

Optimal age for selection in breeding clonal *Tectona grandis*

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Abstract

Teak is one of most widely planted species in the tropics due to its high wood value. Two main questions motivated this research, how early can be performed genetic selection? and which is the optimal age selection in clonal *Tectona grandis*? A clonal test was established at northern Pacific of Costa Rica with 32 clones. Measurements were taken at ages 3.2, 3.6, 4.4, 4.9, 5.9, 8.9, 9.7, 10.6, 11.8, and 12.9 years old for diameter at breast height (DBH), commercial height (estimated), tree quality (assessed) and commercial volume. Genetic parameters and genetic correlations across ages for all variables were obtained through SELEGEN software (REML/BLUP). Individual DBH clonal heritability (H^2_{gi}) ranged from 0.02 to 0.11, while clonal mean heritability (H^2_{mc}) ranged from 0.43 to 0.82. Highest mean clonal heritability for commercial volume was registered between 8.9 and 9.7 years ($H^2_{mc}=0.74$ and 0.77), thus 8.9 became as the target selection age. Significant genetic correlations were found ($r_g=0.74$) between DBH at 4.9 years and commercial volume at 8.9 years. Spearman rank correlation and graphical analysis determined high clonal DBH ranking stability after 4.9 years. Maximum selection efficiency for commercial volume was registered at age 5. Therefore, 9 years-old can be defined as the target age for selection in clonal teak, while early selection can be practiced under low risk through DBH ranking at 5 years, supported by an age-age genetic correlation of $r_g=0.74$. Graphical analysis of ranking splitted in thirds proved to be an effective method to verify ranking stability across ages.

Key words: teak; clonal forestry; early selection; genetic correlations; genotype-age interaction

Introduction

Tectona grandis Linn f. is a valuable timber tree known for its attractive aesthetic heartwood appearance as well as its good physical and mechanical properties (Moya et al., 2013). Its easy propagation, establishment, management, and moderate growth rate have positioned teak as one of the most

valuable cultivated tree in tropical regions (Monteuuis et al. 2011; Camino and Morales, 2013).

Results from breeding efforts and better silvicultural practices are slowly reducing rotation lengths in teak, from the usual 20 to 24 years to 16 and 18 years (Badilla and Murillo 2022; Murillo et al., 2013; Murillo et al., 2019). Similarly, intensive clonal silviculture based on elite materials are motivating for a more efficient and shorter genetic selection protocols (Badilla and Murillo 2022). Conceptual early selection theory in tree improvement was established in the 1980s, which provided a framework for implementing new strategies (Lambeth, 1980; Zobel and Talbert, 1984; Lambeth et al., 1983; Cotterill and Dean, 1988). Juvenile-adult genetic correlations, known also as age-age correlations, is the foundational principle behind and usually applied for economically important traits, such as diameter and commercial volume. Analytical efforts typically focus on predicting future genetic ranking at the earliest possible age, under the lowest risk, thus, allowing safe selection decisions some years before (Zobel and Talbert 1984; Sun et al., 2017).

However, early selection can lead to two types of error risks: 1) elimination of high genetic merit genotypes but, with a poor initial performance, and 2) selection of genotypes with low genetic merit, due to an acceptable good performance at early ages, caused by favorable and non-repetitive environmental effects. Both error types may cause a reduction of the genetic gain in the breeding program (Zobel and Talbert 1984).

For a better understanding of this issue, it is necessary to clarify two interrelated but different concepts. First, what is the best age of selection? which is usually accepted as the age where highest genetic gain is obtained (Zobel and Talbert 1984; Lambeth 1980). In simple terms, it will occur when heritability reaches its highest value (Farfán et al. 2002). Secondly, how early this optimal selection age can be predicted? Therefore, observance of behavior and stability of genetic parameters across ages is crucial. Heritability values, juvenile-adult genetic correlations, genetic variation magnitude and its respective accuracy estimation, need to be frequently monitored. An early selection approach in teak provenances, was studied in Tanzania for growth and stem quality with promising results at 5 and 17 years (Pedersen et al. 2007). Other

perspectives of early selection have been also undertaken through the area of genomic selection, where there are some recent and promising results in teak (Callister et al., 2024). Given the potential impact of shortening selection and breeding cycles in forestry, this study was conducted with the objective of determining the earliest and optimal selection age in clonal breeding *Tectona grandis*.

