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Genetic parameters and correlation between growth traits in young progenies of *Corymbia torelliana* (F.Muell.) KD Hill and LAS Johnson

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SILVICULTURE

ABSTRACT

Background: *Corymbia torelliana* is a promising alternative for the forestry sector due to its rapid growth, resistance, and high-quality wood for charcoal and biomass production. However, there is limited information regarding its genetic performance under Brazilian conditions. This study aimed to estimate genetic parameters and evaluate correlations between growth traits in young half-sib progenies. The experiment was conducted in Lavras, MG, with 28 progenies evaluated in a randomized complete block design, with eight replications and five plants per plot. Height (H) and diameter at breast height (DBH) were measured at 12, 18, and 24 months, and genetic estimates were obtained using the REML/BLUP method, including analyses of genotypic and phenotypic correlations.

Results: Narrow-sense heritabilities showed moderate magnitude (0.18 to 0.22), as well as progeny selection accuracy (0.64 to 0.68). Individual genetic variation coefficients ranged from 8.3% to 12.8%, indicating genetic variability among individuals. The environmental effect among plots was significant, with a determination coefficient above 0.10. Average DBH ranged from 2.4 to 5.3 cm with increasing age, and mean height reached 2.91 m at 12 months. High genetic and phenotypic correlations suggest potential for simultaneous selection, although indirect selection accuracy was lower than direct selection.

Conclusion: The results confirm the genetic potential of *C. torelliana* for selective gains, particularly in DBH at 24 months. The study highlights the importance of improving management practices and selection strategies to mitigate environmental effects and enhance the accuracy of genetic estimates.

Keywords: Forestry, forest breeding; heritability; indirect selection.

HIGHLIGHTS

Moderate heritability indicates potential for genetic selection in *C. torelliana*.
Accuracy of estimates was satisfactory despite experimental heterogeneity.
Correlations across ages indicated limitations for early indirect selection.
Findings support silvicultural diversification and strengthen breeding programs.

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INTRODUCTION

Brazilian silviculture has traditionally relied on a few exotic species of the genus *Eucalyptus*, such as *E. grandis* W.Hill ex Maiden, *E. urophylla* S.T. Blake, and their hybrids (Assis et al., 2015; Barros et al., 2022), valued for their productivity, adaptability, and extensive scientific knowledge. However, dependence on a small number of species poses challenges amid environmental issues and the need for diversification and sustainability in forest production systems.

Non-traditional species such as *Corymbia torelliana* represent viable alternatives for expanding the cultivated genetic base and addressing region-specific requirements (Melo et al., 2024). *C. torelliana* demonstrates rapid growth, tolerance to adverse environmental conditions, and produces high-density wood suitable for biomass, charcoal, and timber products (Loureiro et al., 2021; Massuque et al., 2022; Pereira et al., 2021). Its silvicultural characteristics support its suitability for cultivation in tropical and subtropical regions (Silva et al., 2023).

Interspecific hybrids can be produced between *C. torelliana* and species collectively referred to as Spotted gums, including *C. citriodora* (Hook.) K.M.P.Conn. & B.H.F.P., *C. henryi* (S.T.Blake) K.D.Hill & L.A.S.Johnson, and *C. maculata* (Hook.) K.D.Hill & L.A.S.Johnson (Brune, 2021). According to this author, these hybrids demonstrate enhanced resistance to both biotic and abiotic stresses compared to the pure species and exhibit adaptability to diverse environments. Moreover, *C. torelliana* contributes a maternal effect during hybridization that improves the rooting success of mini-cuttings in clonal production (Assis, 2015) and increases hybrid seed yield by a factor of four relative to the pure species (Lee, 2007). Therefore, scientific data and the identification of superior genotypes are required to facilitate the development of hybrids involving *C. torelliana*.

Although this species offers significant ecological and economic benefits, limited information exists on the genetic performance of its progenies in Brazil. Progeny testing and estimation of genetic parameters, including heritability and variance among progenies, are critical for developing effective selection strategies and achieving sustainable genetic improvement (Santos et al., 2021). Mixed models, utilizing Restricted Maximum Likelihood and Best Linear Unbiased Prediction (REML/BLUP), efficiently account for random effects and yield accurate genetic value predictions, even with unbalanced experimental data (Resende, 2016).

