

# New Forests

## Statistical selection of native and exotic species for genetic breeding in the Brazilian Atlantic Forest --Manuscript Draft--

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<b>Abstract:</b>	<p>The study aimed to test different statistical methods of selection in high dense spacing trees and evaluate, statically, the growth potential of a forest plantation in South of Bahia, Brazil composed by several Brazilian Atlantic Forest and exotic species. The experiment was carried out in the Comissão Executiva do Plano da Lavoura Cacaueira (CEPLAC) forest arboretum located in the South of Bahia state, Brazil. A total of 58 species were tested with three replications with plot areas 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 industrial 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 area. The combination of these traits should be performed after mixed models' analyses using a predicted value for each trait. The top two ranked species were <i>Pterygota brasiliensis</i> Allemão and <i>Plathymenia reticulata</i> Benth., which adapted well to a tropical climate, such as the climate in South Bahia, Brazil. From this study, it was possible to establish genetic breeding strategies through 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.</p>

# Statistical selection of native and exotic species for genetic breeding in the Brazilian Atlantic Forest

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## 1 - ABSTRACT

The study aimed to test different statistical methods of selection in high dense spacing trees and evaluate, statically, the growth potential of a forest plantation in South of Bahia, Brazil composed by several Brazilian Atlantic Forest and exotic species. The experiment was carried out in the Comissão Executiva do Plano da Lavoura Cacaueira (CEPLAC) forest arboretum located in the South of Bahia state, Brazil. A total of 58 species were tested with three replications with plot areas containing 36 individuals that were arranged in  $2 \times 2$  m spacing. Experimental parameters indicated high variability among species to high density spacing, which is favorable to commercial pure stands practiced in the industrial 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 area. The combination of these traits should be performed after mixed models' analyses using a predicted value for each trait. The top two ranked species were *Pterygota brasiliensis* Allemão and *Plathymenia reticulata* Benth., which adapted well to a tropical climate, such as the climate in South Bahia, Brazil. From this study, it was possible to establish genetic breeding strategies through 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:** Forest breeding; Selection index; Statistics; Breeding strategy.

## 2 - 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 (Cornacini et al. 2017). 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 (Moraes et al. 2013).

Brazil is considered the country that holds the greatest biodiversity on the planet considering ecosystems, species, populations, individuals, and genes (Myers et al. 2000). 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. Despite the relevance of native forest species, investments in research for the selection and improvement of populations of these species are still limited (Zaninovich et al. 2016). 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*, which are exotic species (Gonçalves et al. 2013; Thomas et al. 2014). The *Eucalyptus* spp. and *Pinus* spp. together account for about 7.3 million hectares of forests currently planted in Brazil, while native forest species account for less than 0.59 million hectares (IBA 2017).

The small participation of native species in the Brazilian forest sector is due to their low development in relation to *Eucalyptus* and *Pinus*, and a scarcity of basic information for their domestication. 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<sup>3</sup> ha<sup>-1</sup>.y<sup>-1</sup>, 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 of a high degree of investment in their breeding programs, which are in advanced stages with some species improving to their third generation of advancement (Pires et al. 2011). Thus, genetic breeding studies concerning native Brazilian Atlantic Forest species is

extremely important in order to make 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 (Melo et al. 2013). 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; Sujii et al. 2017).

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), and rubber tree (*Hevea brasiliensis* Willd. ex A. Juss) (Oliveira et al. 2015). 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. In spite of these studies, a wide range of genetic materials with timber potential has not yet been evaluated, mainly in the region of the South of 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. The study of characters is given according to the model  $P = G + E$ , where P is a phenotype or phenotypic value measured in the individuals, as a result of a genotype (G)

action influenced by an environment (E) (Cruz 2010). 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 (Cruz 2010).

Almost all selection of higher individuals of native forest species are based on mass selection (Oliveira; Farias Neto 2008). 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.

Considering all these aspects, the objective of the present work was to test different statistical methods of selection in high dense spacing trees and evaluate the growth potential of a forest plantation in South of Bahia, Brazil composed of several Brazilian Atlantic Forest and exotic species.

### **3 - MATERIALS AND METHODS**

#### ***3.1 Genetic Materials***

Genetic materials were originated from a 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 14°45'28.0 "S and 39°13'49.5" W with an altitude of 58 meters (Af climate according to Köppen classification, Alvares et al. 2013). 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 56 species was analyzed using most native species from the Brazilian Atlantic Forest (Table 1).

