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EVALUATION OF *Myracrodruon urundeuva* Fr.All. PROGENIES FOR DIFFERENT PLANTING SYSTEMS AIMING AT GENETIC CONSERVATION[1]

AVALIAÇÃO DE PROGÊNIES DE *Myracrodruon urundeuva* Fr.All. EM DIFERENTES SISTEMAS DE PLANTIO PARA FINS DE CONSERVAÇÃO GENÉTICA[1]

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ABSTRACT - *Myracrodruon urundeuva* is a highly explored native tree species. The objective of this work was to evaluate the genetic variation for silvicultural traits, survival and sex ratio, in two tests of progenies of *Myracrodruon urundeuva*, aiming to provide subsidies for *ex situ* conservation. Thirty progenies were analyzed in two progeny tests in different planting systems - mixed (TP-MUE) and homogeneous (TP-DES). The silvicultural characters evaluated were height (H), diameter at breast height (DBH), average crown diameter (DMC), survival (SOB), number of trees with male flowering (Nm), female flowering (Nf), monoecious trees (Mo) and without flowering (Sf). Estimates of genetic parameters were obtained using the REML / BLUP procedure. The SOB rate was high for both tests (> 80%). The mean for H ranged from 7.58 m (TP-MUE) to 10.02 m (TP-DES); for 8.24 cm DAP (TP-MUE) to 10.91 cm (TP-DES). The heritability of the average of progenies varied from moderate to high (from 0.39 to 0.72). In the TP-MUE, the sex ratio was 2♂:1♀ and in the TP-DES 4♂:1♀. The effective size (Ne) of the TP-MUE represented 38 % of the expected Ne and in the TP-DES it was 12 %. Therefore, there is genetic variability for *ex situ* genetic conservation of *M. urundeuva* in the short term.

Keywords: Aroeira; Genetic parameters; Effective size; Progeny test.

RESUMO - *Myracrodruon urundeuva* é uma espécie arbórea nativa muito explorada. O objetivo deste trabalho foi avaliar a variação genética para caracteres silviculturais, a sobrevivência e a proporção sexual, em dois testes de progênies de *Myracrodruon urundeuva*, visando fornecer subsídios para conservação *ex situ*. Foram analisadas 30 progênies, em dois testes de progênies em sistemas de plantio distintos - misto (TP-MUE) e homogêneo (TP-DES). Os caracteres silviculturais avaliados foram altura (ALT), diâmetro à altura do peito (DAP), diâmetro médio de copa (DMC), sobrevivência (SOB), número de árvores com florescimento masculino (Nm), florescimento feminino (Nf), árvores monóicas (Mo) e sem florescimento (Sf). As estimativas dos parâmetros genéticos foram obtidas pelo procedimento REML/BLUP. A taxa de SOB foi alta para os dois testes (> 80%). A média para ALT variou de 7,58 m (TP-MUE) a 10,02 m (TP-DES); para DAP de 8,24 cm (TP-MUE) a 10,91 cm (TP-DES). A herdabilidade da média de progênies variou de moderada a alta (de 0,39 a 0,72). No TP-MUE, a proporção sexual foi de 2♂:1♀ e no TP-DES de 4♂:1♀. O tamanho efetivo (Ne) do TP-MUE representou 38 % do Ne esperado e no TP-DES foi de 12%. Existe variabilidade genética para conservação genética *ex situ* de *M. urundeuva* a curto prazo.

Palavras-chave: Aroeira; Parâmetros genéticos; Tamanho efetivo; Teste de progênies.

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1 INTRODUCTION

Processes such as deforestation represent a recurring and worrying environmental problem nowadays. Among the main consequences is the origin of fragments derivate of natural vegetation that, in general, are small and can be isolated in the landscape. Forest fragmentation represents a reduction in population size, causing the effect of a genetic bottleneck, with a reduction in genetic diversity and effective population size (Tambarussi et al., 2017a).

Myracrodruon urundeuva, known as aroeira, is a native tree species, with high commercial value in the market, good wood quality due to the its strength characteristic. The heartwood shows high resistance to rot in contact with the soil, due to the high amount of phenolic extracts associated with lignin (Queiroz et al., 2002). The wood is quite heavy, with a density of up to 1.19 g cm^{-3} and, therefore, it exhibits high mechanical resistance (Lorenzi, 2014).

Its geographical distribution is predominant in the Cerrado biome (Brazilian Savannah), but it can also be found in the Caatinga and Atlantic Forest (Carvalho, 2003). In primary forests, concomitant occurrence with other species is common, but in areas under some degree of disturbance, it occurs almost homogeneously (Freitas et al., 2006). It is a dioecious species, although there are reports of monoecia and hermaphroditism (Carvalho, 2003; Sant'ana, 2017). The fruits are produced in the cold and dry period, and maturation depends on the temperature rise (Nunes et al., 2008). The dioecious sexual system is characterized by the presence of male and female individuals within plant populations (Lenza e Oliveira, 2005). Studies on reproductive biology have pointed out that Cerrado plants and forests depend on sexual reproduction for their regeneration and dispersion (Oliveira e Gibbs, 2000).