As a complementary strategy for implementing breeding programs, analyzing correlations between growth traits can guide the simultaneous selection of multiple traits (Oliveira et al., 2021; Santos et al., 2021). Positive and significant correlations enable indirect selection, in which the improvement of one trait can reflect gains in another of interest, optimizing selection efforts (Santos et al., 2021).

In this context, the present study aims to estimate genetic parameters and evaluate correlations between growth traits in young half-sib progenies of *Corymbia torelliana*. By providing information on the performance and genetic variability of these progenies, the study seeks to expand the available silvicultural options, stimulate technological innovation in the sector, and reduce reliance on traditionally used species. Such information enables tree breeders to understand the species' potential for early selection, identify the most relevant silvicultural traits to be evaluated when aiming at wood production, assess the species' performance in the region, and support decision-making in future genetic improvement programs involving the species.

MATERIAL AND METHODS

Study site and experiment establishment

The study was conducted at Fazenda Muquém, located at the Federal University of Lavras (UFLA) in Lavras, Minas Gerais (MG), at coordinates 21º14'S and 45º00'W. At this site, in August 2022, a progeny test with the species *Corymbia torelliana* was established, comprising 28 half-sib progenies derived from mother trees sampled in populations located at different sites in Minas Gerais, Brazil. The experiment followed a randomized complete block design with eight replications and five plants per plot, spaced at 3.0 m × 1.0 m, occupying approximately 0.4 ha. Border trees were planted around the trial to minimize edge effects and were not included in the evaluations.

The climate is Cwa according to Köppen, characterized by cold, dry winters and hot, humid summers (Alvares et al., 2013). The annual mean temperature is 20.4°C, and the mean annual precipitation is 1460 mm (Dantas et al., 2007). During the coldest months, mean temperatures range from 17.1°C to 18.6°C, while in the warmest months, they range from 22.1°C to 22.8°C, at an approximate altitude of 918 m (Dantas et al., 2007). The soil of experimental area was a Red-Yellow Argisol.

Before planting, leaf-cutting ants were controlled through the application of granular ant bait. Subsequently, the area was cleared using a tractor-drawn mechanical brush cutter. Thirty days after clearing, a desiccant herbicide was applied at a rate of 4 L ha^{-1}. Soil preparation was then carried out using a subsoiler, which reached a depth of 60 cm.

At the time of planting, 150 g of single superphosphate per planting hole was applied. Irrigation was performed immediately after planting and again four days later due to the period of water deficit, with approximately 2 L of water applied per seedling in each irrigation. Leaf-cutting ant control was maintained through weekly inspections during the first six months and subsequently through monthly rounds, using the same ant bait previously mentioned.

Top-dressing fertilizations were performed at 6, 12, and 24 months after planting, with the application of 100 g of NPK 20-05-10 fertilizer per plant. Weed control was conducted at 5, 12, and 18 months using a manual mechanical brushcutter, in addition to the application of glyphosate herbicide at a dose of 4 L ha^{-1}. Additionally, at 18 months, supplementary fertilization was carried out with 10 g of zinc sulfate and 17 g of boric acid per plant.

Experiment evaluation

The experiment evaluations were conducted at 12, 18, and 24 months: height (H) was measured using a graduated ruler (m), and diameter at breast height (DBH) was obtained by measuring the circumference at 1.30 m above the ground with a measuring tape (cm) and subsequently converted to diameter.

The estimation of variance components and genetic parameters was carried out using the Restricted Maximum Likelihood / Best Linear Unbiased Prediction (REML/BLUP) procedure, based on the statistical model (Eq. 1).

$$y = Xr + Za + Wp + e \qquad (1)$$

Where: y is the data vector; r is the replication vector, assumed as a fixed effect; a is the vector of additive genetic effects; p is the vector of plot effects; e is the residual vector; the uppercase letters X, Z, and W represent the incidence matrices of the effects above, respectively. The vectors are random effects, except for the vector r.

