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Selection of Atlantic Forest species in South Bahia, Brazil

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Abstract
The study aimed to evaluate the growth potential of several Atlantic Forest species in South Bahia, displayed in high dense grid and select the best trees through selection indexes. The experiment was carried out in the Comissão Executiva do Plano da Lavoura Cacaueira (CEPLAC) located in the South of Bahia state, Brazil. A total of 44 Atlantic Forest species were tested with three replications with plot containing 36 individuals that were arranged in 2 × 2 m spacing. Experimental parameters indicated high variability among species to high density spacing, which is favorable to commercial pure stands practiced in the forestry sector. Statistical selection of native species was evaluated using selection indices based on volumetric production and survival traits. These indices allowed select species by their adaptation into the experimental region. The top two ranked species were *Pterygota brasiliensis* Allemão (Folheiro ou pau-rei) and *Plathymenia reticulata* Benth. (Vinhático), which adapted well to a tropical, humid, and rainy weather, such as the climate in South Bahia, Brazil. From this study, it was possible to subsidize the selection of ideal species and individuals for seed collection, indication of materials to assemble breeding populations, cloning, and orientate future studies in South Bahia state, Brazil.

Keywords
Tree breeding — Brazilian native tree species — Selection index — Breeding strategy — Wood species

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1. Introduction

Forest breeding plays an important role in the economics of industrial products and timber used in the construction of houses, buildings, and furniture. Besides economic interests, using improved trees promotes high levels of carbon sequestration and helps to preserve native forests from forest degradation (Laverdière et al., 2022). Native forests in Brazil contain many species with a high potential to be introduced in breeding programs oriented towards timber production. In order to use all these germplasms, breeders need to consider statistical parameters and strategies to select the best materials with favorable silvicultural characteristics as high diameter, total height and straight form (Garuzzo et al., 2021; Santos et al., 2022).

Brazil is considered the country that holds the greatest biodiversity on the planet considering ecosystems, species, populations, individuals, and genes. However, the replacement of native forests has been the subject of discussions in the last few decades. Especially concerning the extinction of some endemic species that may have participate in the economy and social development of Brazil in the short-term future (Fernandes et al., 2023). Despite the relevance of native forest species, investments in research for the selection and improvement of populations of these species are still limited. This fact presents a great challenge to the native species productive sector, especially due to the scarcity of silvicultural and genetic breeding not related to *Eucalyptus* and *Pinus* genus, which are exotic (Santos et al., 2022).

The native species in the Brazilian have a small participation in the forest sector in relation to *Eucalyptus* and *Pinus*. Native species have lower yield than *Eucalyptus* and *Pinus*, and scarcity of basic information for their domestication, which can be pointed out as one of the critical reasons for small commercial use. This leads to higher production costs coupled with longer rotation cycles in relation to these exotic species. For example, paricá (*Schizolobium parahyba* var. amazonicum Huber ex Ducke) produces an average of 22 $m^3 ha^{-1}.y^{-1}$, which represents almost half of the productivity of *Eucalyptus* forests (Gonçalves et al., 2013). The higher yield capabilities of exotic species in relation to native ones is a result

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of a high degree of investment in their breeding programs, which are in advanced stages with some species improving to their third generation of breeding (Romão et al., 2023). Thus, genetic breeding studies concerning native Brazilian Atlantic Forest species is extremely important to orientate the progress with timber germplasm in breeding programs.

The need for replenishment of native forests in the Legal Reserve Areas has long been recognized and was instituted by Law 6,660 in August 2008. However, the unavailability of improved seeds, physiological quality of seed, and adequate seed quantity has contributed to a low coverage of majority planted areas of these species in some research institutes in Brazil. Forest restoration using native forest species with some degree of improvement would give degraded areas an *ex situ* conservation aspect and contribute to the conservation of native species other than for sustainable use (Melo et al., 2013).

Currently, studies are being carried out with some native forest species using the genetic variability existing among and within populations. Special emphasis has been given to species with economic potential such as yerba mate (*Ilex paraguariensis* St. Hil.) (Sturion et al., 2017), paricá (*Schizolobium parahyba* var. amazonicum Huber ex Ducke Barneby) (Ohashi et al., 2010), rubber tree (*Hevea brasiliensis* Willd. ex A. Juss) (Oliveira et al., 2015), *Cariniana legalis* (Mart.) Kuntze*, Cordia trichotoma* (Vell.) Arrab. ex Steud*, Plathymenia foliolosa* Benth *and Zeyheria tuberculosa* (Vell.) Bureau ex Verl (Garuzzo et al., 2021; Santos et al., 2022, 2023). However, other species have conserved their genetic identities through intensive exploitation of their natural populations, such as “aroeira” (*Myracrodruon urundeuva* Fr. All.) (Pupin et al., 2017), “baru” (*Dipteryx alata* Vogel) (Canuto et al., 2015) and “capitão-do-campo” (*Terminalia argentea* Mart. et Succ.) (Otsubo et al., 2015). All studies highlight the wide genetic variability within populations and suggest success for the selection of future breeding and genetic conservation programs. Despite these studies, a wide range of genetic materials with timber potential has not yet been evaluated, mainly in the region of South Bahia, Brazil. Thus, it is necessary to increase the knowledge base about the adequacy of Brazilian native species breeding programs with potential for wood production.

