Genetic control of wood quality of *Myracrodruon urundeuva* populations under anthropogenic disturbance

Lara Comar Riva[1], Marcela Aparecida de Moraes[2]*, José Cambuim[1], Daniele Fernanda Zulian[1], Luciane Missae Sato[1], Francieli Alves Caldeira[1], Alan Rodrigo Panosso[3] and Mario Luiz Teixeira de Moraes[1]

Abstract: *Forest fragmentation in the Cerrado biome exposes the tree species Myracrodruon urundeuva to the risk of extinction. Thus, the objective of the study was to evaluate silvicultural characteristics related to wood quality, based on genetic parameters estimated in two M. urundeuva progenies from natural populations, assessed in Bauru-SP (PBAU) and Selvíria-MS (PSEL), 31 years after planting. The genetic parameters were estimated according to the REML/BLUP (Restricted maximum likelihood/Best Linear Unbiased Prediction) method using a mixed linear model. The progeny tests detected genetic variation. In PSEL, more positive genetic correlations and a greater number of clusters were observed. Based on the heartwood/sapwood ratio, a higher genetic gain was predicted for PBAU, and for the basic wood density, the genetic gain of the populations was approximately the same. Consequently, the areas of the two progeny tests may be used as future seed orchards to ensure wood quality and long-term ex situ conservation.*

Keywords*: Cerrado, genetic conservation, genetic variation, risk of extinction, tree breeding, seed orchard.*

INTRODUCTION

Brazil is the country with the greatest diversity of tree species in the world, with about 8.715 species, corresponding to 14.5% of the species registered worldwide, of which almost 50% (4.333) are endemic to the country (Beech et al. 2017). One of them is *Myracrodruon urundeuva* Fr. All (Anacardiaceae)*,* found in four Brazilian biomes: Caatinga, Atlantic Forest, Cerrado and Pantanal, as well as in the Chaco region of Paraguay, Bolivia, and Argentina. It is also noteworthy that the conservation status of this and most other species is unknown, since intense deforestation is causing fragmentation of the natural vegetation. This raises questions about the extent to which these fragments are resistant and/or resilient to disturbances, their capacity to maintain the local and regional biodiversity, and about the ability to maintain carbon stocks in vegetation and soils.

The best conservation strategy is *in situ* conservation, however due to the rapid fragmentation of vegetation patches, another option has been adopted, namely *ex situ* conservation. For this conservation form of the species, not necessarily in

***Corresponding author:**
E-mail: marcela.apmoraes@gmail.com
ORCID: 0000-0003-3572-9291

[1] Faculdade de Engenharia de Ilha Solteira da UNESP, Avenida Brasil 158, 15.385-000, Ilha Solteira, SP, Brazil
[2] Faculdade de Ciências Agronômicas da UNESP, Fazenda Lageado, Portaria I: Rua José Barbosa de Barros, 1780, 18.610-307, Botucatu, SP, Brazil
[3] Faculdade de Ciências Agrárias e Veterinária de Jaboticabal da UNESP, Via de Acesso Prof. Paulo Donato Castellane, s/n, 14.884-900, Jaboticabal, SP, Brazil

its natural habitat, the routine progeny tests of selection or breeding programs can be used. By this procedure, genetic parameters can be estimated, which is essential for the choice of the best conservation and breeding strategies of *M. urundeuva*. In this way, the selection of the best trees of the progeny tests can be used for the implementation of an active germplasm bank in the form of seedling seed orchards, where improved seeds can be produced, according to the target traits of selection and with a broader genetic base (Sebbenn et al. 2007).

However, to conduct a breeding program, knowledge about the genetic variation in the study populations and genetic control of breeding traits of interest is imperative to ensure a more effective selection. Quantitative, economically important traits are useful to estimate genetic variation, heritability, genetic gains and genetic correlations between these variables. Based on these estimates, the most appropriate strategies can be determined for the selection of superior genotypes to constitute the parent population of improved generations (Silva et al. 2012).

Among the economically relevant traits for breeding of tree species for wood production are growth (height), diameter at breast height (DBH), stem form and adaptation (survival). Estimates of genetic parameters for these traits in *M. urundeuva* indicate genetic variation among and within provenances, which can be used for genetic conservation and breeding purposes (Freitas et al. 2007, Tung et al. 2011, Moraes et al. 2012, Pupin et al. 2017, Canuto et al. 2017, Martins et al. 2018).