**Table 1** List of species studied in the arboretum of Comissão Executiva do Plano da Lavoura Cacaueira (CEPLAC) located in the South of Bahia state, Brazil, named Experimental Station Arnaldo Medeiros (Esarm)

Scientific name	Family	Common name	Planting year
<i>Acacia glomerosa</i>	Fabaceae	barauna-mogno	-
<i>Acanthosyris paulo-alvini</i>	Santalaceae	mata-cacau	-
<i>Alibertia edulis</i>	Rubiaceae	arariba-branca	1973
<i>Andira stipulacea</i>	Fabaceae	angelim-coco	1972
<i>Bauhinia fusconervis</i>	Fabaceae	unha-de-vaca	1975
<i>Cariniana estrellensis</i>	Lecythidaceae	jequitibá-cipó	1975
<i>Cedrela odorata</i>	Meliaceae	cedro-rosa	-
<i>Cedrela odorata</i>	Meliaceae	cedro-rosa	-
<i>Cetrolobium robustum</i>	Fabaceae	putumuju-mirim	1972
<i>Cetrolobium robustum</i>	Fabaceae	putumuju-mirim	1972
<i>Cetrolobium robustum</i>	Fabaceae	putumuju-mirim	1972
<i>Cetrolobium tomentosum</i>	Fabaceae	putumuju-piloso	1972
<i>Copaifera</i> sp.	Fabaceae	Pau-óleo, copaiba	-
<i>Copaifera</i> sp.	Fabaceae	Pau-óleo, copaiba	-
<i>Cordia trichotoma</i>	Boraginaceae	claraíba-parda	1972
<i>Cordia trichotoma</i>	Boraginaceae	claraíba-parda	1972
<i>Dalbergia nigra</i>	Fabaceae	jacaranda-da-bahia	1972

<i>Dalbergia nigra</i>	Fabaceae	jacaranda-da-bahia	1972
<i>Dalbergia nigra</i>	Fabaceae	jacaranda-da-bahia	1972
<i>Delonix regia</i>	Fabaceae	flamboyant	1975
<i>Dialium guianenses</i>	Fabaceae	jitaí-preto	1972
<i>Erythrina velutina</i>	Fabaceae	eritrina-mulungu	1973
<i>Eugenia florida</i>	Myrtaceae	murta	1975
<i>Gallesia scorodendron</i>	Phytolataccaceae	pau-d'álho	1972
<i>Genipa americana</i>	Rubiaceae	jenipapo	1975
<i>Goniorrachis marginata</i>	Fabaceae	Itapicuru	1972
<i>Hymeea aurea</i>	Fabaceae	jatobá-piloso	1972
<i>Joanesia princeps</i>	Euphorbiaceae	Dandá, boleira	1975
<i>Lecythis pisonis</i>	Lecythidaceae	sapucaia	1972
<i>Libidibia ferrea</i>	Fabaceae	pau-ferro	-
<i>Libidibia ferrea</i>	Fabaceae	pau-ferro	-
<i>Machaerium pedicellartum</i>	Fabaceae	mucitaiba-amarela	1975
<i>Manilkara elata</i>	Sapotaceae	maçaranduba-vermelha	-
<i>Parapitadenia pterosperma</i>	Fabaceae	viola	-
<i>Parkia pendula</i>	Fabaceae	juerana-prego	1972
<i>Paubrasilia echinata</i>	Fabaceae	Pau-brasil, ibirapitanga	1972
<i>Paubrasilia echinata</i>	Fabaceae	Pau-brasil, ibirapitanga	1972
<i>Paubrasilia echinata</i>	Fabaceae	Pau-brasil, ibirapitanga	1972
<i>Peltogyne</i> sp.	Fabaceae	pau-roxo	1975



<i>Piptadenia</i> sp.	Fabaceae	sucupiruçu	-
<i>Plathymenia reticulata</i>	Mimosaceae	vinhático	-
<i>Pradosia kuhlmannii</i>	Sapotaceae	buranhém	1972
<i>Protium heptaphyllum</i>	Buseraceae	amescla-mirim	1972
<i>Pterygota brasiliensis</i>	Malvaceae	Folheiro, pau-rei	1972
<i>Samanea tubulosa</i>	Fabaceae	casqueiro	1974
<i>Spondias dulcis</i>	Anacardiaceae	cajarana	1972
<i>Spondias mombin</i>	Anacardiaceae	Cajá, taperebá	1975
<i>Swietenia macrophylla</i>	Meliaceae	mogno	1974
<i>Tachigalia multijuga</i>	Fabaceae	ingá-açu	1972
<i>Tachigalia multijuga</i>	Fabaceae	ingá-açu	1972
<i>Tacoyena bullata</i>	Rubiaceae	jenipapo-bravo	1974
<i>Tecoma stans</i>	Bignonaceae	ipê-de-jardim	1974
<i>Tecoma stans</i>	Bignonaceae	ipê-de-jardim	1974
<i>Tectona grandis</i>	Verbenaceae	teca	1974
<i>Terminalia brasiliensis</i>	Combretaceae	araçá-d'água	1975
<i>Virola officinalis</i>	Myristicaceae	bicuíba-branca	-