Statistical genetics assumes an important role in genetic breeding programs in selection of individuals and genitors. Statistical genetics is based on quantitative genetics, and experimentation is the main source of reliable information for decision making. The study of characters is given according to the influence of environment in the phenotype of an individual and genetic effects (Resende et al., 2021). The phenotype of an individual is what can be observed or measured. The genotype represents the inheritable and non-inheritable effects generated by the genes of an individual. The influence of the environment is characterized by conditions of temperature, humidity, soil fertility, precipitation, and luminosity. This influence can bias genetic selection, by phenotypically equating genetically distinct individuals (Grattapaglia, 2022; Heinemann et al., 2022). Thus, experimentation is crucial to enable access to the genetic values of an individual and the isolation of systematic and environmental effects, which can mislead the selection. Almost all selection of higher individuals of Brazilian native forest species are based on mass selection. This method has been used to select seed donors located in natural areas and is based only on phenotypical observation. However, the absence of a statistical analysis can bias the genetic selection and delay genetic progress with selection since erroneous genotypes can be top ranked (Santos et al., 2022).

Considering all these aspects, our work aimed to evaluate the growth potential of several Atlantic Forest species in South Bahia, displayed in high dense grid and select the best trees through selection indexes.

2. Material and Methods

2.1 Forest species

The species were originated from Comissão Executiva do Plano da Lavoura Cacaueira (CEPLAC) forest arboretum located in the South of Bahia state, Brazil. Data was collected from the Arnaldo Medeiros Experimental Station (Esarm) located in the municipality of Ilhéus, at the geographical point 14º45'28.0 ”S and 39º13'49.5” W with an elevation of 58 meters, typical eutrophic haplic gleisol (Santana et al. 2016), Af climate according to Köppen classification (Alvares et al., 2013). A more detailed climatic characterization of the experimental area is presented in Figure 1. Climatic data of the experimental area were obtained using the EnvRtype package (Costa-Neto et al., 2021) implemented in R software (R Core Team 2024). The trial was set in a tropical, humid, and rainy weather, such as the climate of South Bahia, Brazil. The experiment was planted in 1970 and 1971 consisting of plots with 36 individuals of the same species in each plot arranged in 2 × 2 m spacing and three replications for each species. The growth potential of 44 species was analyzed using most native species from the Brazilian Atlantic Forest (Table S1). There were some plots of exotic species as *Eucalyptus saligna* Sm and *Tectona grandis* L.. used for comparison with native ones.