Due to the high deforestation and fragmentation of the Cerrado biome, the natural habitat of *M. urundeuva*, the maintenance of the few remaining natural fragmented areas and recovered degraded areas where the species occurs has become a major environmental challenge. In view of this situation, since 1987, several *M. urundeuva* populations have been conserved *ex situ* in provenance and progeny trials at the Fazenda de Ensino, Pesquisa e Extensão (FEPE) of the Faculdade de Engenharia de Ilha Solteira (FEIS/UNESP). However, it is very important to quantify the genetic variability retained in the tests, which could get lost due to natural causes, for example fire. After the tests, these trees can be subjected to selection and used as seedling seed orchards. The seeds of these orchards contain substantial genetic variability and can be sold to supply the demand for reforestation programs.

In this context, the genetic variability, heritability, genetic correlation, dissimilarity distance and genetic gain were estimated for growth, wood quality and survival traits of two groups of *M. urundeuva* progenies tested for selection. The objective was to use the trees of these trials as a seedling seed orchard, to provide seeds of genetically improved trees in terms of wood quality for commercial and reforestation programs.

MATERIAL AND METHODS

In forest fragments of two transition areas between the Atlantic Forest (Seasonal Semideciduous Forest) and the Cerrado, under strong anthropogenic disturbance, in Bauru-SP (lat 22º 18' 54" S; long 49º 03' 39" W, alt 526 m asl) and Selvíria-MS (lat 20º 22' 02" S; long 51º 25' 08" W, alt 357 m asl), seeds were collected from 28 open-pollinated trees in 1986, from one natural *M. urundeuva* population in each transition area (PBAU and PSEL) (Moraes et al. 1992). According to Köppen's climate classification, the region of Bauru is Aw, with an annual rainfall of 1.331 mm and a mean annual temperature of 22.6 ºC (CEPAGRI/UNICAMP 2018). Two types of soil predominate in this region: Argissolos Vermelho-Amarelo and Latossolos Vermelho-Amarelo (Rossi 2017). The climate type of the region of Selvíria is also Aw, with a mean annual precipitation of 1.309.4 mm and mean annual temperature of 24.8 ºC (UNESP 2018). The regional soil is a Latossolo Vermelho Distroférrico típico (Santos et al. 2018).

Two progeny tests of *M. urundeuva* were installed in December 1987, at the Fazenda de Ensino, Pesquisa e Extensão (FEPE), of the Faculdade de Engenharia de Ilha Solteira (FEIS/UNESP), in Selvíria-MS. A randomized block design with 28 treatments (progenies), three replications (blocks) and 10 plants per and plot, spaced 3 x 3 m apart, was used in both tests. After cutting, only six plants per plot were left to grow. To transform the area into a seed orchard, after 31 years, the growth and survival traits were measured and the poorest trees were cut. The evaluated traits were: *i*) Height (H, m), *ii*) diameter at breast height (*DBH*, cm) and *iii*) mean canopy diameter (MCD, m); *iv*) survival rate (SUR,%); and *v*) stem form (SF), based on a score scale (Otsubo et al. 2015). The characters related to the wood quality of the felled trees were measured: *vi*) basic wood density (*BWD*) according to the Brazilian Standard NBR: 11941 (ABNT 2003) measured in disks (thickness 5 cm), cut at *DBH* of the trees felled in the plots; *vii*) heartwood/sapwood ratio (H/S ratio) determined in the disks at the trunk base (Pereira et al. 2013). The *BWD* and *H/S* ratio were estimated by multiple regression equations

($BWD_i = b_0 + b_1 H_i + b_2 DBH_i$) for each progeny, using the R program (R Core Team 2013), for the trees that were not felled but left to grow in the plots, for the formation of the seedling seed orchard.