Materials and Methods

The study was performed based on a clonal teak test with continuous measurements until 13 years old. The trial was established in Nicoya, Guanacaste province, northern Pacific of Costa Rica, under geographical coordinates at 10°06'10" North and 85°22'24" West.

The area is located at 100 m elevation with an average annual precipitation of 2200 mm, concentrated from May to November, and an average temperature of 25 °C.

The site was very uniform, previously utilized in crops and did not undergo any soil preparation at the time of establishment. A total of 31 clones derived from plus tree selections in the northern Pacific of Costa Rica were evaluated (Murillo et al. 2019), along with two commercial bulked seed lots as controls from local Guanacaste organizations. Plants were vegetatively propagated as cuttings in greenhouse conditions at Centro Agrícola Cantonal de Hojancha, close to the trial site.

The trial was established following conventional experimental design utilized by the Tree Improvement Cooperative (GENFORES) in Latin America (Murillo et al., 2019). Which is basically based on a model for a randomized complete block design with six replications, with three 2-tree plots per clone (6 ramets per block in total), randomly distributed within each block. Therefore, each clone was represented by 36 ramets in the trial. The initial planting density was 625 trees per hectare, with a spacing of 4 m by 4 m.

The trial was evaluated in ten occasions (3.2, 3.6, 4.4, 4.9, 5.9, 8.9, 9.7, 10.6, 11.8, and 12.9 years of age). All trees were measured for diameter at breast height (DBH), and the commercial height was estimated based on the number of potential logs per tree (2.5 meters in length). The visual estimation of the number of commercial logs per tree (2.5 meters in length) and the quality assessment of each commercial log were carried out using a scale ranging from 1 to 4, according to the methodology proposed by Murillo and Badilla (2004; Murillo et al., 2019). A value of "1" corresponds to a log without stem visible defects and of the highest quality and potential for sawing. Meanwhile, a value of "4" was assigned to a non-merchantable log for sawing due to stem defects, suitable only for biomass. However, this trait was included only for a better estimation of commercial height, and therefore, for a better commercial volume estimation, since teak is a hardwood with a high wind damage susceptibility, that can reduce its commercial value (Murillo et al. 2013).

Data analysis

All measurements were consolidated into a unified database, ensuring its correspondence at each individual tree over time. This allowed for the analysis of genotypes' performance in the genetic ranking, at each specific age.

An estimate of commercial volume was obtained through the DBH value, commercial height based on the number of effective 2.5m-length logs and scoring the log quality separately for each of the first four logs, as explained previously. Commercial height was finally adjusted to a minimum diameter of 12 cm based on the teak tapering algorithm (Fallas 2017), through the Forest Appraisal Program, developed by Murillo and Badilla (2011, version 2024).

Database was standardized in Excel, and the trial was analyzed using SELEGEN-REML/BLUP software, which utilizes REML/BLUP (Restricted Maximum Likelihood/Best Linear Unbiased Prediction) statistical procedure (Resende 2016), suitable for analyzing unbalanced genetic data and provides more accurate estimates of genetic parameters, such as variance components and genetic ranking, among others (Resende et al., 2018).

A randomized complete block design was utilized for a set of unrelated clones, multiple plants per plot and established in one single site. The statistical model is described in equation (1), and the genetic parameters obtained are presented in Table 2.

$$Y = Xr + Zg + Wp + e \quad (1)$$

Where "y" is the vector of data, i.e., the dependent variable; "r" is the vector of repetition effects (block assumed as fixed); "g" is the vector of genetic effects (the clone assumed as random); "p" is the vector of plot or experimental unit effects (assumed as random); "e" is the vector of residual errors (assumed as random). The uppercase letters (X, Z and W) represent the incidence matrices of the identified effects (Resende 2016).

Based on SELEGEN, each trait was analyzed independently to obtain their genetic parameters and its respective ranking. Each age was treated as an independent variable associated to each trait, like DBH4.4, DBH8.9, VolCom8.9, etc, instead of including age as an effect in the model. Thus, it facilitated data analysis, its interpretation and avoided possible discrepancies in measurements across ages.