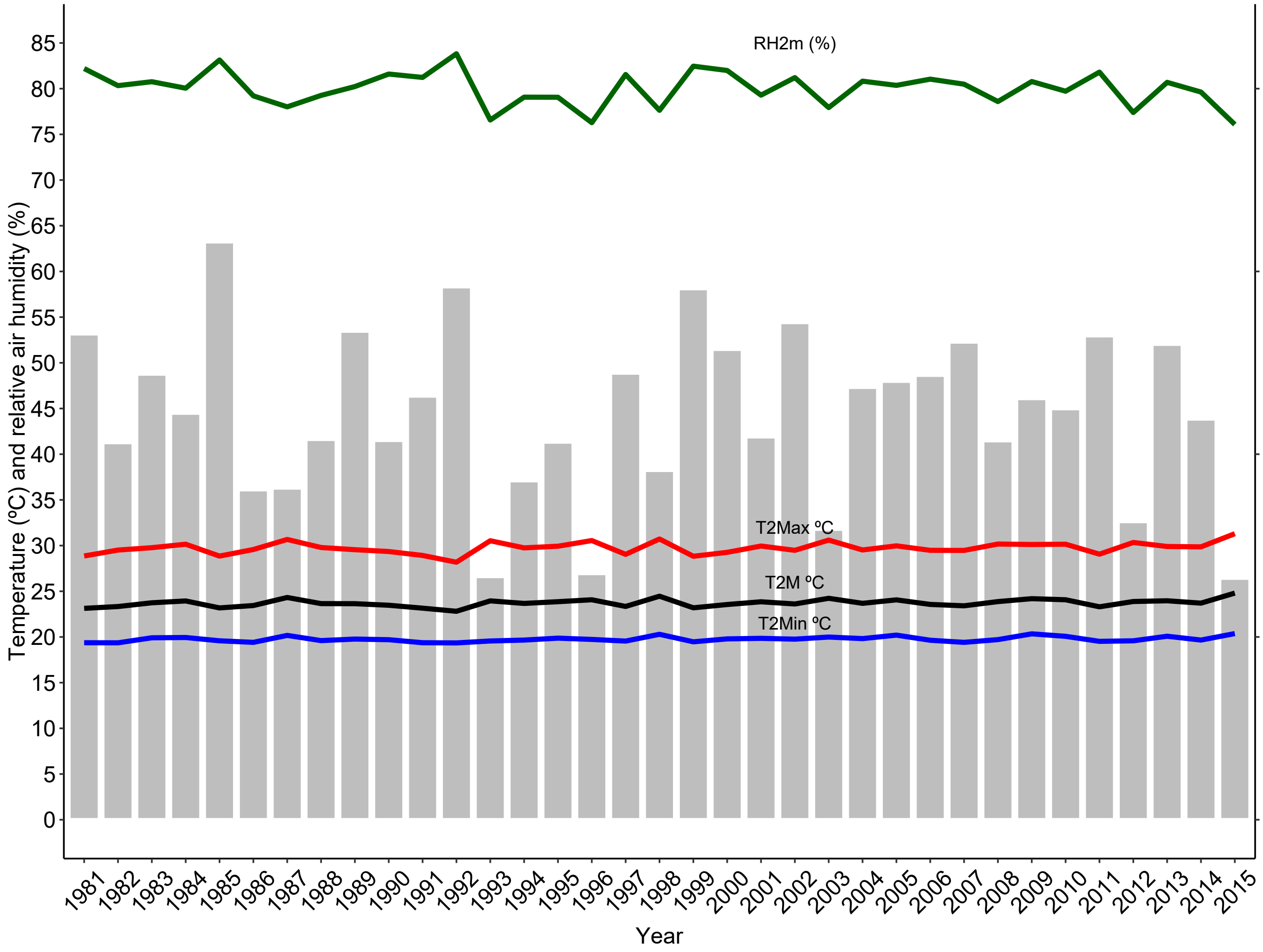

Figure 1. Climatic variables total rainfall per year (mm) represented with the bars, relative air humidity at 2 m above the surface of the earth (%, R2HM), daily average temperature at 2 m above the surface (ºC, T2M), maximum air temperature at 2 m above the surface of the earth (ºC, T2Max), minimum air temperature at 2 m above the surface of the earth (ºC, T2Min) for the most part of the experiment period, located South of Bahia state, Brazil, in the municipality of Ilhéus, at the geographical point 14º45'28.0 "S and 39º13'49.5" W.

2.2 Data collection

Tree-growth data were collected in 2014 and 2015 for the traits circumference at breast height (CBH, m), total height (TH, m) and commercial height (CH, m). The same plots were measured in different years. The CBH was measured with a flexible measuring tape, and height was measured with a hypsometer. Each trait in each year was considered as a different trait so that a total of six traits were measured. Moreover, survival was counted as 1 for alive trees and 0 for dead trees.

2.3 Phenotypic index

In order to use the information from all years and records, appropriately standardized by the standard deviation, a phenotypic index (PI) was created by multiplying all traits measured in each tree (Nunes et al. 2017):

$$PI = \left(\frac{CBH_{2014}}{S_{CBH_{2014}}}\right) \times \left(\frac{TH_{2014}}{S_{TH_{2014}}}\right) \times \left(\frac{CH_{2014}}{S_{CH_{2014}}}\right) \times \left(\frac{CBH_{2015}}{S_{CBH_{2015}}}\right) \times \left(\frac{TH_{2015}}{S_{TH_{2015}}}\right) \times \left(\frac{CH_{2015}}{S_{CH_{2015}}}\right) \quad (1)$$

In which:PI = phenotypic index; CBH_{2014}= circumference at breast height measured in 2014; $S_{DBH_{2014}}$= standard deviation of circumference at breast height measured in 2014; TH_{2014}= total height measured in 2014; $S_{TH_{2014}}$= standard deviation of total height measured in 2014;CH_{2014}= commercial height measured in 2014; $S_{CH_{2014}}$= standard deviation of commercial height measured in 2014; CBH_{2015}= circumference at breast height measured

	CBH2014	CBH2015	CH2014	CH2015	PI	TH2014	TH2015
TH2015	0.82	0.83	0.85	0.82	0.95	0.98	1
TH2014	0.82	0.79	0.84	0.78	0.94	1	0.97
PI	0.92	0.93	0.93	0.89	1	0.94	0.95
CH2015	0.69	0.69	0.97	1	0.89	0.8	0.82
CH2014	0.77	0.7	1	0.97	0.93	0.81	0.84
CBH2015	1	1	0.77	0.6	0.87	0.82	0.77
CBH2014	1	0.99	0.68	0.56	0.85	0.77	0.74

Figure 2. Pearson correlation between predicted values in M1 (above the diagonal) and M2 (below diagonal) of the traits circumference at breast height measured in 2014 (CBH_{2014}), commercial height measured in 2014 (CH_{2014}), total height measured in 2014 (TH_{2014}), circumference at breast height measured in 2015 (CBH_{2015}), commercial height measured in 2015 (CH_{2015}), total height measured in 2015 (TH_{2015}) and phenotypic index (PI). M1: model 1 without covariable. M2: model with survival as a covariable

in 2015; $S_{CBH_{2015}}$= standard deviation of circumference at breast height measured in 2015; TH_{2015}= total height measured in 2015; $S_{TH_{2015}}$= standard deviation of total height measured in 2015; CH_{2015}= commercial height measured in 2015; $S_{CH_{2015}}$= standard deviation of commercial height measured in 2015. Equal relative economic weights were assigned to all traits, i.e., this index was interpreted as an objective trait for genetic breeding.

2.4 Mixed model analysis

Two statistical models were tested. Model 1 (M1) consisted of each trait analyzed without covariable:

M1: $y = Xr + Zg + e$

where: y, r, g, and e are vectors of data or PI, general mean and repetitions (fixed), effects of species (random), and random errors, respectively. In addition, X and Z are the incidence matrices for r and g.

Model 2 (M2) considered survival (0 and 1) as a covariable aiming to correct random effects of dead trees.

M2: $y = Xr + \beta Cov + Zg + e$

where: y, r, g, and e are vectors of data, general mean and repetitions (fixed), effects of species (random), and random errors, respectively. In addition, X and Z are the incidence matrices for r and g. The β coefficient refers to the regression associated with covariable. All analyses were conducted using the Selegen-REML/BLUP software (Resende, 2016). Graphs were prepared in R software (R Core Team 2024) with ggplot2 package (Wickham, 2016) .