### 3.2 Data collection

Tree-growth data were collected in 2014 and 2015 with measured attributes that included tree circumference at breast height (CBH, m), total height (TH, m) and commercial height (CH, m). The CBH was measured with a flexible measuring tape, and height was measured with a

hypsoneter. 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.

### 3.3 Phenotypic index

A phenotypic index (PI) was created by multiplying all traits measured in each tree:

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

In which:  $PI$  = phenotypic index;  $CBH_{2014}$  = circumference at breast height measured in 2014;  $S_{CBH_{2014}}$  = 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 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.

### 3.4 Mixed model analysis

In order to analyze the data, two statistical models were tested. Model 1 (M1) consisted of each trait analyzed without covariable:  $y = Xr + Zg + e$ , where:  $y$ ,  $r$ ,  $g$ , and  $e$  are vectors of data, general mean (fixed), effects of species plot (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:  $y = Xr + \beta\text{Cov} + Zg + e$ , y, r, g, and e are vectors of data, general mean and repetitions (fixed), effects of species plot (random), and random errors, respectively. In addition, X and Z are the incidence matrices for r and g. The  $\beta$  coefficient refers to the regression associated with covariable. All analyses were conducted using the Selegen-REML/BLUP software (Resende 2016). Graphics were done using the package ggplot2 in the software R (R Core Team 2019).

Distributions and structures of means and variances of the mixed model equations:

$$E[y \ g \ e] = [Xr \ 0 \ 0] ; \quad Var[g \ e] = [I\sigma_g^2 \ 0 \ 0 \ I\sigma_e^2] ; \quad [X'X \ X'Z \ Z'X \ Z'Z + I\lambda_1][r^{\wedge} \ g^{\wedge}] = [X'y \ Z'y]$$

$$\lambda_1 = \frac{\sigma_e^2}{\sigma_s^2} = \frac{1-c_{sp}^2}{c_{sp}^2}; \quad c_{sp}^2 = \frac{\sigma_s^2}{\sigma_s^2 + \sigma_e^2} : \text{species determination coefficient of individual selection.}$$

$$Acuracy = \sqrt{\frac{n \times c_{sp}^2}{1 + (n-1) \times c_{sp}^2}}; \quad n: \text{number of individuals per species}; \quad c_{sp_m}^2: Acuracy^2$$

$$\sigma_s^2 = \text{variance among species plot}; \quad \sigma_e^2 = \text{residual variance.}$$

$$CVs\% = 100 \times \left( \frac{\sqrt{\sigma_g^2}}{m} \right) = \text{coefficient of variation among species plot}; \quad m = \text{general mean of the experiment.}$$

$$CVe\% = 100 \times \left( \frac{\sqrt{\sigma_e^2}}{m} \right) = \text{coefficient of residual variation.}$$

$$CVr = \left( \frac{CVs\%}{CVe\%} \right) = \text{coefficient of relative variation.}$$

Variance components estimators via REML and EM algorithm:

$$\sigma_e^2 = \frac{[y'y - r^{\wedge'} X' y - g^{\wedge'}]}{[N - r(x)]}; \quad \sigma_s^2 = \frac{[g^{\wedge'} g^{\wedge} + \sigma_e^2 (tr) C^{22}]}{q}$$

$$C^{22} \text{ can be found in: } C^{-1} = [C_{11} \ C_{12} \ C_{21} \ C_{22}]^{-1} = [C^{11} \ C^{12} \ C^{21} \ C^{22}]$$

In which: C is the coefficient matrix of mixed models equations; tr: trace matrix operator; r(x): rank of matrix X; N,q = total number of data and species respectively.

### 3.5 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.

## 4 - RESULTS AND DISCUSSION

### 4.1 Parameters and correlation between traits

Variability among species was considered relatively high according to analysis using M1 once the species determination coefficients for individual selection ( $c^2_{sp}$ ) for a majority of traits were greater than 0.50 (Table 2). Moreover, the variability among species was statically significant at 1% of probability according to the Likelihood Ratio Test (Table 3). According to Resende (2002), 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. The presence of high genetic 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.

