

Comparative assessment of LiDAR and conventional methods in evaluating genetic parameters of eucalypt progeny trials

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Abstract: *This study compared Light Detection and Ranging (LiDAR) and conventional methods in progeny trials of Eucalyptus cloeziana and E. saligna. Two populations, derived from open-pollinated progenies, were evaluated by using a randomized complete block design. Measurements were taken six years after planting for E. cloeziana and three years for E. saligna. The study aimed to assess genetic parameters and select individuals at typical breeding evaluation ages in Brazil. Both methods demonstrated strong alignment, with high correlations in genetic parameters and values at both progeny and individual levels. Correlations exceeded 97% for progenies and 81% for individuals when analyzing the genetic values of diameter at breast height and height. The methods aligned closely under lower selection intensities but diverged under higher selection intensities. While the accuracy of LiDAR can be improved through refinement, the choice between these methods ultimately depends on operational factors such as the availability of skilled labor and equipment.*

Keywords: *Forestry evaluation techniques, selection intensity, growth phenotyping, Eucalyptus cloeziana, E. saligna*

INTRODUCTION

Brazil is a leading global supplier of products derived from planted forests, including paper, pulp, timber, and energy charcoal. As of 2023, Brazil's planted forest area reached 10.2 million hectares (IBÁ Annual Report 2024), of which 7.8 million hectares are dedicated to eucalypt cultivation. The success of eucalypt plantations has been attributed to the species' rapid growth and adaptability to Brazil's diverse environmental conditions (Araujo et al. 2019). A key component of forest management and experimental trials is the efficient, accurate measurement of tree traits, which is essential for the selection of superior individuals in breeding programs.


Traditionally, forest inventory methods have been used to assess productivity. However, these methods face several challenges, including shortages of skilled labor, data handling errors, and measurement biases (Scolforo and Mello 2006, Oliveira et al. 2014). These issues are particularly problematic in experimental settings that demand precise assessments, especially for genetic improvement

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efforts, where genetic parameters are estimated, and the best individuals are selected. To address these limitations, Light Detection and Ranging (LiDAR) has emerged as a promising solution. LiDAR enhances data acquisition by measuring tree height, diameter, and volume while generating detailed 3D forest images (Leite et al. 2020).

Eucalyptus cloeziana and *E. saligna* are particularly noteworthy for their robust growth and adaptability to a wide range of climatic and soil conditions. Their wood properties make them highly valuable for diverse applications, including construction and energy production (Paludzyszyn Filho et al. 2006, Reis et al. 2017, Silva et al. 2023).

To optimize genetic improvement efforts, it is crucial to understand the quantitative traits of these species' populations. This understanding enables breeders to predict genetic gains and effectively direct breeding programs. It also facilitates the efficient use of quantitative data within breeding programs, refining selection methods (Moraes et al. 2008, Costa et al. 2015, Tambarussi et al. 2018, Araujo et al. 2021).

This study aimed to obtain and compare genetic parameters and correlations for selecting individuals and progenies using conventional methods and LiDAR. The analysis focused on one breeding population of *Eucalyptus cloeziana* at six years old and another of *E. saligna* at three years old, reflecting the typical evaluation ages in Brazilian breeding programs.

MATERIAL AND METHODS

Study area

Research was conducted at Experimental Station of Forestry Sciences (EECFI), Luiz de Queiroz College of Agriculture (ESALQ), University of São Paulo (USP), in the city of Itatinga (lat 23° 10' S, long 48° 40' W), state of São Paulo (SP), Brazil (Figure 1). According to the Köppen-Geiger (1928)'s climate classification, the region is classified as Cwa (humid subtropical), with an average annual temperature of 20 °C and an average annual precipitation of 1,350 mm.