A genetic correlation matrix among all variables was then generated using an option of SELEGEN as described by Flôres et al. (2021). Commercial volume was selected for the early selection analysis since it is the most economically relevant trait. Thus, ages with highest heritability values were recorded, as the most appropriate time for selection. Numerous authors define it as the ideal selection age due to its greater reliability, accuracy, and when highest estimation of genetic gain will converge (Lambeth et al., 1983; Zobel and Talbert 1984; Coterill and Dean 1988; Dean et al., 2006; Zimback et al., 2011; Moraes et al., 2014; Resende et al., 2018; Murillo et al., 2019; Hernández et al., 2021).

Once the optimal selection age (named as target age) was determined, the genetic correlations between all measurement ages were examined to determine how early the target age could be predicted with an acceptable accuracy level.

Early selection efficiency was determined based on the procedure suggested by Sun et al. (2017) as follows:

$$SE = r_g \sqrt{R_x T_2} / \sqrt{R_y T_1} \quad (2)$$

Where T_1 and T_2 are the two ages for trait x and desired trait y respectively, r_g is the genetic correlation between the trait at both ages, $\sqrt{R_x}$ and $\sqrt{R_y}$ are the square roots of heritability (repeatability). The analysis was performed separately for DBH and commercial volume and, for individual clonal heritability (H^2g) and mean clonal heritability (H^2mc).

As a complementary approach, safety of early selection was assessed by visually examining the behavior of the genetic ranking across selected ages, following the methodology proposed by Murillo et al. (2019). Each ranking was subdivided into three thirds, that is, upper third, middle third, and lower third. Thus, clonal behavior in ranking position across ages was directly and visually assessed.

Subdivision into thirds was determined based on:

Interval = (Maximum genetic value of the variable - Minimum genetic value of the variable)/3

This subdivisions grouped different number of clones in each, since it was based on the whole magnitude of variation of that trait.

When a clone changed its ranking position to the next third, it was assessed as a simple genotype-age interaction type. On the other hand, if a clone changed in ranking position from the first third to the third group, or vice versa, it was assessed as a

severe or a complex genotype-age interaction type (Resende et al., 2018).

In addition, the non-parametric Spearman's Rank Correlation test was conducted, which essentially determined the significance and magnitude of ranking changes at different ages.

$$P = 1 - \frac{6 \sum D^2}{n(n^2 - 1)}$$

Where "D" is the absolute difference in positions of the same clone in both rankings, and "n" is the number of clones in the ranking.

Results

All genetic parameters are shown in Table 1, where DBH exhibited higher heritability values than commercial volume at all ages. Meanwhile commercial volume had a larger coefficient of variation across ages. Heritability values for DBH and commercial volume exhibited an age increment tendency, although somewhat discontinuous. Highest heritabilities were reached between 8 and 10 years-old in all genetic parameters.

In Figure 1 can be observed these behavior patterns of both, individual and clonal mean heritability across ages. Which shows a continuous increase until 8-10 years reaching peak values.

In Table 2 is shown the correlation matrix among all variables at different ages, which exhibit a significant genetic correlation between DBH3.2age and DBH4.9 age with commercial volume at age target 8.9 ("r" value of 0.5 and 0.74 respectively).

Table 1

Individual heritability (H^2g), mean clonal heritability (H^2mc), and genetic coefficient of variation (Cvg%) for diameter at breast height (DBH) and commercial volume of teak (*Tectona grandis* Linn f.) in Nicoya, Pacific region of Costa Rica.

Age (year)	H^2g		H^2mc		Cvg (%)	
	DBH	Com.Vol.	DBH	Com.Vol.	DBH	Com.Vol.
3.2	0.02	0.00	0.43	0.09	2.85	2.35
3.6	0.02	0.04	0.43	0.56	2.40	5.30
4.4	0.12	0.01	0.79	0.08	7.79	2.35
4.9	0.09	0.09	0.79	0.77	3.01	7.09
5.9	0.06	0.03	0.73	0.54	2.40	3.90
8.9	0.11	0.07	0.82	0.74	3.04	5.62
9.7	0.10	0.09	0.74	0.77	2.78	7.09
10.6	0.09	0.06	0.73	0.67	2.67	4.80
11.8	0.11	0.06	0.79	0.68	3.06	5.20
12.9	0.11	0.08	0.80	0.73	3.31	6.00