The REML/BLUP procedure (restricted maximum likelihood/best linear unbiased prediction), using mixed linear model methodology, was used for individual analyses to estimate the genetic parameters of each of the traits evaluated in the progeny tests. For these estimates, software SELEGEN (Resende 2016) was used, with the statistical model group (1), using models 93 and 110 and 112 ($s = 0.2$) of model group (2). In addition, the genetic correlations (r_g) among traits were estimated using "model 102".

$$y = X_r + Z_a + W_p + T_s + e, \qquad (1)$$

$$y = X_r + Z_a + W_p + e, \qquad (2)$$

where y, r, a, p, s and e are vectors of the data, replication, genetic, plots, population and of errors. The incidence matrices for the above effects are represented by uppercase letters: X, Z, W and T (Resende 2007). For the traits H, DBH, MCD, SF, BWD and H/S ratio, the genetic divergence was analyzed using Mahalanobis' distance as dissimilarity measure, by which the different genotypes were grouped using the hierarchical method UPGMA and Tocher optimization. The clustering was validated by the UPGMA method, determined by the co-phenetic correlation coefficient of Sokal and Rohlf (1962). The significance of this coefficient was calculated by the Mantel test with 10.000 permutations (Mantel 1967) and the cut-off point was defined by the Mojena (1977)'s method. The relative contribution of the traits to genetic divergence was determined, using the criterion proposed by Singh (1981). For these genetic-statistical analyses we used software GENES (Cruz 2013).

RESULTS AND DISCUSSION

The survival rate of 31-year-old trees of the PBAU (80%) and PSEL (76%) progeny tests indicated high adaptation of the populations to the study site. The likelihood ratio test (LTR) detected significant differences among progenies for the *BWD* and *H*/S ratios (Tables 1 and 2), indicating genetic variability for wood quality.

For PBAU, the mean *H* was 11.13 m, *DBH* 14.33 cm and *MCD* 4.44 m. The mean development of PSEL was similar, with a mean H of 11.0 m, *DBH* of 14.19 cm and *MCD* of 4.18 m. According to Martins et al. (2018), the mean *H* was 11.93 m and *DBH* was 14.50 cm when this population was 31 years old. Therefore, the development of *M. urundeuva* populations was similar to that observed in the literature for long-lived tree species, characterized by a slower growth than that of exotic commercial species.

The quality of the stem form (SF) is calculated as the mean (PBAU=2.36; PSEL=2.20) of the scores assigned for the traits straightness and bifurcation (Tables 1 and 2). The higher the mean, the better the SF, which broadens the possibilities

Table 1. Estimates of genetic parameters for height (H, m), diameter at breast height (DBH, cm), basic wood density (BWD, g cm^{-3}), mean canopy diameter (MCD, m), stem form (SF) and heartwood/sapwood ratio (H/S ratio) in a progeny test of 31-year-old *Myracrodruon urundeuva* trees, assessed in Bauru-SP (PBAU)

Estimates	H (m)	DBH (cm)	BWD (g cm^{-3})	MCD (m)	SF	H/S ratio
$\hat{h}^2_a$	0.11±0.06	0.01±0.02	0.70±0.15	0.05±0.04	0.00±0.01	0.65±0.15
$\hat{C}^2_p$	0.1555	0.1443	0.1160	0.1898	0.0973	0.0956
$\hat{h}^2_m$	0.33	0.04	0.81	0.18	0.02	0.81
$r_{\hat{a}a}$	0.5748	0.1941	0.8992	0.4244	0.1509	0.9008
$\hat{h}^2_{ad}$	0.09	0.01	0.71	0.04	0.00	0.62
CV_{gi} (%)	8.8	2.1	16.6	8.77	1.7	70.1
CV_{gp} (%)	4.4	1.5	8.3	4.4	0.84	35.0
CV_e (%)	11.0	17.6	7.0	16.4	13.41	29.3
CV_r	0.40	0.08	1.19	0.27	0.06	1.20
$\hat{m}$	11.13	14.33	0.667	4.44	2.36	0.72
LRT (X^2)	1.29	0.01	24.49*	0.30	0	23.44*

*Significant at 1% probability with 1 degree of freedom; $\hat{h}^2_a$ individual heritability of the additive effects; $\hat{C}^2_p$ coefficient of determination of the plot effects; $\hat{h}^2_m$ heritability of the progeny mean; $r_{\hat{a}a}$ accuracy; $\hat{h}^2_{ad}$ additive heritability within a plot; CV_{gi} individual additive genetic variation coefficient; CV_{gp} coefficient of genotypic variation among progenies; CV_e experimental variation coefficient; CV_r relative variation coefficient; $\hat{m}$ overall mean; LRT: Likelihood ratio test; X^2 Deviance based chi-square value.