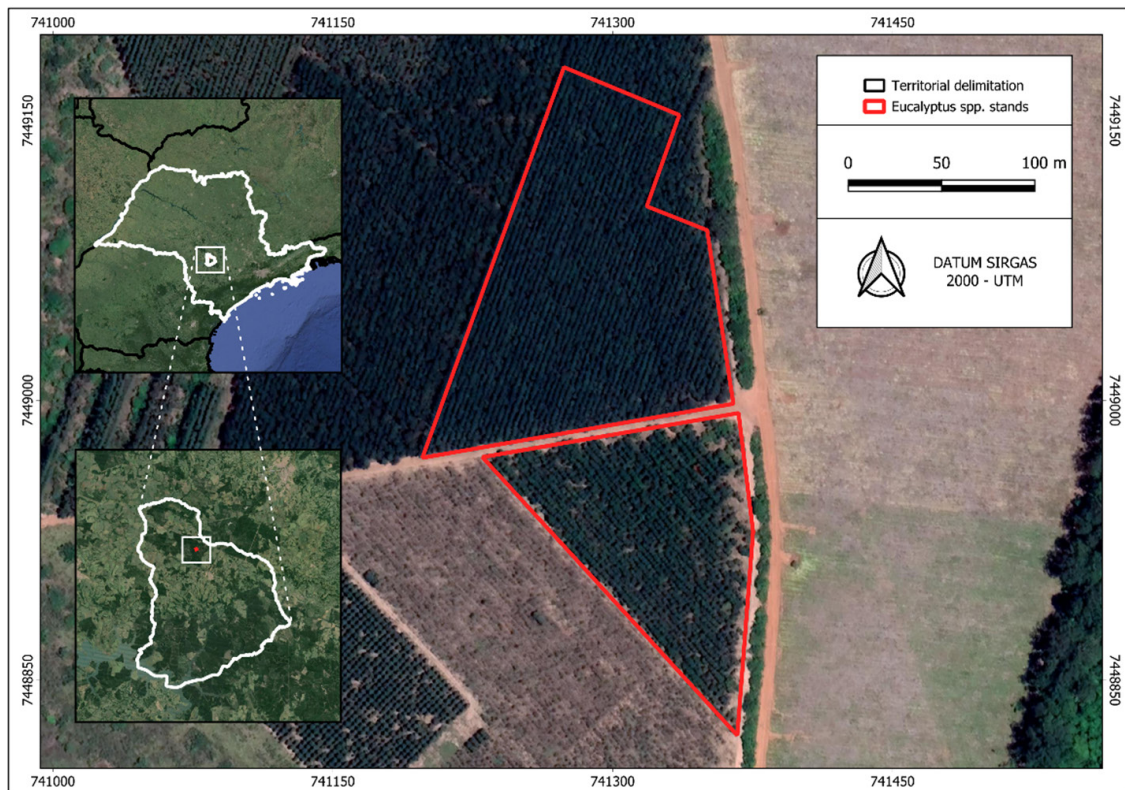


Figure 1. Study area comprising the progeny tests of *Eucalyptus cloeziana* (top) and *E. saligna* (bottom) at Itatinga Experimental Station, city of Itatinga, state of São Paulo, Brazil

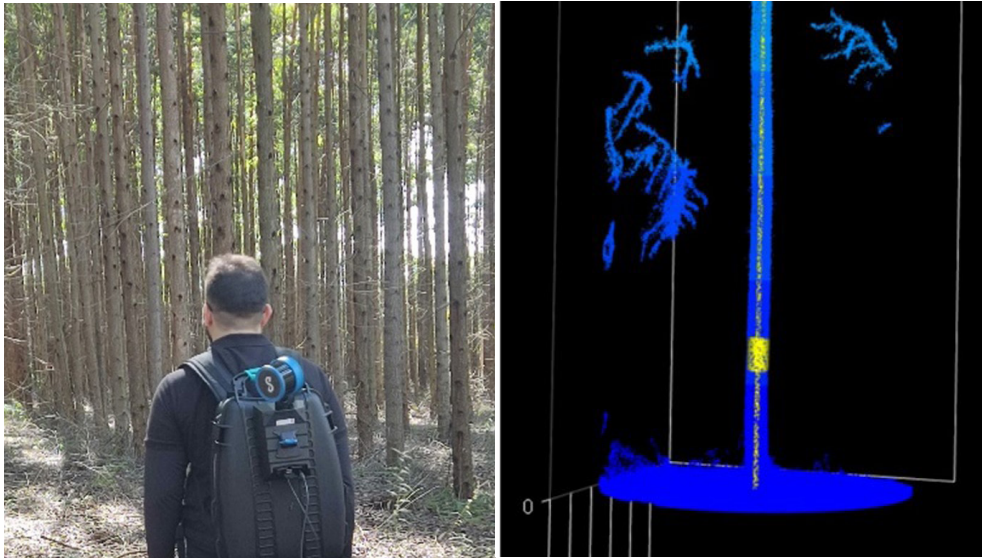


Figure 2. Data collection using the LiDAR Hovermap STX system and the point cloud representation of an *E. cloeziana* tree in the progeny test.

