genetic material should be selected independently for each site.

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AUTHORSHIP CONTRIBUTION

Project Idea: OPS

Database: OPS

Processing: OPS, BMRTV

Analysis: LVM,

Writing: LVM, EVT

Review: LVM, EVT, OPS, BMRTV

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