Table 1. Experimental parameters estimated from data analysis of species according to M1 and M2 for the traits circumference at breast height (CBH_{2014}), commercial height measured in 2014 (CH_{2014}), total height measured in 2014 (TH_{2014}), circumference at breast height measured in 2015 (CBH_{2015}), commercial height measured in 2015 (CH_{2015}), total height measured in 2015 (TH_{2015}) and phenotypic index (PI)

	Model/Trait													
	M1	**M2**	**M1**	**M2**	**M1**	**M2**	**M1**	**M2**	**M1**	**M2**	**M1**	**M2**	**M1**	**M2**
Parameters	**CBH2014**		**CH2014**		**TH2014**		**CBH2015**		**CH2015**		**TH2015**		**PI**	
c2sp	0.50	0.15	0.48	0.23	0.38	0.18	0.51	0.15	0.48	0.24	0.40	0.19	0.49	0.20
c2spm	0.87	0.86	0.87	0.91	0.82	0.88	0.87	0.86	0.86	0.91	0.83	0.89	0.87	0.89
Accuracy	0.93	0.93	0.93	0.95	0.91	0.94	0.93	0.93	0.93	0.95	0.91	0.94	0.93	0.94
CVs%	47.64	43.11	51.07	60.87	27.73	32.75	47.71	42.07	46.14	55.32	28.86	33.42	37.49	39.00
CVe%	47.89	102.55	53.60	112.23	35.50	69.12	47.03	99.93	47.79	98.38	35.56	68.67	37.97	78.25
CVr	0.99	0.42	0.95	0.54	0.78	0.47	1.01	0.42	0.97	0.56	0.81	0.49	0.99	0.50
Mean	0.80	0.28	5.25	1.84	15.19	5.58	0.82	0.28	5.75	2.03	16.10	5.79	10.85	3.80

c^2sp: individual determination coefficient of species; c^2spm: determination coefficient of species at mean level; Accuracy: accuracy of species selection; CVs%: individual coefficient of variation among species; CVe%: residual coefficient of variation among species; CVr: relative coefficient of variation. M1: model 1 without covariable. M2: model with survival as a covariable.

2.5 Index of survival correction

An index of growth corrected by survival was created from predicted values of PI for each species. This index was calculated with predicted values from mixed model analysis for PI and allowed penalization of those species with a low rate of survival:

$$ISC = PV_{PI} \times PV_{Survival}$$

In which:ISC = Index of survival correction; PV_{PI} = predicted value for PI for each species; $PV_{Survival}$ = predicted value for survival of each species. Equal relative economic weights were assigned to all traits, i.e., this index was interpreted as an objective trait for genetic breeding.

3. Results and Discussion

3.1 Parameters and correlation between traits

Variability among species was considered relatively high according to analysis using M1 (without covariable) once the species determination coefficients for individual selection (c^2sp) for most traits were greater than 0.50 (Table 1). Moreover, the variability among species was statically significant at 1% of probability according to the Likelihood Ratio Test (Table 2). When it comes to heritability, determination values for individual selection of genotypes ranging from 0.01 to 0.15 are considered low, 0.15 to 0.50 values are considered moderate, and values greater than 0.50 are considered high (Santos et al., 2022). In this sense, by drawing a parallel between this scale and the coefficient of determination between species, one can understand the great possibility of gain from the selection of species in the present study. The presence of high variability for growth traits was also observed in *Jacaranda cuspidifolia* (Moraes et al., 2013), *Dipteryx alata* progenies (Santos et al., 2014) and *Astronium fraxinifolium* (Cornacini et al., 2017), confirming the high potential to be explored in breeding programs of Brazilian native forest species.

This high variability estimated in the population demonstrated different responses of species to dense spacing. In commercial stands, genotypes adapted to dense spacing are important to wood production in quantity and quality. According to Moraes et al. (2013), spacing is crucial for well silvicultural development of trees and success in the industrial products generated from a uniform plantation. A plant breeding dilemma is to select on a mixed population and expect high yielding in pure stands. The competition effects among plants can mislead selection and harm the success of forestry breeding and its efficiency (Ferreira et al., 2024). Experimental designs must allow superior materials to be selected in an optimized and accurate way (Cappa & Cantet, 2008; Mendes et al., 2014). Thus, the dense spacing adopted allowed testing the response of different species and individuals to genotypic competition, which simulated a commercial stand.

The use of M2 (survival as a covariable) resulted in moderate values of c^2sp. The coefficient of variation among species (CVs) was similar between M1 and M2 for all traits, and the coefficient of residual variation (CVe%) for M2 was higher than the CVe% for M1 for all traits. An important parameter to understand the relation between variation among species and residuals is the coefficient of relative variation (CVr). This parameter was estimated

Table 2. Likelihood ratio test (LRT) for variance among species using M1 and M2 (represented as c^2sp) for the traits circumference at breast height in 2014 (CBH_{2014}), commercial height measured in 2014 (CH_{2014}), total height measured in 2014 (TH_{2014}), circumference at breast height measured in 2015 (CBH_{2015}), commercial height measured in 2015 (CH_{2015}), total height measured in 2015 (TH_{2015}) and phenotypic index (PI)

	Model/Trait													
	M1	**M2**	**M1**	**M2**	**M1**	**M2**	**M1**	**M2**	**M1**	**M2**	**M1**	**M2**	**M1**	**M2**
	CBH2014		**CH2014**		**TH2014**		**CBH2015**		**CH2015**		**TH2015**		**PI**	
DCM	-729.6	2433.6	3125.8	11492	4366.6	23474	-717.8	2939.5	3030.4	13096	4412.2	24294	3800.9	19331
DRM	-424.3	1705.7	3535.9	10758	4664.3	21314	-417.4	2098.9	3447.9	11942	4711.2	21893	4157.9	17476
LRT	305.34	727.9	410.11	734.72	297.66	2159.7	300.35	840.59	417.48	1153.8	299.03	2400.5	356.99	1855
Significant at 1%	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES	YES

DCM: deviance of the complete model; DRM: deviance of the reduced model; LRT: Likelihood ratio test. Chi-square tab at 1%: 6.63. M1: model 1 without covariable. M2: model with survival as a covariable.

as the ratio between CVs and CVe (%). The CVr values for M2 were lower than those for M1, which was evidence of residual variance inflation in the analysis using M2. Thus, the cause of lower values of c^2sp for M2 is a result of higher residual variance pointed in M2. These findings indicated the need for the consideration of plant mortality as a covariable in statistical models to improve selection of different species. Moreover, the accuracy of selection (Accuracy) was slightly higher (Resende & Alves, 2022) for M2 in almost all traits (Table 1).