Two populations, formed by open-pollinated progenies, were selected for evaluation. Both were established using a randomized complete block design with linear plots of five plants and five replications. The *Eucalyptus cloeziana* population (I-45B-190), consisting of 98 progenies, was assessed at six years of age, while the *E. saligna* population (I-46A-203), comprising 12 progenies, was evaluated at three years. These evaluation ages align with standard practices in Brazilian eucalypt breeding programs, where six years is also the typical cutting age for most commercial plantations. Planting was conducted with a spacing of 3 m × 1.5 m in linear plots of five plants. All silvicultural practices, including soil preparation, fertilization, ant control, and weed management, followed commercial recommendations for eucalypt plantations in the region.

In June 2023, a full inventory was conducted, measuring 100% of the trees in both trials. Data collection used a measuring tape and a Haglöf EC II digital clinometer to record silvicultural variables, such as diameter at breast height (DBH) and height. After completing the conventional inventory, LiDAR scanning was performed in both experimental areas, which were located adjacent to each other. The LiDAR Hovermap STX system was used for scanning, which was carried in a backpack (Figure 2). Scanning was performed by walking every four planting rows to enhance the capture of plantation details.

Estimation of genetic parameters and selection gain

Analyses were conducted separately for each trial using a mixed-effects model. Calculations were performed by using the “lme4” package (Bates et al. 2015) for R (R Core Team 2023) and the Selegen-REML/BLUP software (Resende 2016). The model used is shown below:

$$y = Xr + Za + Wp + e$$

Where:

y = phenotypic vector of observations for a trait; r = vector of replication effects (assumed as fixed), added to the general mean; a = vector of individual additive genetic effects (assumed as random); p = vector of plots effects (assumed as random); e = vector of errors or residuals (random). The matrices X , Z , and W are the incidence matrices corresponding to the respective effects. Using the mixed model adjustment, the following variance components and heritability estimates were obtained: additive genetic variance ($\hat{\sigma}_a^2$); phenotypic variance ($\hat{\sigma}_y^2$); narrow-sense heritability

(h_a^2); progeny mean heritability (h_m^2); accuracy in progeny selection (\hat{r}_{aa}); coefficient of genetic variation among progenies (CV_{gp} (%)); coefficient of individual additive genetic variation (CV_{gi} (%)); and coefficient of experimental variation (CV_e (%)).

Following the estimation of genetic parameters, progenies and individuals were ranked based on their genetic values by using the best linear unbiased prediction (BLUP) method. Pearson correlations were also evaluated at both the progeny and individual levels. Coincidences were assessed exclusively at the individual level when comparing LiDAR with conventional inventory measurement methods. This ranking made it possible to simulate selection based on the top 1%, 5%, and 10% of genetic values of individuals for cloning purposes. Additionally, the top 30% were selected for establishing a Seedling Seed Orchard, aligning with the selection intensity recommended for orchard composition (Araujo et al. 2023).

To estimate the selection gain for both methods, the same selection intensities used for the coincidence levels were applied. The comparison included conventional measurements and LiDAR to evaluate the variation in genetic gain between the two methods. Genetic gain was calculated using the mean breeding values of selected individuals and the phenotypic mean of the trait, as follows:

$$Genetic\ gain\ (G\%) = \left(\frac{\overline{BV}}{\mu_{Trait}} - 1 \right) \times 100$$

Where:

\overline{BV} = mean breeding values of selected individuals; μ_{Trait} = phenotypic mean of the trait.

RESULTS AND DISCUSSION

Estimation of genetic parameters and selection gain

The average DBH and height values obtained using both methodologies were similar, indicating good growth performance for both species (Table 1). These results align with those reported for other eucalypt species with high productivity in Brazil at comparable ages (Oliveira et al. 2018, Silva et al. 2019a, Silva et al. 2019b, Silva et al. 2021).