Table 2. Estimates of genetic parameters for height (H, m), diameter at breast height (DBH, cm). basic wood density (BWD, g cm⁻³), mean canopy diameter (MCD, m), stem form (SF) and heartwood/sapwood ratio (H/S ratio) in a progeny test of 31-year-old *Myracrodruon urundeuva* trees, assessed in Selvíria-MS (PSEL)

Estimates	H (m)	DBH (cm)	BWD (g cm⁻³)	MCD (m)	SF	H/S ratio
$\hat{h}_a^2$	0.11±0.07	0.01±0.02	0.80±0.15	0.12±0.07	0.03±0.04	0.58±0.15
$\hat{C}_p^2$	0.2071	0.1550	0.0824	0.1257	0.0941	0.1791
$\hat{h}_m^2$	0.22	0.04	0.88	0.29	0.11	0.68
$r_{\hat{a}a}$	0.4743	0.1981	0.9372	0.5395	0.3365	0.8259
$\hat{h}_{ad}^2$	0.11	0.01	0.80	0.10	0.03	0.62
CV_{gi} (%)	7.9	3.2	17.4	10.0	4.9	53.7
CV_{gp} (%)	3.9	1.6	8.9	5.0	2.5	26.8
CV_e (%)	12.7	18.0	5.7	13.4	12.7	31.7
CV_r	0.31	0.09	1.55	0.37	0.19	0.85
$\hat{m}$	11.00	14.19	0.693	4.18	2.20	0.76
LRT (X^2)	0.53	0.01	39.41*	0.93	0.09	11.29*

[*] Significant at 1% probability with 1 degree of freedom; $\hat{h}_a^2$ individual heritability of the additive effects; $\hat{C}_p^2$ coefficient of determination of the plot effects; $\hat{h}_m^2$ heritability of the progeny mean; $r_{\hat{a}a}$ accuracy; $\hat{h}_{ad}^2$ additive heritability within a plot; CV_{gi} individual additive genetic variation coefficient; CV_{gp} coefficient of genotypic variation among progenies; CV_e experimental variation coefficient; CV_r relative variation coefficient; $\hat{m}$ overall mean; LRT: Likelihood ratio test; X^2 Deviance based chi-square value.

of wood use on rural properties. In other words, a score closer to 5 indicates a straighter and less bifurcated tree trunk, suitable for fence posts and other purposes. In this study, the trees had low scores (PBAU=2.36; PSEL=2.20), limiting the possibilities of wood use.

The wood density (*BWD*) is a complex but important trait for physical and mechanical properties, influenced by several anatomical factors. It can vary between different species, in the same species or in different parts of a same tree (Foelkel et al. 1971). This fact explains the significant differences among progenies in the two progeny tests. In both, the approximate means were 0.677 g cm⁻³ and 0.693 g cm⁻³ for PBAU and PSEL, respectively (Tables 1 and 2). Other studies with the same species reported highest *BWD* between 0.750 g cm⁻³ and 0.741 g cm⁻³ (Tung et al. 2011, Silva et al. 2017). According to the IPT (1956)'s classification, a wood density between 0.500 and 0.720 g cm⁻³ is considered medium and above 0.720 g cm⁻³ high. This indicates medium to high wood density of the studied *M. urundeuva* progenies, with values within these intervals.

The heartwood/sapwood (H/S) ratio of the two populations (PBAU=0.72 and PSEL=0.76) was also similar. According to the expression used, a H/S ratio of 0.33 indicates the same proportion of heartwood and sapwood. Thus, the H/S ratio of > 0.70 found in both populations indicates the presence of a larger heartwood than sapwood area of the disc. This ratio is an essential parameter for defining the wood use, be it for the production of charcoal, paper, cellulose, timber or wooden panels (Pereira et al. 2013).

The coefficient of genetic variation (CV_g) expresses the extent of genetic variation in relation to the environmental characteristics (Resende et al. 1991). Almeida et al. (2019) mention that CV_g show good selection potential when the evaluated traits are significant, in the case of BWD and H/S ratio (Tables 1 and 2). The coefficient of experimental variation (CV_e) was considered medium, except for the H/S ratio that exceeded 20%, indicating a high variation among trees for this trait. The coefficient of determination of environmental effects between plots ($\hat{C}_p^2$) in both populations was generally moderate (< 20%) for all traits. Values above 10% indicate environmental heterogeneity within the plots (Sturion and Resende 2010).