Pearson correlation between traits evidenced the possibility of indirect selection (Nunes et al., 2016). The correlation between CBH and TH in both 2014 and 2015 years of measurement were high. According to Nunes et al. (2016), indirect selection assumes crucial importance in tree selection processes, once there are traits of difficult and high costs measurements, being the easier ones an efficient form to improve breeding programs. Thus, easier measurement traits as CBH can be used to select species for difficult measurements traits, such as TH, and accelerate selection process (Figure 2).

The magnitude of the correlations between CBH and CH was smaller than those for CBH and TH, specially among CBH2015 - CH2015 and CBH2014 - CH2015. Since CH is made by standardizing the commercial stem, that is, the portion to be used by the timber sector, different results are indeed expected. Nevertheless, the correlation remains positive and moderate between CBH and CH, which may also make indirect selection for CH viable. High levels of correlation among traits allow indirect selection of traits of difficult measurement (Fereidoonfar et al., 2018). The tree height measurement is prone to wind effects, which is a difficult procedure and may cause errors. Moreover, statistical models to estimate tree height can be built from CBH data using a good tree height database as reference in the case of similar sites, which optimize field work and reduce costs (Santos et al., 2014). These correlations obtained through M1 and M2 differed slightly with correlations from M2 being lower than those from M1 likely due to competition effects removed through M2. Although these differences existed, correlations were high for all traits for both models M1 and M2.

3.2 Selection of species

The top 20 species were ranked according to predicted value for Index of Survival Correction (ISC - obtained after mixed model analysis of PI and survival using M1), phenotypic index analyzed by M1 (PI_M1), and phenotypic index analyzed by M2 (PI_M2) in order to compare different forms of species selection (Table S2). The gains with selection were estimated in relation to the general mean of the arboretum. The PI_M1 and PI_M2 rankings showed a high correlation of 0.80 but predicted values in PI_M2 were lower than those in PI_M1. This was likely a consequence of covariable survival correction, which occurs when a growth potential of an individual is favored by its neighbor's death and the accompanying model can be used to correct this.

The correspondence of ranking position between M1 and M2 were high, which meant that the main difference between these two approaches was only the magnitude in predicted values. The ISC presented low correlation between predicted values for PI_M1 (0.19) and PI_M2 (0.45). The ISC simultaneously considered the growth potential and the number of individuals per species in the experimental area. Thus, species with a low number of individuals will hardly be penalized in the total predicted value of ISC.

The species *Eucalyptus saligna*, *Samanea tubulosa,* and *Gallesia integrifolia* were top ranked in PI_M1 and occupied low positions for ISC. These species presented a low number of individuals, which was evidence of the low adaptability of these species in the area (Figure 3). An important point on selection of top ranked species for genetic breeding is the adaptation of genotypes in the