After fitting the model, a deviance analysis and a likelihood ratio test (LRT) were conducted, adopting a significance level of 5% ($p < 0.05$), based on the chi-square distribution, to verify the significance of the additive genetic effects and the plot effect. For the variables and ages that proved significant, genotypic and phenotypic correlations were estimated using analysis of covariance, based on the additive genetic and phenotypic covariance matrices.

The statistical analyses were conducted using the Selegen-REML/BLUP software (Resende, 2016). For this, the equations for the components of additive genetic variance ($\hat{\sigma}_a^2$, Eq. 2); environmental variance between plots ($\hat{\sigma}_c^2$, Eq.3); residual variance ($\hat{\sigma}_e^2$, Eq. 4); and individual phenotypic variance ($\hat{\sigma}_p^2$, Eq. 5), are presented:

$$\hat{\sigma}_a^2 = \frac{\hat{a}' A^{-1}\hat{a} + \hat{\sigma}_e^2 tr\left(A^{-1}C^{22}\right)}{q} \qquad (2)$$

$$\hat{\sigma}_c^2 = \frac{\hat{c}'\hat{c} + \hat{\sigma}_e^2 trC^{33}}{s} \qquad (3)$$

$$\hat{\sigma}_e^2 = \frac{y'y - r'X'y - \hat{a}'Z'y - \hat{c}'W'y}{N - r\left(x\right)} \qquad (4)$$

$$\hat{\sigma}_p^2 = \hat{\sigma}_a^2 + \hat{\sigma}_c^2 + \hat{\sigma}_e^2 \qquad (5)$$

Where: $\hat{a}$ is the vector of estimated additive genetic values; $\hat{a}'$ is the transposed vector of estimated additive genetic values; A^{-1} is the inverse of the additive correlation matrix between the individuals evaluated; C^{22}, C^{33} are derived from the inverse of C; C is the matrix of coefficients of the mixed model equations; $\hat{c}'$ is the transposed vector of the random effects of plots; $\hat{c}$ is the vector of the random effects of plots; y is the vector of observed data; tr is the trace operator; $r(x)$ is the rank of matrix X; N, q, s are, respectively, the numbers of data, individuals and plots. The descriptions of the equations for the genetic parameters and the genotypic and phenotypic correlations are presented in Table 1.

Values of genotypic and phenotypic correlations were shown in heatmap graphs, generated using R software (R Core Team, 2024) with the ggplot2 (Wickham et al., 2025) and ggcorrplot (Kassambara, 2023) packages. Additionally, a principal component analysis (PCA) was performed on the statistically significant variables and ages, again using R software (R Core Team, 2024) and the ggplot2 package (Wickham et al., 2025).

Based on the accuracy of progeny selection (Ac_{prog}) and genetic correlations ($\hat{r}_{gxy}$), values of indirect selection accuracy were calculated (ASI; Eq. 6), according Resende (2002), where:

$$ASI = \hat{r}_{gxy}\ Ac_{prog} \qquad (6)$$

ASI was calculated for pairs of variables, with variable x being the one measured to obtain a response in variable y, which was the target of indirect or early selection. Thus, ASI is compared with Ac_{prog} of y variable, to verify whether there is an advantage in indirect selection and early selection.

RESULTS

Deviance analysis (Table 2) show a significant progeny effect for height at 12 months (H12) based on the LRT at a 5% error probability, indicating genetic variability among progenies at this early stage. However, no differences were observed for height at 18 and 24 months (H18 and H24), suggesting a decline in genetic variability for this trait over time. In contrast, the progeny effect for diameter at breast height at 12, 18, and 24 months (DBH12, DBH18, and DBH24) was significant, indicating the preservation of genetic variability for this trait.

Regarding the estimated genetic parameters, H12 presented $\hat{\sigma}_a^2$ of 0.05. For DBH, an increase in $\hat{\sigma}_a^2$, $\hat{\sigma}_c^2$, $\hat{\sigma}_e^2$, $\hat{\sigma}_p^2$ over the time evaluated, being approximately double from one age to another (Table 3).