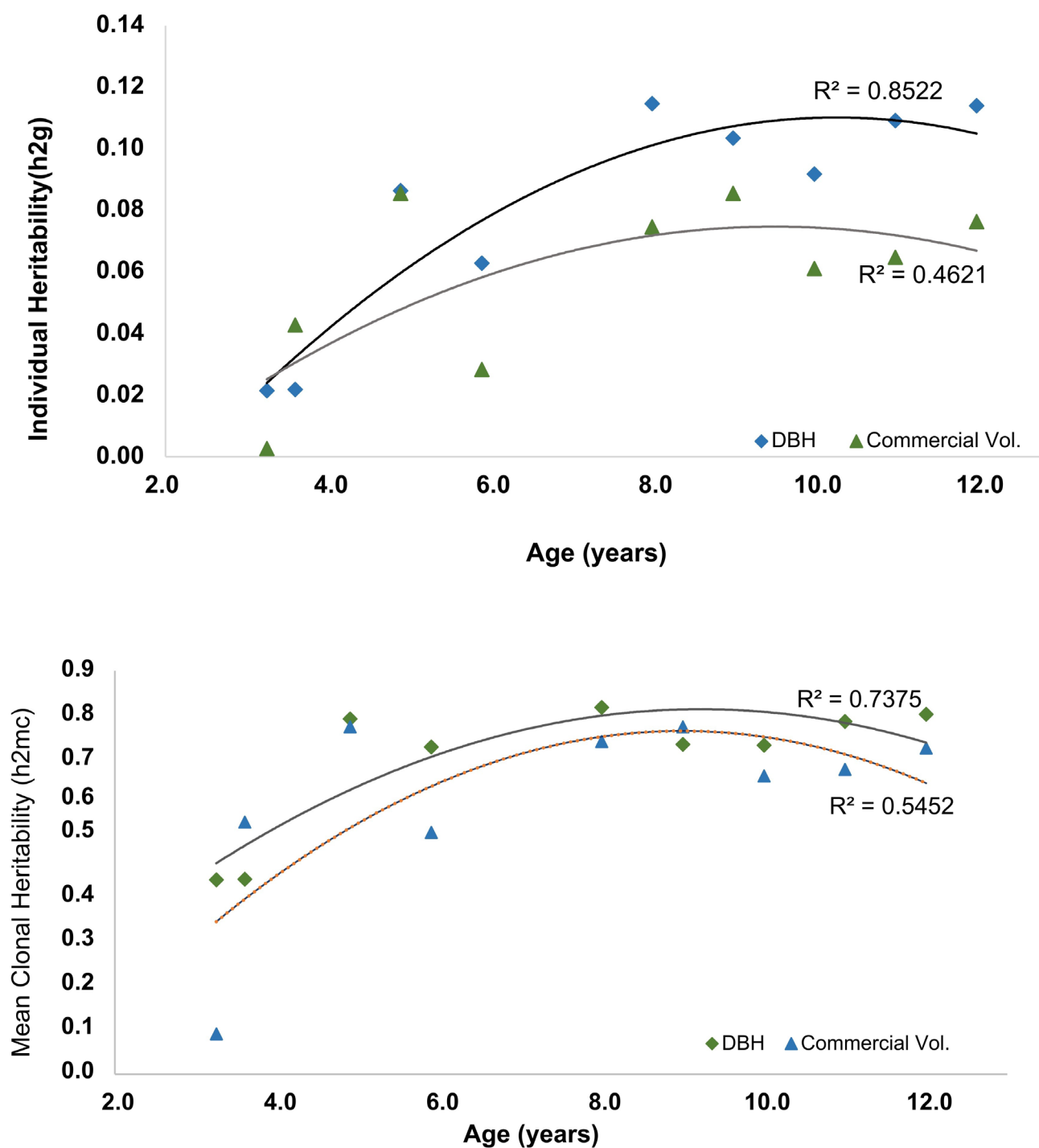


Figure 1

Clonal individual heritability (H^2gi , 1a), clonal mean heritability (H^2mc , 1b) across years for diameter at breast height and commercial volume of teak (*Tectona grandis* Linn f.) in Nicoya, Pacific region of Costa Rica. Individual heritability (figure 1a) exhibits a strong increment over years in both traits, although steadier in DBH. Meanwhile, mean clonal heritability (figure 1b) shows a similar increment pattern for diameter and commercial volume curves, although DBH exhibits a steeper and more predictable function.