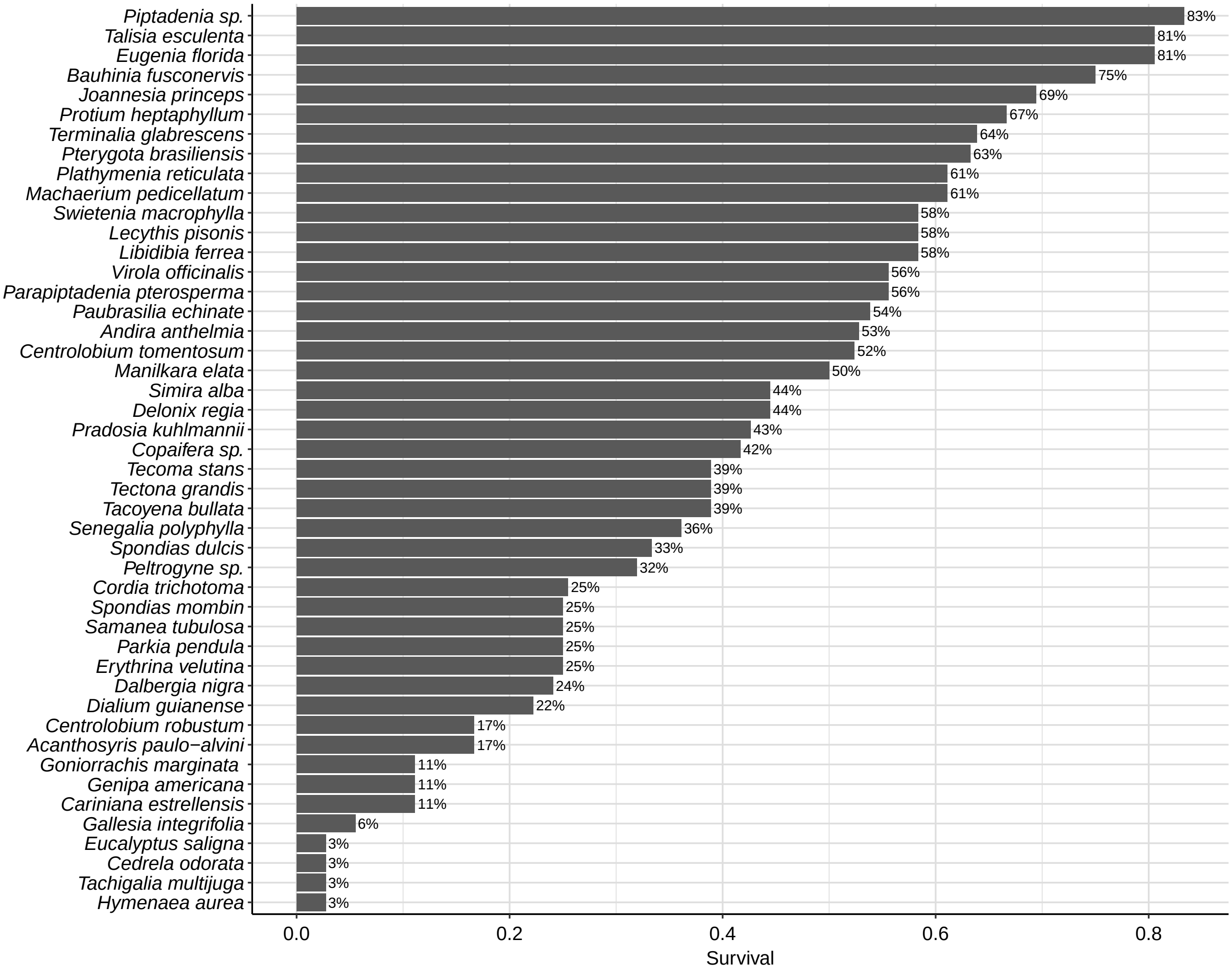

Figure 3. Survival rate ranging from 0 to 0.83 (0% to 83%) of species studied in the arboretum of Comissão Executiva do Plano da Lavoura Cacaueira (CEPLAC) located in the South of Bahia state, Brazil.

experimental area, which is representative of the main region of cultivation (Cornacini et al., 2017).

Survival can represent the adaptation of a species and the adequacy of this species in densely spaced conditions. Moreover, in relation to PI_M1 and PI_M2, ISC penalized the predicted values and allowed a more realistic selection for species adaptation compared to PI_M2. According to Nunes et al. (2017), selection indices based on post mixed model analysis, such as ISC, are more accurate than phenotypic indices (preparation of the combination of two traits before statistical analysis). Nunes et al. (2017) compared different indices for tree selection and reported that genotypic indices, such as ISC, provided an accurate ranking. This ranking accounted for the accuracy and heritability of both traits expressed in its predicted values before combination into a unique aggregate. Considering these aspects, ISC was the best index to use in species selection since it analyzed the behavior of a species individual survival under highly competitive conditions.

Considering ISC, the two top-ranked species was *Pterygota brasiliensis* and *Plathymenia reticulata*. The species *P. brasiliensis* presented the best growth potential in a dense spaced system with a gain with selection of 163.71% in relation to general mean (Figure 4). These species adapted well to a tropical, humid, and rainy weather, such as the climate of South Bahia, Brazil (Figures 1 and 3). Mendonça et al. (2017) also reported *P. brasiliensis* as a good timber producer. These authors demonstrated that *P. brasiliensis* was one of the most indicated species to produce sawn timber based on silvicultural characteristics. Although this species presented