Variances showed some differences between the methodologies. The estimated phenotypic variance ($\hat{\sigma}_f^2$) was lower, particularly for *E. cloeziana* (the older population), when analyzing the height trait. This result was expected due to LiDAR's higher accuracy in measuring this variable. Conventional height measurements are less reliable, as they are influenced by environmental factors such as wind and population density as well as by methodological challenges such as equipment accuracy and operator skill. Narrow-sense heritability (h_a^2) values were lower when using LiDAR for both traits in *E. cloeziana*. These ranged from 0.54 to 0.43 for DBH and 0.66 to 0.47 for height. Interestingly, the differences between methodologies were more pronounced in *E. cloeziana* than in *E. saligna*, which showed greater similarity (Table 1). This disparity may be attributed to differences in size and canopy structure between the species. The taller, denser canopy of *E. cloeziana* could complicate conventional height measurements. Despite the differences, the observed heritability values fall within the broad range reported in the literature for growth traits in eucalypts at comparable ages (Hamilton and Potts 2008,

Table 1. Estimates of variances and genetic parameters for diameter at breast height (DBH) (cm) and height (m) traits in progeny tests of *Eucalyptus cloeziana* at 6 years of age and *Eucalyptus saligna* at 3 years of age

Parameters	Conventional		LiDAR	
	DBH	H	DBH	H
<i>Eucalyptus cloeziana</i>				
$\hat{\sigma}_a^2$	5.21	5.38	4.75	2.78
$\hat{\sigma}_f^2$	9.50	8.12	10.96	5.84
h_a^2	0.54	0.66	0.43	0.47
h_m^2	0.82	0.82	0.76	0.76
CV_{gp} (%)	7.54	5.680	7.10	4.13
CV_{gi} (%)	15.08	11.36	14.19	8.26
CV_e (%)	18.91	12.18	20.03	10.90
\hat{r}_{aa}	0.91	0.90	0.87	0.875
\bar{x}	15.14	20.42	15.36	20.19
<i>Eucalyptus saligna</i>				
$\hat{\sigma}_a^2$	1.86	3.22	2.19	3.69
$\hat{\sigma}_f^2$	10.93	10.35	11.37	9.85
h_a^2	0.17	0.31	0.19	0.37
h_m^2	0.46	0.60	0.49	0.68
CV_{gp} (%)	6.04	6.05	6.20	6.27
CV_{gi} (%)	12.08	12.10	12.41	12.55
CV_e (%)	26.42	18.95	25.67	18.36
\hat{r}_{aa}	0.67	0.77	0.70	0.82
\bar{x}	11.31	14.83	11.92	15.30

$\hat{\sigma}_a^2$: additive genetic variance; $\hat{\sigma}_f^2$: phenotypic variance; h_a^2 : narrow-sense heritability; h_m^2 : progeny mean heritability; CV_{gp} : coefficient of genetic variation among progenies; CV_{gi} : coefficient of individual additive genetic variation; CV_e : coefficient of experimental variation; \hat{r}_{aa} : accuracy on progeny selection; \bar{x} : mean of the trait.

Li et al. 2017, Oliveira et al. 2018).

In the restricted heritability estimates for *E. saligna*, both assessment methods yielded low values, suggesting a stronger environmental influence. This result may also be partially attributed to the younger age of the population. However, heritability values for *E. cloeziana* ranged from moderate to high, which is consistent with the classification by Resende et al. (1995). For the height trait in *E. saligna*, the h^2 value was slightly higher when measured using LiDAR compared to the conventional method. This suggests that the observed differences were primarily driven by genetic variation between populations rather than by the measurement methodology itself. This finding is encouraging, as heritability primarily reflects the genetic potential of the population being evaluated, independent of the tools used for assessment.

The coefficient of experimental variation ($CV_e(\%)$) was higher for the DBH trait in *E. cloeziana* when measured using the LiDAR methodology. Two factors may explain this: first, the scanning density employed, as denser scanning along planting rows could improve point cloud capture. Second, the algorithm used for processing the data may require further refinement, though these potential improvements were not addressed in this study. Similarly, the coefficient of individual additive genetic variation ($CV_{gi}(\%)$) was lower for LiDAR measurements in *E. cloeziana*. For *E. saligna*, however, the ($CV_e(\%)$) was slightly lower for both DBH and height when measured with LiDAR, while the ($CV_{gi}(\%)$) increased. Accuracy (\hat{r}_{aa}) was high (> 0.7) for both methodologies (Resende et al. 1995). This indicates that both measurement methods allow for precise selection in breeding programs.