Table 2

Genetic correlation matrix in a teak (*Tectona grandis* Linn f.) clonal trial among diameter at breast height (DBH) and commercial volume (Vol), at different ages in Nicoya, Pacific region of Costa Rica. Target correlations in bold.

Variable	DBH 4.9	DBH 5.9	DBH 8.9	DBH 9.7	DBH 10.6	DBH 11.8	Vol 3.2	Vol 4.9	Vol 5.9	Vol 8.9	Vol 9.7	Vol 10.6	Vol 11.8	Vol 12.9
DBH3.2	0.58	0.29	0.37	0.35	0.36	0.33	0.92	0.59	0.40	0.50	0.48	0.47	0.46	0.49
DBH4.9		0.78	0.79	0.68	0.71	0.64	0.62	0.99	0.69	0.74	0.66	0.66	0.61	0.61
DBH5.9			0.90	0.82	0.84	0.79	0.37	0.77	0.73	0.67	0.63	0.61	0.60	0.61
DBH8.9				0.92	0.96	0.93	0.40	0.77	0.64	0.80	0.78	0.77	0.79	0.78
DBH9.7					0.97	0.95	0.37	0.66	0.48	0.64	0.80	0.69	0.73	0.74
DBH10.6						0.98	0.38	0.69	0.55	0.74	0.81	0.79	0.82	0.82
DBH11.8							0.33	0.62	0.46	0.67	0.76	0.73	0.82	0.81
Vol3.2							0.63	0.52	0.57	0.54	0.53	0.49	0.54	
Vol4.9									0.68	0.73	0.66	0.66	0.60	0.60
Vol5.9										0.87	0.73	0.78	0.70	0.70
Vol8.9											0.88	0.95	0.90	0.88
Vol9.7												0.94	0.92	0.91
Vol10.6												0.96	0.95	
Vol11.8													0.98	

Other important juvenile correlations with target age (Vol8.9 years) were commercial volume at 4.9 years ($r = 0.73$) and commercial volume at 5.9 years ($r = 0.87$), both highly significant (table 2). The non-parametric Spearman's rank correlation test showed highly significant values ($r = 0.70^*$) among genetic ranking across ages, consistently with conventional genetic correlations at same ages (Table 2). Selection efficiency results show clearly (Table 3) that at age 4.9 (in both DBH and commercial volume) can be achieved the best and earliest selection of target age for commercial volume, supported by highest individual and clonal mean heritabilities, consistent with the matrix of genetic correlations (Table 2). Another way of verifying these results can be determined through the graphical method of splitting the ranking in thirds (Table 4). Clonal allocation in the first third of the genetic ranking for commercial volume (target 8.9 age), displayed a similar clonal position for (DBH) at ages 3.2 and 4.9, in the same first third of their genetic ranking respectively. All clones from the top third at DBH 3.25 and 4.9 years are included in the first third of the commercial volume

ranking at 8.9 years. However, 50 % of the best genotypes in the 8.9-year ranking (first third) are not included in the first third of the genetic ranking at both juvenile ages. Nonetheless, all these top genotypes were positioned within the second third, with the only exception of clone 05CM.

In the other way of analysis, it is observed that none of the clones allocated in the worst ranking placement at 8.9 years (last third), were positioned in the first third at an early age. That means, this type of early selection error would not occur. Changes observed in ranking position across ages (genotype $\times$ age interaction) are all of small scale or simple in nature. That is, changes from the first third to the second third and vice versa. If all seven clones from the first third at DBH4.9 were selected, the only early selection error would occur with the omission of clone 05CM. It was allocated in the lowest third at that age, but in the third position at age 8.9. That would represent a 3,2 % early selection error. While all best seven clones from DBH4.9 were also allocated in best positions at commercial volume 8.9 years.

Table 3

Selection efficiency (SE) for commercial volume at target age (8.9 years), based on early measurements of DBH and commercial volume, in a teak clonal trail in Nicoya, Pacific region of Costa Rica.