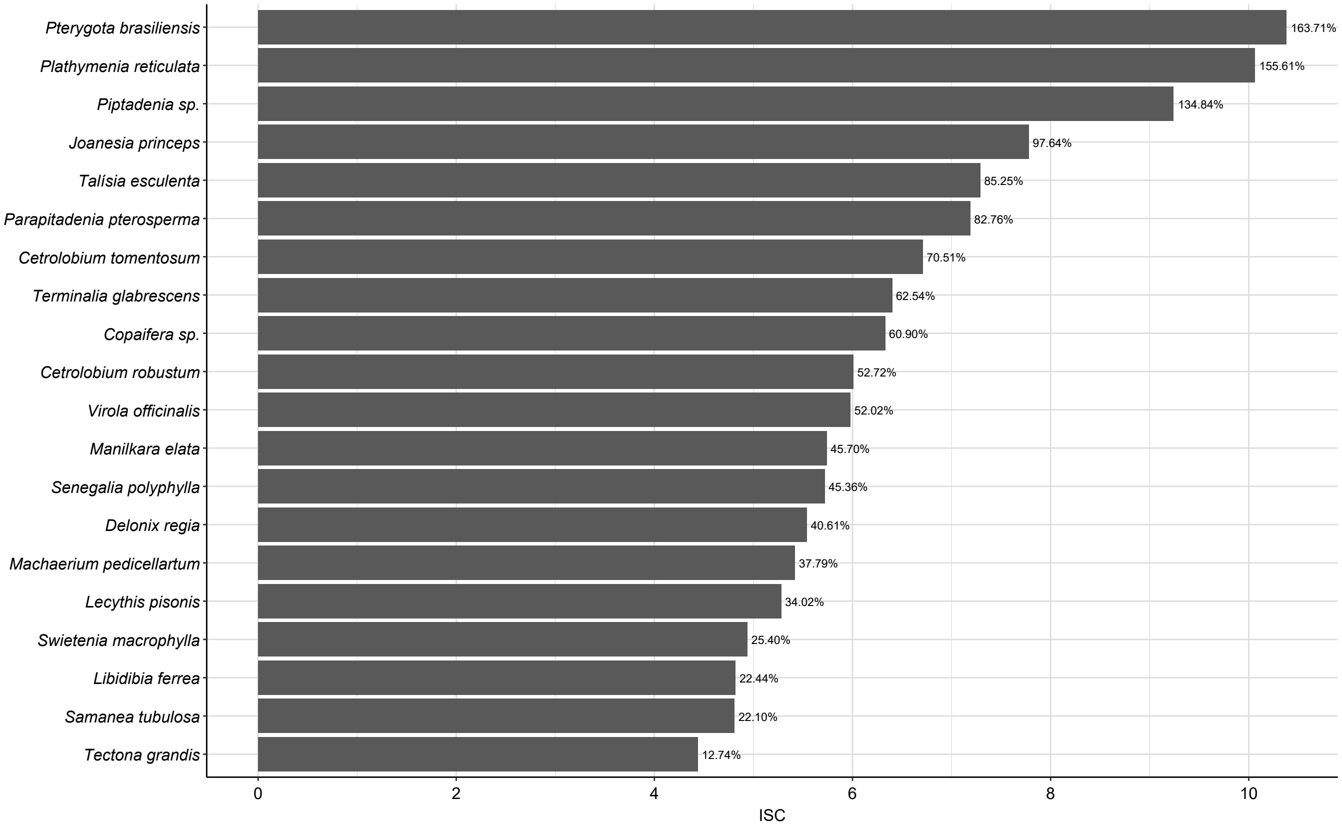

Figure 4. Gain in percentage (%), calculated in relation to general mean of the population for the top 20 species according to predicted value for Index of Survival Correction (ISC - obtained after mixed model analysis of PI and survival using M1).

high volumetric production, the basic density of the wood was moderate to low, which promotes the species to dominate the wood veneer industry (Mendonça et al., 2017). Rolim et al. (2018), classified *P. brasiliensis* wood's basic density as moderate and indicated this species may be used in soft structures, furniture, coatings, packaging, and utensils. Moreover, this species should be used as shader in consortiums due to its uniform tree top design (Rolim et al., 2018).

The species *Platymenia reticulata* also presented good adaptation and volumetric development with a gain of 155.61% in relation to the general mean of the experiment. Opposingly, *P. reticulata* had potential to be used in the timber industry due to high quality wood and volumetric development (Lacerda et al., 2002). Therefore, these two species should be considered ideal genetic breeding examples in regions with similar characteristics to the experimental area studied here.

The species *P. brasiliensis*, *P. reticulata*, *Piptadenia* sp., *Joannesia princeps,* and *Talisia esculenta* presented high gains with selection (Figure 3). Individuals of these species can be used as donors for cloning propagules to compose a clonal recombination orchard. These clonal propagules require clonal techniques such as graft, somatic embryogenesis, or clonal propagation using minicuttings. Considering seed collection, the use of the only 36 individuals in the experiment as seed donors may reduce genetic variability and growth mean of the breeding population due to endogamy (Nunes, 2021). Even if seed collection were carried out from the best individuals on the plot, receiving pollen from other consanguineous neighbors could result in the generation of seeds with a high rate of inbreeding. Inbreeding is a natural phenomenon of finite populations, which occurs when the offspring was the result of a cross between two individuals that shared the same ancestry (Woolliams et al., 2015).

Potential seed donors trees of *P. brasiliensis*, *P. reticulata*, *Piptadenia* sp., *Joannesia princeps,* and *T. esculenta* can be the target of research in South Bahia forest fragments. Knowledge about the effects of crosses between individuals is important in forest genetic improvement since selection gains can be compromised with endogamy. This phenomenon can also reduce the production of viable seeds and cause decreases in genetic variance within the population due to the reduction of heterozygosity and a loss of unfavorable alleles (Wei et al., 1998; Fernandes et al., 2023). In this context, is important to consider seed donors from different locations of South of Bahia state, Brazil, in order to assemble a breeding population with adequate genetic representativeness of this selected species.

4. Conclusion

The top two ranked species were *P. brasiliensis* and *P. reticulata*, which adapted well to a tropical, humid, and rainy weather, such as the climate of South Bahia, Brazil. This species will be the target of conservation genetics and breeding studies directed for industrial timber production.

Statistical selection of native species may consider the selection index based on volumetric production and survival traits. This combination should be made after mixed models' analyses with a predicted value for each species that allowed for the selection of species with high output volume and adaptation to the site.

The study provides subsidies to orientate selection of ideal species adapted to the study area and individuals for seed collection, breeding populations assembling of selected species and to guide future studies of native Brazilian Atlantic Forest species.

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Author Statements

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TREED0272 - Supplementary Material

Selection of Atlantic Forest species in South Bahia, Brazil

Andrei Caíque Pires Nunes **et al., 2024.**

Table S1 List of species studied in the arboretum of Comissão Executiva do Plano da Lavoura Cacaueira (CEPLAC) located in the South of Bahia state, Brazil. This area is named Experimental Station Arnaldo Medeiros (Esarm)

Scientific name	Family	Common name
Senegalia polyphylla (DC.) Britton & Rose	Fabaceae	barauna-mogno
Acanthosyris paulo-alvini G.M. Barroso	Santalaceae	mata-cacau
Andira anthelmia (Vell.) Benth.	Fabaceae	angelim-coco
Bauhinia fusconervis (Bong.) Steud.	Fabaceae	unha-de-vaca
Cariniana estrellensis (Raddi) Kuntze	Lecythidaceae	jequitibá-cipó
Cedrela odorata L.	Meliaceae	cedro-rosa
Centrolobium robustum (Vell.) Mart. ex Benth.	Fabaceae	putumuju-mirim
Centrolobium tomentosum Guillem. ex Benth.	Fabaceae	putumuju-piloso
Copaifera sp.	Fabaceae	pau-óleo, copaíba
Cordia trichotoma (Vell.) Arráb. ex Steud.	Cordiaceae	claraíba-parda
Dalbergia nigra (Vell.) Allemão ex Benth.	Fabaceae	jacaranda-da-bahia
Delonix regia (Bojer ex Hook.) Raf.	Fabaceae	flamboyant
Dialium guianense (Aubl.) Sandwith	Fabaceae	jitaí-preto
Erythrina velutina Willd.	Fabaceae	eritrina-mulungu
Eugenia florida DC.	Myrtaceae	murta
Gallesia integrifolia Spreng.	Phytolataccaceae	pau-d'álho
Genipa americana L.	Rubiaceae	jenipapo
Goniorrachis marginata Taub.	Fabaceae	itapicuru
Hymenaea aurea Y.T.Lee & Langenh.	Fabaceae	jatobá-piloso