The mean heritability among progenies ($\hat{h}_m^2$) of most traits was higher than heritability in the narrow sense ($\hat{h}_a^2$) and within progenies ($\hat{h}_{ad}^2$). This indicated selection at the mean progeny level as the most appropriate selection strategy that will achieve highest genetic gains. In open-pollinated progenies, the expected pattern for quantitative traits is that the $\hat{h}_m^2$ values are higher than $\hat{h}_a^2$ and $\hat{h}_{ad}^2$ (Resende 2002). The heritability coefficients vary according to the plant age. Until there is complete establishment and balance in the field, there may be an environmental effect on the expression of growth traits, be it high or low (Ettori et al. 2006). This was confirmed by Canuto et al. (2017), who studied nine progenies of six natural *M. urundeuva* populations at different ages (3, 10, 15 and 20 years), and observed great variation

in the heritability coefficients for growth traits. Thus, the $\hat{h}^2_m$ values for DBH and SF in PBAU and PSEL (0.02 to 0.11) may be higher in future assessments, in response to the thinning of the 31-year-old trees. The highest h_m^2 was observed for BWD and H/S ratio (> 0.67), reinforcing that selection at the progeny level can maximize genetic gains. Similarly, the coefficient of relative variation (CV_r) was higher for BWD (1.19) and H/S ratio (1.20) in PBAU (Table 1) and for BWD (1.55) and H/S ratio (0.85) in PSEL (Table 2). According to Vencovsky and Barriga (1992), the higher the CV_r, the greater is the genetic control of the traits and little influenced by environmental factors. Thus, higher selection gains are expected for BWD and H/S. Moreover, selection accuracy ($r_{\hat{a}a}$) was highest (> 0.8) for H and H/S in both tests.

There were significant differences in the correlations between the studied traits, which allows direct and indirect selection of the provenance and progeny tests (Table 3). It is worth mentioning the negative correlation between DBH and BWD. In case of a significant and positive genetic correlation, the selection for one trait can lead to indirect gains for another (Sampaio et al. 2000). Thus, the significant and positive correlations between growth and wood quality traits in PSEL indicated the possibility of indirect selection for these traits via H, DBH or MCD, with the exception of DBH *vs* BWD, which were negatively correlated. Thus, significant and positive correlations between the growth and wood quality traits in PSEL will be a clear recommendation of indirect selection for these characters via H, DBH or MCD, with the exception of DBH *vs* BWD, which were negatively correlated. With regard to the wood quality-related traits, BWD and H/S were strongly correlated in this population. As the estimation of BWD is very laborious, direct selection for H/S would be interesting. According to Pereira et al. (2013), heartwood generally has a higher density and this relationship between wood density and heartwood percentage is usually observed in trees with a high percentage of adult wood. This may explain the positive correlation between the two traits BWD and H/S. Genetic correlation coefficients above 0.50 can be considered high (Aguiar et al. 2019). Thus, the results indicated strong correlations between H x DBH and DBH x MCD in PBAU and H x DBH in PSEL. Therefore, indirect selection for MCD, for example, is possible if trees with higher DBH in PBAU are chosen. This strategy of direct and indirect selection allows more effective selection gains and time optimization in the breeding of the species. According to Vencovsky and Barriga (1992), the high correlation between

Table 3. Estimates of genotypic correlations for PBAU (above the diagonal) and PSEL (below the diagonal) between wood growth and quality traits of 31-year-old *Myracrodruon urundeuva* trees

Trait	H (m)	DBH (cm)	BWD (g cm⁻³)	MCD (m)	SF	H/S ratio
H	-	0.72*	0.23	0.45*	0.21	0.25
DBH	0.76*	-	-0.02	0.67*	0.22	0.29*
BWD	-0.07	-0.41*	-	0.00	0.00	-0.09
MCD	0.36*	0.40*	-0.22	-	0.08	0.05
SF	0.22	0.30*	-0.19	0.25	-	-0.012
H/S ratio	0.34*	-0.01	0.48*	0.26*	-0.16	-

* Significant at 5% probability by the t test.