				DBH		Commercial Volume			
Age	r	H ² g	H ² mc	SE H ² g	SE H ² mc	H ² g	H ² mc	SE H ² g	SE H ² mc
3.6	0.5	0.02	0.43	0.213	0.362	0.04	0.56	0.378	0.435
4.4		0.12	0.79			0.01	0.08		
4.9	0.74	0.09	0.79	0.669	0.726	0.09	0.77	0.839	0.755
5.9	0.67	0.06	0.73	0.495	0.632	0.03	0.54	0.439	0.572
8.9		0.11	0.82			0.07	0.74		

r = genetic correlation; H²g individual heritability; H²mc = mean clonal heritability

Table 4

Comparisons of clonal position changes in the genetic ranking for commercial volume at 8.9 years (target age) in *Tectona grandis*, relative to clonal positions in the DBH ranking at 3.2 and 4.9 years, in Nicoya, Pacific region of Costa Rica.

	DBH 3.2	Vol 8.9	DBH 4.9
1	04CM	48EXP	49EXP
2	49EXP	33CM	48EXP
3	107CM	05CM	08EXP
4	48EXP	11CM	102CM
5	06CM	106CM	06CM
6	102CM	04CM	33CM
7	37CM	102CM	04CM
8	106CM	49EXP	06SE
9	32CM	107CM	107CM
10	08EXP	06CM	34CM
11	34CM	66CM	11CM
12	11CM	37CM	07EXP
13	85CM	08EXP	03EXP
14	83CM	85CM	66CM
15	68CM	83CM	85CM
16	33CM	06SE	37CM
17	07EXP	34CM	72CM
18	02CM	07EXP	05SE
19	12CM	72CM	106CM
20	30CM	02CM	94CM
21	94CM	94CM	83CM
22	05SE	50CM	02CM
23	66CM	12CM	50CM
24	72CM	05SE	22CM
25	50CM	98CM	12CM
26	06SE	68CM	05CM
27	03EXP	22CM	98CM
28	05CM	32CM	32CM
29	22CM	03EXP	68CM
30	67CM	67CM	67CM
31	98CM	30CM	30CM

Clone 05CM is showing a strong and complex genotype-age interaction, changing its position in the genetic ranking from the lowest allocation at year 4.9, moving to the top of the ranking at 8.9 years age.

Discussion

In this study we conducted an age-age systematic analysis which provided valuable guidance for early selection of teak clones. Individual heritability values were relatively low for variables DBH and commercial volume before eight years, as reported in other teak studies (Narayanan et al. 2009; Goh et al., 2013; Molina 2017; Murillo et al., 2019; Badilla and Murillo 2022). Low genetic variability can be explained by the origin of these materials, which came from selections in commercial

plantations established at the time when there were no tree improvement programs. That is, seeds coming from small seed stands with a narrow genetic variability (Murillo et al., 2013). Besides, there are some reports denoting relatedness evidence within breeding populations in Costa Rican teak companies (Murillo, et al. 2019; Ramírez 2020, Badilla and Murillo 2022).

Individual and clonal mean heritability values for DBH tend to be higher than those for commercial volume. Which could be attributed to direct measurements of diameter, while commercial volume is a product of diameter and an estimation of commercial height. In addition, wind usually affects severely young teak plantations, causing crown breakage, reducing commercial height and therefore, affecting commercial volume as well (Guzmán et al., 2017). This situation conditions commercial height at an early age, while DBH continues to increase as the tree matures.

Individual and clonal mean heritability followed an expected increment from 3.3

years to 4.9 years for both traits, DBH and commercial volume. At year 5.9 there is a reduction in both parameters explained by a first rouging that removed 50 % of the worst trees. As a result, the trial lost a significant number of observations, leading to a temporary reduction in the overall variability and in the genetic parameters as well. It is important to mention, that after rouging the trial generated a more robust genetic analysis by comparing the best remaining individuals from each accession. The coefficient of genetic variation (Cvg%) for both traits clearly expresses the thinning effect in a reduction of values at different ages. The Cvg% for commercial volume almost doubles DBH values due to the quadratic effect of diameter in the volume function.

Individual heritability (Figure 1a) and mean clone heritability (Figure 1b) followed a steady pattern with age, reaching highest values around eight years for both parameters. A similar pattern has been reported for *Gmelina arborea* in tropical regions, where the peak value is reached at four years (Hernández-Castro et al., 2021), at 10 years in *Pinus taeda* in southern Brasil (Flôres et al. 2021), at 5 to 6 years in *Larix kaempferi* (Sun et al., 2017), as well as at two years of age for *Eucalyptus* in Brazil (Beltrame et al., 2012). Higher consistency of DBH genetic parameters compared to commercial volume can be attributed to diameter as a variable measured directly in the field. While volume is calculated by the diameter and an estimation of commercial height (Figure 1a). In addition, commercial height may remain the same over the years, due to crown breakage caused by wind, as mentioned before. This may explain why genetic variation and heritability increases more rapidly across years for DBH than for commercial volume. Regarding the behavior of clonal mean heritability in both traits (Figure 1b), it is shown a clear tendency of higher values with the years, approaching the same peak age that in individual heritability as expected.