The h_a^2 between the traits and ages evaluated presented values ranging from 0.18 to 0.22, while the values of h_{ad}^2 ranged to 0.23 to 0.34. Values of h_{mp}^2 were higher, shown 0.42 for H12 and varying between 0.41 and 0.47 for DBH. Values of Ac_{prog} were close for both traits and evaluation ages, being 0.65 for H12 and ranging from 0.64 to 0.68 for DBH. However, the highest value of Ac_{prog} was obtained for DBH24.

At all ages evaluated, $CV_{gi}\%$ was higher for DBH compared to H12. However, the highest $CV_{gi}\%$ value was shown in DBH12, which also occurred for $CV_{gp}\%$. $CV_e\%$ for H12 was lower than DBH at any age; however, it is noteworthy that $CV_e\%$ values for DBH decreased across the ages evaluated. CV_r values were similar for both traits and ages, ranging from 0.29 to 0.33.

The c_p^2 values were similar for H12 and DBH12, showing 0.45 and 0.44, respectively. However, they decreased for DBH between the ages of assessments. DBH growth from 12 to 18 months was higher (57%) than growth from 18 to 24 months (38%).

Table 1: Description of equations for estimating genetic parameters and genotypic and phenotypic correlations.

Parameters	Equations	Components
Narrow sense individual heritability (h_a^2)	$h_a^2 = \frac{\hat{\sigma}_a^2}{\hat{\sigma}_p^2}$	Additive variance ($\hat{\sigma}_a^2$) Phenotypic variance $\hat{\sigma}_p^2$
Narrow sense heritability within plots (h_{ad}^2)	$h_{ad}^2 = \frac{\hat{\sigma}_a^2}{\hat{\sigma}_a^2 + \hat{\sigma}_e^2}$	Additive variance ($\hat{\sigma}_a^2$) Residual variance $\hat{\sigma}_e^2$
Coefficient of determination of plot effects (c_p^2)	$c_p^2 = \frac{\hat{\sigma}_c^2}{\hat{\sigma}_p^2}$	Environment variance between plots ($\hat{\sigma}_c^2$) Phenotypic variance ($\hat{\sigma}_p^2$)
Mean heritability of progenie (h_{mp}^2)	$h_{mp}^2 = \frac{\hat{\sigma}_g^2}{\hat{\sigma}_g^2 + \frac{\hat{\sigma}_c^2}{r} + \frac{\hat{\sigma}_e^2}{rn}}$	Genetic variance ($\hat{\sigma}_g^2$) Residual variance $\hat{\sigma}_e^2$ Environment variance between plots ($\hat{\sigma}_c^2$) Number of plots per progeny (*r*) Number of plants per progenies (*n*)
Accuracy of progeny selection (Ac_{prog})	$Ac_{prog} = \sqrt{h_{mp}^2}$	Mean heritability of progenie (h_{mp}^2)
Coefficients of individual additive genetic variation (CV_{gi}%)	$CV_{gi} = \frac{\sqrt{\hat{\sigma}_a^2}}{\hat{m}}.100$	Additive variance $\hat{\sigma}_a^2$ Overall mean ($\hat{m}$)
Coefficient of genetic variation between progenies (CV_{gp}%)	$CV_{gp} = \frac{\sqrt{\hat{\sigma}_g^2}}{\hat{m}}.100$	Genetic variance ($\hat{\sigma}_g^2$) Overall mean ($\hat{m}$)
Residual coefficient of variation (CV_e%)	$CV_e = \frac{\sqrt{\hat{\sigma}_e^2}}{\hat{m}}.100$	Residual variance $\hat{\sigma}_e^2$ Overall mean ($\hat{m}$)
Relative coefficient of variation (CV_r)	$CV_r = \frac{CV_{gi}}{CV_e}$	Coefficients of individual additive genetic variation (CV_{gi}) Residual coefficient of variation (CV_e)
Genetic correlation $\hat{r}_{\hat{g}_{xy}}$	$\hat{r}_{\hat{g}_{xy}} = \frac{\hat{\sigma}_{gxgy}}{\sqrt{\hat{\sigma}_{gx}^2 . \hat{\sigma}_{gy}^2}}$	Genetic correlation coefficient ($\hat{r}_{\hat{g}_{xy}}$) Average gene product ($\hat{\sigma}_{gx}^2 \cdot \hat{\sigma}_{gy}^2$) estimated in the correlation for characters X and Y
Phenotypic correlation ($\hat{r}_p$)	$\hat{r}_p = \frac{Cov(xy)}{\hat{\sigma}_x \hat{\sigma}_y}$	*Cov*(*xy*) = Covariance between characteristics *X* and *Y*. $\hat{\sigma}_x \hat{\sigma}_y$ = Standard deviation of characteristics *X* and *Y*.