Table 4. Clustering of 28 *Myracrodruon urundeuva* progenies by the Tocher method, based on the Generalized Distance of Mahalanobis (D²), of 31-year-old trees in Bauru-SP (PBAU) and Selvíria-MS (PSEL)

Clusters	PBAU	PSEL
1	1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28	12, 17, 2, 7, 28, 10, 23, 5, 19, 16, 25
2	14	21, 27, 20, 3
3	-	1, 15
4	-	11, 18
5	-	8, 14
6	-	24
7	-	22
8	-	13
9	-	4
10	-	9
11	-	26
12	-	6

H and DBH can be explained by the growth of the trees, which also increases H, suggesting that these growth traits are largely influenced by the same pleiotropic genes.

Mahalanobis' distance is widely used to determine the choice of superior genotypes for crosses to explore heterosis. Cluster analysis by the Tocher method based on Mahalanobis' generalized distance clustered 28 *M. urundeuva* progenies in only two groups in PBAU and 28 *M. urundeuva* progenies in 12 groups in PSEL (Table 4), suggesting that this population has greater genetic diversity among progenies. As the objective of this study is to transform the progeny test areas into seed orchards, with a view to conserving the genetic variability, it would be interesting to select progenies in such way that they represent all the proposed clustered groups (Table 4).

With regard to gains with selection, the overall mean of H/S did not differ largely between PBAU and PSEL (0.720 and 0.762, respectively) (Table 5). However, the genetic gain by selection in the populations was high. When applying a selection intensity of 30%, choosing eight progenies out of 28, the gain prediction for PBAU was 53% and for PSEL 32.1%. High selection gains were expected because H/S had high $\hat{h}_a^2$ values in both populations. The predicted genetic gains of BWD were lower than for H/S, although the expected value was also high (Table 6). The mean BWD of the selected progenies was 0.750 g. cm^{-3} for PBAU and 0.760 g. cm^{-3} for PSEL, corresponding to a genetic gain of 12.5 and 11.0%, respectively. Our results are important as: a) information about *M. urundeuva* growth, adaptation and wood quality traits from different origins, in the long term, for the purposes of *ex situ* conservation as well as breeding; b) suggestion of updated management measures and experimental planting arrangements to promote better plant architecture (improve the SF); c) support of assessments of variability and genetic control at the site, with a view to establishing seed orchards of improved seedlings in the future, to supply the seedling market for reforestation and breeding programs addressing wood quality. Finally, this study detected genetic variability in both *M. urundeuva* progeny populations, which allows the

Table 5. Prediction genetic gain in the selection of the eight best progenies of *Myracrodruon urundeuva* for the H/S ratio in relation to POP-BAU and POP-SEL at 31 years old

	POP-BAU			POP-SEL	
Ind	Prog	Mean	Ind	Prog	Mean
1	14	1.45	1	19	1.11
2	26	1.19	2	26	1.04
3	19	1.11	3	23	1.01
4	27	1.06	4	14	1.00
5	10	1.03	5	17	0.98
6	8	1.01	6	2	0.97
7	16	0.99	7	5	0.96
8	13	0.97	8	7	0.95
Mean of the Progenies		1.10	Mean of the Progenies		1.00
Overall Mean		0.72	Overall Mean		0.76
Selection Gain (%)		53.00	Selection Gain (%)		32.10

Table 6. Prediction genetic gain in the selection of the eight best progenies of *Myracrodruon urundeuva* for the WD in relation to POP-BAU and POP-SEL at 31 years old

	POP-BAU			POP-SEL	
Ind	Prog	Mean (g cm^{-3})	Ind	Prog	Mean (g cm^{-3})
1	25	0.779	1	18	0.775
2	24	0.767	2	17	0.773
3	4	0.761	3	12	0.772
4	12	0.756	4	26	0.771
5	23	0.745	5	16	0.769
6	19	0.737	6	2	0.767
7	26	0.731	7	23	0.765
8	9	0.726	8	27	0.762
Mean of the Progenies		0.750	Mean of the Progenies		0.770
Overall Mean		0.667	Overall Mean		0.693
Selection Gain (%)		12.46	Selection Gain (%)		11.00

transformation into seedling seed orchards, by progeny selection by thinning. The genetic variation for wood density and H/S indicates the possibility of considerable gains with selection. The greater number of divergent groups within the PSEL was due to the higher genetic variability than in PBAU.