**Table 2** Experimental parameters estimated from data analysis of species displayed as plots in the experiment according to M1 and M2 for the traits circumference at breast height (CBH<sub>2014</sub>), commercial height measured in 2014 (CH<sub>2014</sub>), total height measured in 2014 (TH<sub>2014</sub>), circumference at breast height measured in 2015 (CBH<sub>2015</sub>), commercial height measured in 2015 (CH<sub>2015</sub>), total height measured in 2015 (TH<sub>2015</sub>) and phenotypic index (PI)

Model/Trait														
	M1	M2	M1	M2	M1	M2	M1	M2	M1	M2	M1	M2	M1	M2
Parameters	CBH <sub>2014</sub>		CH <sub>2014</sub>		TH <sub>2014</sub>		CBH <sub>2015</sub>		CH <sub>2015</sub>		TH <sub>2015</sub>		PI	
c <sup>2</sup> <sub>sp</sub>	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
c <sup>2</sup> <sub>spm</sub>	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<sup>2</sup><sub>sp</sub>: individual determination coefficient of species; c<sup>2</sup><sub>spm</sub>: 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.

8 This high variability estimated in the population demonstrated different responses of  
9 species to dense spacing. In commercial stands, genotypes adapted to dense spacing are  
10 important to wood production in quantity and quality. According to Moraes et al. (2013),  
11 spacing is crucial for well silvicultural development of trees and success in the industrial  
12 products generated from a uniform plantation. A plant breeding dilemma is to select on a  
13 mixed population and expect high yielding in pure stands (Griffing 1967). Experimental  
14 designs must allow superior materials to be selected in an optimized and accurate way (Cappa  
15 and Cantet 2006; Mendes et al. 2013). Thus, the dense spacing adopted allowed testing the  
16 response of different species and individuals to genotypic competition, which simulated a  
17 commercial stand.

18 The use of M2 (survival as a covariable) resulted in moderate (Resende 2002) values  
19 of  $c^2_{sp}$ . The coefficient of variation among species (CVs) was similar between M1 and M2  
20 for all traits, and the coefficient of residual variation (CVe%) for M2 was higher than the  
21 CVe% for M1 for all traits. An important parameter to understand the relation between  
22 variation among species and residuals is the coefficient of relative variation (CVr). This  
23 parameter was estimated as the ratio between CVs and CVe (%). The CVr values for M2 were  
24 lower than those for M1, which was evidence of residual variance inflation in the analysis  
25 using M2. Thus, the cause of lower values of  $c^2_{sp}$  for M2 is a result of higher residual  
26 variance pointed in M2. These findings indicated the need for the consideration of plant  
27 mortality as a covariable in statistical models to improve selection of different species.  
28 Moreover, the accuracy of selection (Accuracy) was slightly higher for M2 in almost all traits  
29 (Table 2).

**Table 3** Likelihood ratio test (LRT) for variance among species using M1 and M2 (represented as c<sup>2</sup>sp) for the traits circumference at breast height in 2014 (CBH<sub>2014</sub>), commercial height measured in 2014 (CH<sub>2014</sub>), total height measured in 2014 (TH<sub>2014</sub>), circumference at breast height measured in 2015 (CBH<sub>2015</sub>), commercial height measured in 2015 (CH<sub>2015</sub>), total height measured in 2015 (TH<sub>2015</sub>) and phenotypic index (PI)

Model/Trait														
	M1	M2	M1	M2	M1	M2	M1	M2	M1	M2	M1	M2	M1	M2
	CBH <sub>2014</sub>		CH <sub>2014</sub>		TH <sub>2014</sub>		CBH <sub>2015</sub>		CH <sub>2015</sub>		TH <sub>2015</sub>		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.



Correlations 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 (Table 4).

As correlations between CBH and TH were higher than 0.70, indirect selection can be adopted as a powerful tool. High levels of correlation among traits can be used for logic relationships, which allowed indirect selection of traits of difficult measurement (Fereidoonfar et al. 2018). The TH measurement is prone to wind effects, which is a difficult procedure and may cause errors. Moreover, statistical models to estimate TH can be built from CBH data using a good TH database as reference in the case of similar sites, which optimize field work and reduce costs.

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. Santos et al. (2014) also found high correlation between CBH and TH for *Dipteryx alata*. These authors concluded that the indirect genetic selection can be adopted considering diameter at breast height instead of TH.