Table 2: Deviance analysis for total height and diameter at breast height in half-sib progenies of *Corymbia torelliana*, at 12, 18, and 24 months after planting, in Lavras, MG.

Total height (H - m)						
Effect	**12 months**		**18 months**		**24 months**	
	DEV	**LRT[1]**	**DEV**	**LRT[1]**	**DEV**	**LRT[1]**
Complete model	-481.06		190.86		739.42	
Progenies$^+$	-476.99	4.07*	191.33	0.47	739.43	0.01
Plot$^+$	-275.34	205.72*	490.58	299.72*	1092.83	353.41*

Diameter at breast height (DBH - cm)						
Effect	**12 months**		**18 months**		**24 months**	
	DEV	**LRT[1]**	**DEV**	**LRT[1]**	**DEV**	**LRT[1]**
Complete model	-97.79		546.47		1084.29	
Progenies$^+$	-93.10	4.69*	550.36	3.89*	1089.80	5.51*
Plot$^+$	101.10	3.31	677.42	130.95*	1188.64	104.35*

[1] Likelihood ratio test, with distribution with 1 degree of freedom; *significant at the 5% probability of error level by the chi-square test; +Deviance of the fitted model without the effects mentioned.

Table 3: Estimation of genetic parameters in testing of half-sibling progenies of *Corymbia torelliana*, at 12, 18, and 24 months after planting, in Lavras-MG.

Parameters	H12	DBH12	DBH18	DBH24
$\hat{\sigma}_a^2$	0.05	0.09	0.15	0.31
$\hat{\sigma}_c^2$	0.12	0.19	0.29	0.47
$\hat{\sigma}_e^2$	0.09	0.14	0.36	0.67
$\hat{\sigma}_f^2$	0.27	0.42	0.81	1.46
h_a^2	0.21 (0.08)	0.22 (0.09)	0.18 (0.08)	0.21 (0.08)
h_{ad}^2	0.32	0.34	0.23	0.25
c_p^2	0.45	0.44	0.36	0.32
h_{mp}^2	0.42	0.44	0.41	0.47
Ac_{prog}	0.65	0.66	0.64	0.68
$CV_{gi}\%$	8.33	12.83	10.14	10.54
$CV_{gp}\%$	4.16	6.41	5.07	5.27
$CV_e\%$	13.78	20.28	16.93	15.83
CV_r	0.30	0.31	0.29	0.33
Average	2.91 m	2.43 cm	3.82 cm	5.29 cm

Figure 1a shows the distribution of progenies based on the first two principal components, with no high correlation between progenies and any specific variable. However, the vectors for H12 and DBH12 are aligned and close, suggesting a positive correlation early in the development of progeny. DBH12 also remains close to DBH18 but moves away from DBH24, indicating that the correlation between diameter increments decreases over time. In turn, the vector for H12 progressively moves away from the vectors for DBH18 and, especially, from DBH24, signaling a decreasing association between initial height and diameter in later stages.