Correlation and ranking coincidence of genotype selection

For DBH, the correlation among progenies was high, exceeding 95%. At the individual level, correlations were slightly lower, above 80%, but still considered high according to Taylor (1990). Regarding coincidence, more intense selection (1%) showed low coincidence values. However, as selection intensity decreased, coincidence values increased, aligning better with the high correlations (Table 2). A similar trend was observed for the height trait in *E. cloeziana*, where the coincidence index increased from 26% to 63% as selection intensity decreased. This pattern occurs due to small variations in the ranking of individuals or progenies, making it challenging to determine the best ones when genetic value differences are minimal. For *E. saligna*, selection was not performed at the 1% intensity level due to the limited number of progenies in the trial. However, as selection intensity decreased, coincidence values also increased for both traits.

In the context of individual tree inventory, LiDAR is already recognized as a viable option (Oliveira et al. 2021). However, the use of LiDAR for obtaining genetic parameters and analyzing coincidences in tree selection is less frequently discussed in the literature, which complicates comparisons with the data obtained in our study, particularly since our scanning was conducted from the ground by walking along the trees. In a study on Norway spruce, tree heights were measured in the field using an ultrasonic system (Liziniewicz et al. 2020) combined with aerial scanning. At the stand level, the average height measured by aerial scanning was 2% higher than the field-measured average. While the estimation of progeny means was highly accurate, the accuracy at the individual level was insufficient for breeding purposes (Liziniewicz et al. 2020). A key difference between our study and the Norway spruce selection study is the use of ground-based scanning, which is likely to improve the quality of individual selection. According to Liao et al. (2022), LiDAR can provide accurate, precise tree phenotyping for breeding purposes; however, its effectiveness depends on the equipment, scanning methodology, and algorithms used.

Selection gains for *E. saligna* and *E. cloeziana* were evaluated using the same selection intensities across the two methodologies (Table 3). When compared to the selection intensity typically used to establish seed orchards (approximately 30% of the trees) in other eucalypt species in Brazil, such as *E. benthamii*, *E. dunnii*, and *E. pellita*, where observed gains

Table 2. Genetic Pearson's correlation and degree of selection coincidence for diameter at breast height (DBH) and height in conventional and LiDAR measurements across two eucalypt populations

Description	<i>E. cloeziana</i>		<i>E. saligna</i>	
	DBH	Height	DBH	Height
Genetic correlation				
Progeny	0.99	0.98	0.97	0.97
Individual	0.81	0.87	0.81	0.97
Degree of coincidence				
Selection (%)	DBH (%)	Height (%)	DBH (%)	Height (%)
1	11	26	NE*	NE*
5	30	35	60	60
10	49	44	60	67
30	73	63	74	77

* Not evaluated due to the small number of trees under high intensity (n=3 trees).

Table 3. Genetic gain (%) for diameter at breast height (DBH) and height in conventional and LiDAR measurements across two eucalypt populations

Description	Genetic gain (%)							
	<i>E. cloeziana</i>				<i>E. saligna</i>			
	Conventional		LiDAR		Conventional		LiDAR	
Selection (%)	DBH (%)	Height (%)	DBH (%)	Height (%)	DBH (%)	Height (%)	DBH (%)	Height (%)
1	21	16	21	9	NE*	NE*	NE*	NE*
5	18	13	17	8	10	10	11	10
10	16	11	15	7	8	9	10	9
30	12	8	11	5	6	7	7	7

* Not evaluated due to the small number of trees under high intensity (n=3 trees).

range from 8% to 13% (Araujo et al. 2021, Araujo et al. 2023, Silva et al. 2023), the gains for *E. cloeziana* were similar, while those for *E. saligna* were slightly lower. For *E. saligna*, the gains across traits were consistent, reflecting the influence of a small population size and prior selection, which reduced genetic variation and subsequent gains. These factors, rather than the methodology, were the primary contributors to the observed results. In contrast, *E. cloeziana* showed more varied gains, particularly for height at the 1% selection intensity. Gains ranged from 16% (with conventional methods) to 9% (with LiDAR). This difference is attributed to the lower data variance observed with LiDAR measurements.

CONCLUSIONS

LiDAR and conventional measurements in progeny trials demonstrated strong alignment, confirming the effectiveness of both methods for assessing genetic parameters and selecting individuals. High genetic correlations and good selection coincidence were observed, particularly at lower selection intensities. With further methodological refinements, the accuracy of LiDAR could be improved. The choice between the two methods ultimately depends on operational factors such as availability of labor and equipment.

DATA AVAILABILITY

The datasets generated and/or analyzed in this study are available from the corresponding author upon reasonable request.

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