**Table 4** Correlation between predicted values in M1 (below the diagonal) and M2 (above diagonal) of the traits circumference at breast height measured in 2014 (CBH<sub>2014</sub>), commercial height measured in 2014 (CH<sub>2014</sub>), total height measured in 2014 (TH<sub>2014</sub>), circumference at breast height measured in 2015 (CBH<sub>2015</sub>), commercial height measured in 2015 (CH<sub>2015</sub>), total height measured in 2015 (TH<sub>2015</sub>) and phenotypic index (PI)

	<b>CBH<sub>2014</sub></b>	<b>CH<sub>2014</sub></b>	<b>TH<sub>2014</sub></b>	<b>CBH<sub>2015</sub></b>	<b>CH<sub>2015</sub></b>	<b>TH<sub>2015</sub></b>	<b>PI</b>
<b>CBH<sub>2014</sub></b>	-	0.68	0.77	0.99	0.56	0.74	0.85
<b>CH<sub>2014</sub></b>	0.77	-	0.81	0.70	0.97	0.84	0.93
<b>TH<sub>2014</sub></b>	0.82	0.84	-	0.79	0.78	0.97	0.94
<b>CBH<sub>2015</sub></b>	1.00	0.77	0.82	-	0.60	0.77	0.87
<b>CH<sub>2015</sub></b>	0.69	0.97	0.80	0.69	-	0.82	0.89
<b>TH<sub>2015</sub></b>	0.82	0.85	0.98	0.83	0.82	-	0.95
<b>PI</b>	0.92	0.93	0.94	0.93	0.89	0.95	-

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

#### 4.2 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 5). 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 covariable in the model M2 was capable of correcting the predicted value of a big tree if its neighbors were deceased.

The correspondence of ranking position between M1 and M2 were high, which meant that the main difference between these two approaches was only the bias 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 scorodendron* were top ranked in PI\_M1 and occupied low positions for ISC (*E. saligna* 53rd position for ISC and *G. scorodendron* 48th position for ISC). These species presented a low number of individuals, which was evidence of the low adaptability of these species in the area. An important point on selection of top ranked species for genetic breeding is the adaptation of genotypes in the 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.

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

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

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 in selection of 163.71% (Table 6). Mendonça et al. (2017) also reported *P. brasiliensis* sp. [ $\equiv$ *Brasiloxylon brasiliensis* (All.) K.Schum.] 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 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* [ $\equiv$ *Brasiloxylon brasiliensis* (All.) K.Schum.] 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 Esarm experimental area studied here.

**Table 6** Ranking and gain with selection 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)

Rank	Scientific name	ISC	Gain (%)*
1	<i>Pterygota brasiliensis</i>	10.38	163.71%
2	<i>Plathymenia reticulata</i>	10.06	155.61%

3	<i>Piptadenia</i> sp.	9.24	134.84%
4	<i>Joanesia princeps</i>	7.78	97.64%
5	<i>Talisia esculenta</i>	7.29	85.25%
6	<i>Parapitadenia pterosperma</i>	7.19	82.76%
7	<i>Cetrolobium tomentosum</i>	6.71	70.51%
8	<i>Terminalia brasiliensis</i>	6.40	62.54%
9	<i>Copaifera</i> sp.	6.33	60.90%
10	<i>Cetrolobium robustum</i>	6.01	52.72%
11	<i>Virola officinalis</i>	5.98	52.02%
12	<i>Manilkara elata</i>	5.74	45.70%
13	<i>Acacia glomerosa</i>	5.72	45.36%
14	<i>Delonix regia</i>	5.54	40.61%
15	<i>Machaerium pedicellartum</i>	5.42	37.79%
16	<i>Lecythis pisonis</i>	5.28	34.02%
17	<i>Swietenia macrophylla</i>	4.94	25.40%
18	<i>Libidibia ferrea</i>	4.82	22.44%
19	<i>Samanea tubulosa</i>	4.81	22.10%
20	<i>Tectona grandis</i>	4.44	12.74%

\*Gain calculated in relation to general mean of the population

The species *P. brasiliensis*, *P. reticulata*, *Piptadenia* sp., *Joanesia princeps*, and *Talisia esculenta* presented high gains with selection (Table 6). 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. 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 individuals of *P. brasiliensis*, *P. reticulata*, *Piptadenia* sp., *Joanesia 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 (Hardner and Potts 1995; Wei et al. 1998; Hedrick et al. 2016). 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.

## 5 - CONCLUSION

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 top two ranked species were *P. brasiliensis* and *P. reticulata*, which adapted well to a tropical climate, 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.

From this study, it was possible to discuss forest genetic breeding strategies, which orientate selection of ideal species 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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