This pattern is corroborated by genotypic ($\hat{r}_{\hat{g}_{xy}}$) and phenotypic ($\hat{r}_p$) correlations, represented in Figures 1b and 1c, respectively. In the genotypic matrix (Figure 1b), high values of $\hat{r}_{\hat{g}_{xy}}$ are observed between diameter increments, such as between DBH12 × DBH18 (0.95) and DBH18 × DBH24 (0.92), reflecting the continuity of growth under strong genetic influence. The correlations between H12 and DBH at different ages are lower, with the lowest value, H12 × DBH24 (0.71), standing out, indicating a more limited contribution of initial height to diameter growth at later ages. In the phenotypic matrix (Figure 1c), $\hat{r}_p$ values maintain the same pattern, although at a slightly lower magnitude, such as DBH12 × DBH18 (0.78) and DBH18 × DBH24 (0.84), suggesting that environmental factors also influence, but to a more moderate extent. The low correlation between H12 and DBH24 (0.56) in this matrix reinforces the visual separation observed in the principal component analysis.

Table 4 presents the indirect selection accuracy (ASI) values, highlighting the potential of early-measured traits (variable x) for the prediction and selection of traits of interest evaluated at later ages (variable y). The ASI values ranged from 0.46 for the H12 × DBH24 combination to 0.63 for DBH12 × DBH18, indicating variation in the efficiency of indirect selection between different pairs of traits. However, it is noteworthy that, in all cases, the ASI values were lower than the direct selection accuracies (Ac_{prog}) obtained for the targeted variables (*y*).

DISCUSSION

The values obtained for individual narrow-sense heritability (h_a^2) were of moderate magnitude for H12 and DBH at all ages, according to the classification proposed by Ziegler and Tambarussi (2022). The parameter h_a^2 expresses the proportion of additive genetic variance in relation to the total phenotypic variance (Covarrubias-Pazaran, 2021). This is an essential parameter in plant breeding, as it guides the choice of selection methods, the experimental design, the number of replications, and the estimation of the expected genetic gain (Borém et al., 2021). Furthermore, it expresses the degree of difficulty or ease in improving the trait, indicating selection efficiency (Borém et al., 2021).

The moderate heritability estimates suggest that a substantial proportion of the phenotypic variation may be attributed to error variance, likely arising from the influence of uncontrolled environmental factors (Covarrubias-Pazaran, 2021). This agrees with the nature of long-term quantitative traits, such as growth traits like H and DBH, are strongly influenced by the environment, especially at an early age due to the greater influence of factors such as planting failures, early mortality, pest damage, and lower genotype expression (Li et al., 2024).