Joannesia princeps Vell.	Euphorbiaceae	dandá, boleira
Lecythis pisonis Cambess.	Lecythidaceae	sapucaia
Libidibia ferrea (Mart. ex Tul.) L.P.Queiroz	Fabaceae	pau-ferro
Machaerium pedicellatum Vogel	Fabaceae	mucitaiba-amarela
Manilkara elata (Allemão ex Miq.) Monach.	Sapotaceae	maçaranduba-vermelha
Parapiptadenia pterosperma (Benth.) Brenan	Fabaceae	viola
Parkia pendula (Willd.) Benth. ex Walp.	Fabaceae	juerana-prego
Paubrasilia echinate (Lam.) Gagnon, H.C.Lima & G.P.Lewis	Fabaceae	pau-brasil, ibirapitanga
Peltrogyne sp.	Fabaceae	pau-roxo
Piptadenia sp.	Fabaceae	sucupiruçu
Plathymenia reticulata Benth.	Fabaceae	vinhático
Pradosia kuhlmannii Toledo	Sapotaceae	buranhém
Protium heptaphyllum (Aubl.) Marchand	Buseraceae	amescla-mirim
Pterygota brasiliensis Allemão	Malvaceae	folheiro, pau-rei
Samanea tubulosa (Benth.) Barneby & J.W.Grimes	Fabaceae	casqueiro
Simira alba (Mart.) Delprete, Margalho & Groppo	Rubiaceae	arariba-branca
Spondias dulcis Parkinson	Anacardiaceae	cajarana
Spondias mombin L.	Anacardiaceae	cajá, taperebá
Swietenia macrophylla King	Meliaceae	mogno
Tachigalia multijuga Benth.	Fabaceae	ingá-açu
Talisia esculenta (A. St. Hil) Radlk	Sapindaceae	Pitomba
Tacoyena bullata (Vell.) Mart.	Rubiaceae	jenipapo-bravo
Tecoma stans (L.) Juss. ex Kunth	Bignonaceae	ipê-de-jardim
Tectona grandis L.f.	Verbenaceae	teca
Terminalia glabrescens Mart.	Combretaceae	araçá-d´água
Virola officinalis Warb.	Myristicaceae	bicuíba-branca

Table S2 Ranking of the top 20 species according to predicted value for Index of Survival Correction (ISC - obtained after mixed model analysis of PI and survival using M1), phenotypic index analyzed by M1 (PI_M1) and phenotypic index analyzed by M2 (PI_M2)

Rank	**Scientific name**	**ISC**	**Scientific name**	**PI_M1**	**Scientific name**	**PI_M2**
1	Pterygota brasiliensis	10.38	Eucalyptus saligna	24.02	Pterygota brasiliensis	7.85
2	Plathymenia reticulata	10.06	Samanea tubulosa	18.24	Plathymenia reticulata	7.76
3	Piptadenia sp.	9.24	Gallesia integrifolia	18.13	Samanea tubulosa	5.83
4	Joannesia princeps	7.78	Plathymenia reticulata	17.08	Senegalia polyphylla	5.75
5	Talisia esculenta	7.29	Pterygota brasiliensis	16.90	Parapitadenia pterosperma	5.46
6	Parapitadenia pterosperma	7.19	Senegalia polyphylla	15.74	Centrolobium tomentosum	5.26
7	Cetrolobium tomentosum	6.71	Acanthosyris paulo-alvini	15.67	Erythrina velutina	5.09
8	Terminalia glabrescens	6.40	Jatropha sp.	15.60	Piptadenia sp.	4.96
9	Copaifera sp.	6.33	Erythrina velutina	15.27	Delonix regia	4.83
10	Centrolobium robustum	6.01	Goniorrachis marginata	14.69	Acanthosyris paulo-alvini	4.78
11	Virola officinalis	5.98	Genipa americana	13.86	Joanesia princeps	4.78
12	Manilkara elata	5.74	Parapitadenia pterosperma	13.35	Manilkara elata	4.53
13	Senegalia polyphylla	5.72	Centrolobium tomentosum	13.11	Jatropha sp.	4.50
14	Delonix regia	5.54	Cariniana estrellensis	12.95	Spondias mombin	4.47
15	Machaerium pedicellartum	5.42	Spondias mombin	12.80	Spondias dulcis	4.43
16	Lecythis pisonis	5.28	Delonix regia	12.61	Gallesia integrifolia	4.43
17	Swietenia macrophylla	4.94	Spondias dulcis	12.11	Eucaliptus saligna	4.34
18	Libidibia ferrea	4.82	Tachigalia multijuga	11.75	Genipa americana	4.28
19	Samanea tubulosa	4.81	Manilkara elata	11.73	Virola officinalis	4.28
20	Tectona grandis	4.44	Joannesia princeps	11.72	Tectona grandis	4.27

M1: model 1 without covariable. M2: model with survival as a covariable