ACKNOWLEDGMENTS

REFERENCES

ABNT - Associação Brasileira de Normas Técnicas (2003) **Determinação da densidade básica em madeira.** NBR 11941-02, Rio de Janeiro, 6p.

Aguiar BI, Freitas MLM, Tavares YR, Tambarussi EV, Zanatto B, Gandara FB, Paludeto DYBO, Moraes MLT, Longui EL, Zanata M and Sebbenn AM (2019) Genetic control of silvicultural characteristics in *Balfourodendron riedelianum* (ENGL.) ENGL. **Silvae Genetica 68**: 73-78.

Almeida GQ, Chaves LJ, Vieira MC and Ganga RMD (2019) Agronomic evaluation of a Hancornia speciosa Gomes germplasm collection from the Brazilian Cerrado. **Crop Breeding and Applied Biotechnology 19**: 8-14.

Beech E, Rivers M, Oldfield S and Smith PP (2017) Global tree search: the first complete global database of tree species and country distributions. **Journal of Sustainable Forestry 36**: 454-489.

Canuto DSO, Silva AM, Freitas MLM, Sebbenn AM and Moraes MLT (2017) Genetic variability in *Myracrodruon urundeuva* (Allemão) Engl. Progeny Tests. **Open Journal of Forestry 7**: 1-10.

CEPAGRI/UNICAMP - Universidade Estadual de Campinas (2018) Centro de Pesquisa Meteriológica e Climáticas Aplicadas a Agricultura. Available at: < https://www.cpa.unicamp.br/>. Accessed on Jan 10, 2019.

Cruz CD (2013) GENES: a software package for analysis in experimental statistics and quantitative genetics. **Acta Scientiarum 35:** 271-276.

Ettori LC, Figliolia MB and Sato AS (2006) Conservação *ex situ* dos recursos genéticos de espécies florestais nativas: situação atual no Instituto Florestal. In Higa AR and Silva LD (eds) **Pomar de sementes de espécies florestais nativas**. FUPEF, Curitiba, p. 203-225.

Foelkel CEB Brasil MAM and Barrichelo LEG (1971) Métodos para determinação da densidade básica de cavacos para coníferas e folhosas. **IPEF 1:** 65-74.

Freitas MLM, Sebbenn AM, Zanatto ACS and Moraes E (2007) Formação de pomar de sementes a partir da seleção dentro de teste progênies de *Myracrodruon urundeuva*. **Revista Instituto Florestal 19**: 65-72.

IPT - Instituto de Pesquisas Tecnológicas do Estado de São Paulo (1956) **Madeiras nacionais: tabelas de resultados de ensaios físicos e mecânicos**. Instituto de Pesquisas Tecnológicas, São Paulo, 60p.

Mantel N (1967) The detection of disease clustering and a generalized regression approach. **Cancer Research 27:** 209-220.

Martins K, Santos WSD, Quadros TMC, Aguiar, AV, Machado JAR, Sebbenn AM and Freitas MLM (2018) Genetic variation and effective population size of a *Myracrodruon urundeuva* (Engler) FR. All in provenance and progeny test. **Journal of Forest Research 2**: 228-236.

Mojena R (1977) Hierarchical grouping methods and stopping rules: an evaluation. **The Computer Journal 20**: 359-363.

Moraes MA, Valério Filho WV, Resende MDV, Silva AM, Manoel RO, Freitas MLM, Moraes MLT and Sebbenn AM (2012) Produtividade, estabilidade e adaptabilidade em progênies de *Myracrodruon urundeuva* F.F. & M.F. Allemão – Anacardiaceae. **Scientia Forestalis 40**: 69-76.

Moraes MLT, Kageyama PK, Siqueira ACMF, Kano NK and Cambuim J (1992) Variação genética em duas populações de aroeira (*Astronium urundeuva* – Fr. All. Engel. – Anacardiaceae). **Revista do Instituto Florestal 4**: 1241-45.

Otsubo HCB, Moraes MLT, Moraes MA, Neto MJ, Freitas MLM, Costa RB, Resende MDV and Sebbenn AM (2015) Variação genética para caracteres silviculturais em três espécies arbóreas da região do Bolsão Sul-mato-grossense. **Cerne 21**: 535-544.