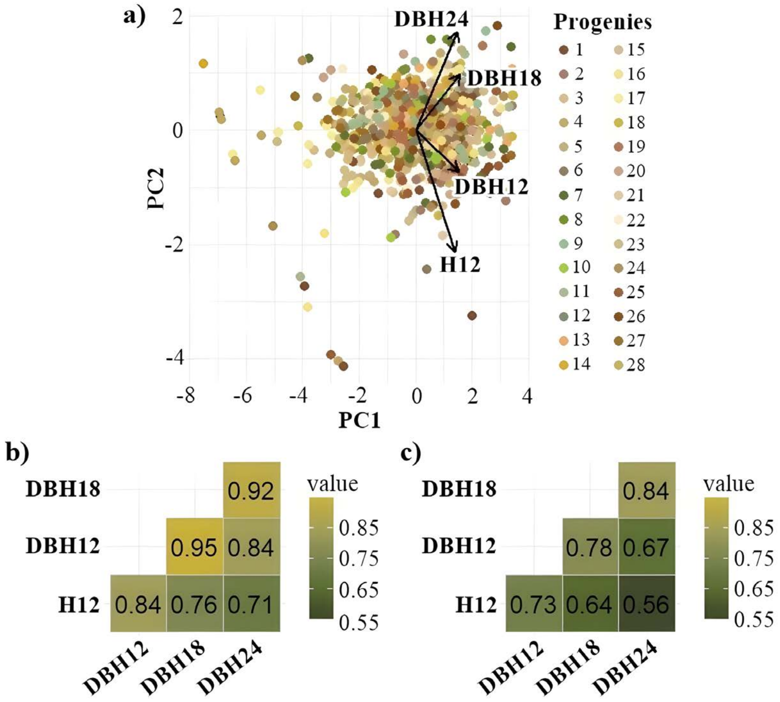

Figure 1: Correlation between early growth traits in half-sib progenies of *Corymbia torelliana*, in Lavras, MG. a) Principal Component Analysis (PCA) based on height (H) at 12 months and diameter at breast height (DBH) at 12, 18, and 24 months. b) Heatmap for genotypic correlations between early growth traits (height at 12 months and DBH at 12, 18, and 24 months). c) Heatmap for phenotypic correlations between early growth traits (height 12 months and DBH at 12, 18, and 24 months).

Table 4: Indirect selection accuracy (ASI) values in progeny testing of *Corymbia torelliana*, in Lavras, MG.

Measured variable (x)	Variable targeted for indirect selection (y)		
	H12	DBH18	DBH24
DBH12	0.55	0.63	0.55
H12		0.49	0.46
DBH18			0.59

Although eucalyptus management is widely established for the most widely cultivated commercial species in Brazil, such as *E. urophylla* and *E. grandis* (Assis et al., 2015; Barros et al., 2022), there are limitations regarding silvicultural practices for non-traditional species such as *C. torelliana*, which may have influenced heritability estimates. Nevertheless, the narrowing difference between h^2_a and h^2_{ad} for DBH across ages indicates that the systematic environmental effect decreased over time, suggesting that environmental heterogeneity had less influence on the trait as trees matured.

Heritability values at the progeny-mean level (h^2_{mp}) for both traits at all ages were also classified as moderate (Ziegler and Tambarussi, 2022). However, when comparing the h^2_{mp} estimated for DBH at 24 months with the results reported by Araujo et al. (2021), the present study indicates a stronger genetic control over family selection. This difference may reflect both the genetic variability captured in the evaluated material and the influence of specific environmental conditions, suggesting greater opportunities for selection gains in the present work. As expected, h^2_{mp} estimates were consistently higher than h^2_a estimates for all traits evaluated. However, the progressive increase in h^2_{mp} for DBH suggests that the progeny average maintained a good ability to discriminate superior genotypes, highlighting selection among families as a possible strategy to be explored. This pattern indicates that non-additive effects, such as dominance and epistasis, may play a relevant role in trait expression and could be efficiently exploited when selection is applied at the progeny level.

The accuracy of progeny selection (Ac_{prog}) was higher than 0.64 for all traits and ages, which can be classified as moderate in magnitude. This parameter represents the correlation between the true genetic value and the predicted genetic value, and is therefore a direct indicator of the reliability of the selections (Resende and Duarte 2007). The observed accuracy suggests that the genetic effects were estimated with good precision, even in the face of environmental influences and possible heterogeneity among plots within the block. Importantly, these results support the feasibility of early selection, since the estimates indicate that predictions are robust enough to guide breeding decisions without compromising genetic gains.

The plot effect was significant for both traits at all ages, with the exception of DBH12. This means that the environmental variance between plots ($\hat{\sigma}^2_c$) presented a value significantly different from zero, representing part of the phenotypic variation. Furthermore, the magnitude of the values of the coefficient of determination of the plot effects (c_p^2)were high according to Resende (2002), being greater than 0.1, indicating high heterogeneity within the blocks, which may compromise the accuracy of the genetic estimates.

However, a tendency for c_p^2 values to decrease for DBH was observed with advancing age, indicating that the environmental influence associated with the interplot effect tends to decrease over time. To mitigate this heterogeneity under similar experimental conditions, reducing the number of plants per plot may be a strategy to reduce c_p^2 e and improve the accuracy of the estimates (Kubota et al., 2015).