The genetic correlation matrix (Table 2) shows consistently the best age-relationship among the traits examined. It identifies the possibility of selection at an early age of the target variable (Vol8.9 age). A strong genetic correlation with target age means that ranking positions between both ages are similar. At age 3.2 a significant correlation of $r = 0.5$ is obtained with target age 8.9. However, one year and a half later (4.9 years) the genetic correlation arises to its peak value ($r = 0.74^*$), which then becomes in the best decision for early selection. Thinning effect may explain the reduction to $r = 0.69$ in the correlation value one year later (5.9 years). It is also observed that even higher correlation values were obtained with commercial volume at vol 3.2 and vol 4.9 years respectively. However, the use of DBH is preferable due to its easier and higher accuracy in field measurements, compared to uncertainty and difficulty when estimating commercial volume, as explained before. Spearman's rank correlation registered a strong and significant value ($r = 0.70^*$) in accordance with the general genetic correlations, for the DBH at 4.9 years and commercial volume at 8.9 years. Which is consistent and confirms the similarities in their ranking allocation of clones.

For teak growing in Tanzania, Pedersen et al. (2007) found strong genetic correlations between growth at age 5 and age 30. While Adu-Bredu et al. in Ghana (2019) found good correlations between 9 and 17 and 28 years. In our investigation we found that at 8.9 years is not only the age where the highest heritability values were recorded, but from that age onwards, a genetic correlation greater than $r = 0.9$ is maintained through 9 to 12 years. This confirms age 8.9 as the target for ranking assessment, along with 5 years as the earliest age that this target age can be predicted.

Similarities in genetic ranking allocation of clones, for commercial volume at 8.9 years and DBH at 3.2 and 4.9 years, can be better observed in detail in Table 4. Splitting the genetic ranking in three third compartments (Murillo et al. 2019), contributes to a more comprehensive visual assessing analysis of the two types of risks associated with early selection. The first risk is not including genotypes that will reach the top third at 8.9 years. It can be observed in general, that in the two first thirds at 3.2 years ranking, or even better, in the first 15 positions only clones 66CM and 05CM are not included (13,3 % risk error). While, in the first 15 positions of DBH4.9 ranking, clones 05CM, 106CM and 83CM wouldn't be included (20 % of mis selection). This result for clone 05CM could be explained as a particular average effect after rouging (at year 5), where its worst adapted ramets were removed, promoting an increment in its new average value. Another explanation is related to some specific genotypes, that exhibit a slow adaptation and retarded initial growth, that affect its ranking position in the first five years, as observed in other teak genetic tests (Naranjo et al., 2012; Murillo et al., 2019). Thus, this case should be considered as a non-expected and non-common in teak ranking change positions across ages.

If there is another early selection scenario, like taking the first two thirds of the ranking distribution, or the best 20 clones, there would be a much lower risk of mis selection with only the 05CM genotype case.

Finally, there is a second risk which deals with including genotypes with lower genetic merit or, selecting genotypes at an early age that later end up in the last third. This happened in this study with genotype 32CM for the DBH variable, which ranked 9th position at 3.2 years, but dropped to the 28th position at 4.9 years. Thus, there would be no risk type 2 if early selection can be performed through DBH at age 4.9, selecting the top 15 positions.

Conclusions

Highest individual (H^2g) and clonal mean heritabilities (H^2mc) for diameter (DBH) and commercial volume were obtained at 8.9 years, therefore, 9 years-old can be defined as the target age for selection in clonal teak.

Maximum selection efficiency for commercial volume was registered at age 5. Therefore, early selection in clonal teak can be performed under low risk through DBH ranking at 5 years, supported by a significant age-age genetic correlation of $r = 0.74$ with target age.

Graphic analysis of ranking splitted in thirds proved to be an effective visual method to verify stability across ages. Early selection can significantly speed up teak breeding programs.

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