Pereira BLC, Oliveira AC, Carvalho AMML, Carneiro ACO, Vital BR and Santos LC (2013) Correlações entre a relação Cerne/Alburno da madeira de eucalipto, rendimento e propriedades do carvão vegetal. **Scientia Forestalis 41:** 217-225.

Pupin S, Freitas MLM, Canuto DSO, Silva AM, Alzate-Marin AL and Moraes MLT (2017) Variabilidade genética e ganhos de seleção em progênies de *Myracrodruon urundeuva* Fr. All. **Nativa 5**: 59-65.

R Core Team (2013) **R: a language and environment for statistical computing.** R Foundation for Statistical Computing, Vienna. Available at <http://www.R-project.org/>. Accessed on Jan 10, 2019.

Resende M, Souza SM, Higa AR and Stein PP (1991) Estudos de variação genética e métodos de seleção em testes de progênies de acácia-negra (*Acacia Mearnsii*) no Rio Grande do Sul. **Boletim de Pesquisa Florestal 22/23**: 45-59.

Resende MDV (2002) **Genética biométrica e estatística no melhoramento de plantas perenes**. Embrapa Informação Tecnológica, Brasília, 975p.

Resende MDV (2007) **SELEGEN-REML/BLUP: sistema estatístico e seleção genética computadorizada via modelos lineares mistos.** Embrapa

Florestas, Colombo, 359p.

Resende MDV (2016) Software Selegen – REML/BLUP: a useful tool for plant breeding. **Crop Breeding and Applied Biotechnology 16:** 330-339.

Rossi M (2017) **Mapa pedológico do Estado de São Paulo: revisado e ampliado.** Instituto Florestal, São Paulo, 118p.

Sampaio PTB, Resende MDV and Araújo AJ (2000) Estimativas de parâmetros genéticos e métodos de seleção para o melhoramento genético de *Pinus caribaea hondurensis*. **Pesquisa Agropecuária Brasileira 7**: 2243-2253.

Santos HG, Jacomine PKT, Anjos LHC, Oliveira VA, Lumbreras JF, Coelho MR, Almeida JA, Araujo Filho JC, Oliveira JB and Cunha TJF (2018) **Sistema brasileiro de classificação de solos**. 5th edn, Embrapa, Distrito Federal, 353p.

Sebbenn AM, Freitas MLM, Zanatto ACS, Moraes E and Moraes MA (2007) Conservação *ex situ* e pomar de sementes em banco de germoplasma de *Balfourodendron riedelianum*. **Instituto Florestal 19**: 101-112.

Silva GAP, Gouvêa LRL, Verardi CK, Resende MDV, Scaloppi Junior JE and Gonçalves OP (2012) Parâmetros genéticos e da correlação em ciclos de medição início em seringueiras. **Euphytica 189**: 625-634.

Silva LLH, Oliveira E, Calegari L, Pimenta MC and Dantas MKL (2017) Características dendrométricas, físicas e químicas da *Myracrodruon urundeuva* e da *Leucaena leucocephala*. **Floresta e Ambiente 24:** 1-8.

Singh D (1981) The relative importance of characters affecting genetic divergence. **The Indian Journal of Genetics and Plant Breeding 41**: 237-245.

Sokal RR and Rohlf FJ (1962) The comparison of dendrograms by objective methods. **Taxon 11**: 30-40.

Sturion JA and Resende MDV (2010) **Avaliação do delineamento experimental utilizado em teste de progênie de erva-mate.** Embrapa Florestas, Colombo, 4p.

Tung ESC, Freitas MLM, Florsheim SMB, Lima IL, Longui EL, Moraes MLT, Santos FW and Sebbenn AM (2011) Variação, divergência e correlações genéticas entre caracteres silviculturais e densidade básica da madeira em progênies de *Myracrodruon urundeuva* (Engler) Fr. Allem. **Revista do Instituto Florestal 23**: 1-12.

UNESP - Universidade Estadual Paulista (2018) **Canal CLIMA da UNESP Ilha Solteira: área de Hidráulica e Irrigação.**

Vencovsky R and Barriga P (1992) **Genética biométrica no fitomelhoramento**. Revista Brasileira de Genética, Ribeirão Preto, 496p.