Regarding the coefficients of individual genetic variation (CV_{gi}%), their values ranged from 8.33% to 12.83%, reflecting the presence of genetic variability among the evaluated individuals (Ziegler and Tambarussi, 2022). Additionally, the coefficients of genetic variation between progenies (CV_{gp}) showed a lower range (4.16% to 6.41%), as expected, since they represent a group rather than an individual average. However, both parameters were only moderately higher than the experimental variation coefficients (CV_e%), with the ratio between CV_{gi} and CV_e (CV_r) ranging from 0.29 to 0.33. These results indicate that existing genetic variability can be useful in the selection process, although the potential gain may be limited by the magnitude of the residual variance ($\hat{\sigma}_e^2$), especially at younger ages.

The progression of the average diameter at breast height (DBH) over time highlights the favorable growth performance of *C. torelliana* under the edaphoclimatic conditions of the experiment. At 24 months after planting, the observed average (5.29 cm) was higher than that reported by Araujo et al. (2021), who obtained 3.81 cm for the same age. This discrepancy may reflect either the occurrence of genetic superiority among the evaluated materials or the influence of more favorable environmental and management conditions in this study. On the other hand, the average DBH recorded here was close to the value was similar to that reported by Gimenez et al. (2025), who observed 5.19 cm, corroborating the potential of the species for production purposes. Taken together, these comparisons suggest that *C. torelliana* not only performs consistently well across different studies but also presents opportunities for genetic selection and site-specific management strategies to further enhance productivity.

Genetic ($\hat{r}_{\hat{g}_{xy}}$) and phenotypic ($\hat{r}_p$) correlations between traits and ages shown high magnitudes, possibly associated with the occurrence of gene linkage or pleiotropy (Ramalho et al., 2021). Gene linkage is a transient phenomenon that tends to be broken during cycles of recombination, gene insertion, or deletion. In contrast, pleiotropy is a permanent condition, since the same gene simultaneously controls two or more traits (Oliveira et al., 2021; Ramalho et al., 2021). Thus, the persistence of high genetic correlations between the same traits evaluated at different ages can be attributed primarily to pleiotropic action. This distinction is relevant because it suggests that selection applied at early stages may remain effective over time, reducing the need for extensive evaluations across multiple developmental phases.

Similar observations were made by Oliveira et al. (2021), who reported genetic correlations greater than 0.70 between H and DBH in *Eucalyptus* spp. clones. These high correlations indicate a strong genetic association between the traits selection, suggesting that selection for one may effectively promote gains in the other. This opens the possibility for more efficient breending strategies through simultaneous trait selection.

However, indirect selection for H12 based on DBH12, as well as early selection for DBH12 targeting gains at later ages, did not prove to be advantageous over direct selection. According to Resende (2002), for indirect selection to be effective, the indirect selection index (ASI) must be greater than the accuracy of the target trait (Ac_{prog}). Furthermore, although the values of $\hat{r}_{\hat{g}_{xy}}$ between ages were high, the ASI indices obtained based on DBH12 for the prediction of DBH18 and DBH24 also did not surpass the respective direct accuracies.

Although there are significant genetic correlations between traits and ages, early selection, especially indirect selection, was not effective in this study. This strategy should be based on consistent quantitative criteria and, whenever possible, combined with multi-trait approaches that maximize genetic gain without compromising the accuracy of the selection process.

The results contribute to advancing the genetic evaluation within the *C. torelliana* breeding program, supporting the continuation of progeny testing to guide new silvicultural trials and strengthen the selection of promising genotypes. Management practices and selection methods will be refined to reduce environmental influences and increase the accuracy of genetic estimates, ensuring that superior individuals are effectively identified and propagated.

CONCLUSION

Heritability estimates revealed moderate genetic control for the growth traits evaluated, confirming the selection potential of *Corymbia torelliana*. The accuracy obtained was satisfactory, even in the presence of experimental heterogeneity, ensuring the reliability of the genetic estimates. Despite variability among individuals and families and significant genetic correlations between traits and ages, early selection, particularly indirect selection, proved ineffective in this study. The results provide relevant information on the performance and genetic variability of the evaluated progenies, indicating that this non-traditional species can contribute to the diversification of the forest base and broadly benefit both economic production and environmental sustainability.

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DATA AVAILABILITY

The datasets analyzed during the current study are available from the corresponding author upon reasonable request.

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