Small forest fragments, often isolated, affect reproductive processes, due to the behavior of pollinators and the processes of migration and dispersion of pollen and seeds (Ramos et al., 2016; Baldoni et al., 2017; Tambarussi et al., 2017a). Isolated individuals may not reproduce, but if this occurs, the reproductive process may happen among a few individuals, resulting in inbreeding depression, which causes negative effects on the survival and fitness of the offspring (Spoladore et al., 2017; Tambarussi et al., 2017b).

The reduction in population size can be reversed by replacing management practices, when the population is at risk of extinction or has high levels of inbreeding (Sebbenn e Ettori, 2001). It is also important to verify the sexual ratio and effective population size of dioic species, in order to better understand the species' behavior and propose more efficient conservation strategies.

One way of mitigating the risk of forest fragmentation is through *ex situ* genetic conservation, which refers to conservation managed by man outside the natural occurrence of the species, and which is an important tool to ensure the maintenance of genetic diversity. Progeny tests are an alternative for genetic conservation of populations, as well as making it possible to estimate the genetic structure and selecting superior individuals as a source of improved seed production based on the selected genotypic value (Shimizu et al., 1982).

Open pollination progenies have been widely used for *ex situ* genetic conservation, in genetic improvement and environmental reforestation programs, due to the low cost, speed and ease of collecting seeds (Moraes et al., 2012). Through progeny tests it is possible to estimate phenotypic and genetic parameters, associations between characters, evaluate the efficiency of selection methods and estimate genetic gains (Paludzyszyn Filho et al., 2002). Genetic variability studies are essential to establish adequate conservation strategies, just as knowledge of the reproductive system is essential for maintaining populations over generations (Berti et al., 2017).

The estimates obtained from genetic parameters for progenies of species such as *Myracrodruon urundeuva*, *Astronium fraxinifolium* and *Terminalia argentea* indicated favorable conditions for selection and a good perspective for genetic conservation programs (Otsubo et al., 2015) as well as other works for tree species carried out in Selvíria-MS (Zaruma et al., 2015; Bertonha et al., 2016; Canuto et al., 2016; Berti et al., 2017; Cornacini et al., 2017).

Given this context, the objective of this work was to evaluate survival, genetic variation for growth traits and sexual proportion, in tests of progenies of *Myracrodruon urundeuva*, installed in different planting systems, aiming to provide subsidies for *ex situ* conservation of the species.

2 MATERIAL AND METHODS

The seeds for seedling production and installation of progeny tests were collected in 30 open pollination matrix trees, in a natural population of *M. urundeuva*, from Ribeirão Preto, State of São Paulo (SP). The positions of matrix trees were registered with GPS and were located in the Germplasm Bank of the University of São Paulo - USP, Ribeirão Preto Campus, in urban areas (parks, squares and quarry), in private rural properties in the surroundings and in municipality access. The species has seeds of the orthodox type, thus, they were conserved *in vitro* in a dry chamber at 5ºC, under laboratory conditions. Years after seed collection, it was found that many parent trees had been cut, which reinforces the importance of *ex situ* conservation. The area of occurrence of natural population is characterized by: region of soils of the typical Dystropheric Red Oxisol type and eutrophic Litholic Neosoil typically (Rossi 2017); climatic type Cwa (subtropical climate with rainy summer and dry winter), according to the Köppen classification; altitude around 608 meters; average annual temperature of 20.9 °C and average annual rainfall of 1,527 mm (Flores et al., 2016).

The seedlings for installation of progeny tests were produced in the nursery of Teaching, Research and Extension Farm (FEPE), from the Faculty of Engineering at Ilha Solteira, State of São Paulo (SP) (FEIS / UNESP), which is located at municipality of Selvíria, State of Mato Grosso do Sul (MS). FEPE is located in Mato Grosso do Sul region, where the Cerrado biome predominates. The soil was classified as a typical distrophic Red Oxisol (Santos, 2018); climatic type Aw (hot and rainy summer and mild, dry winter); altitude at over 335 m; average annual temperature of 23 °C and average annual precipitation of 1,440 mm (Flores et al., 2016). A progeny test was established in two planting systems: mixed, considered to be multi-species (TP-MUE) and homogeneous (TP-DES).

The TP-MUE (progeny test in a multi-species system) was established in July 2006, in the geographic coordinates 20°21'33" S and 51°24'46" O, altitude 0 m, in a randomized block design, with 30 treatments (progenies), 14 replicates and one plant per plot, with each plot, established in a linear form, consisting of four trees, each one belonged to one different native species (Figure 1). The spacing was 3 m × 2 m. Thus, to constitute a plot, each *M. urundeuva* progeny was randomly intercropped with a progeny of *Jacaranda cuspidifolia* (jacaranda-caroba), *Cordia trichotoma* (louro-pardo) and *Mabea fistulifera* (canudo-de-pito). In this study, only *M. urundeuva* was considered. Thus, the spacing between the *M. urundeuva* progenies was 3 m × 8 m.

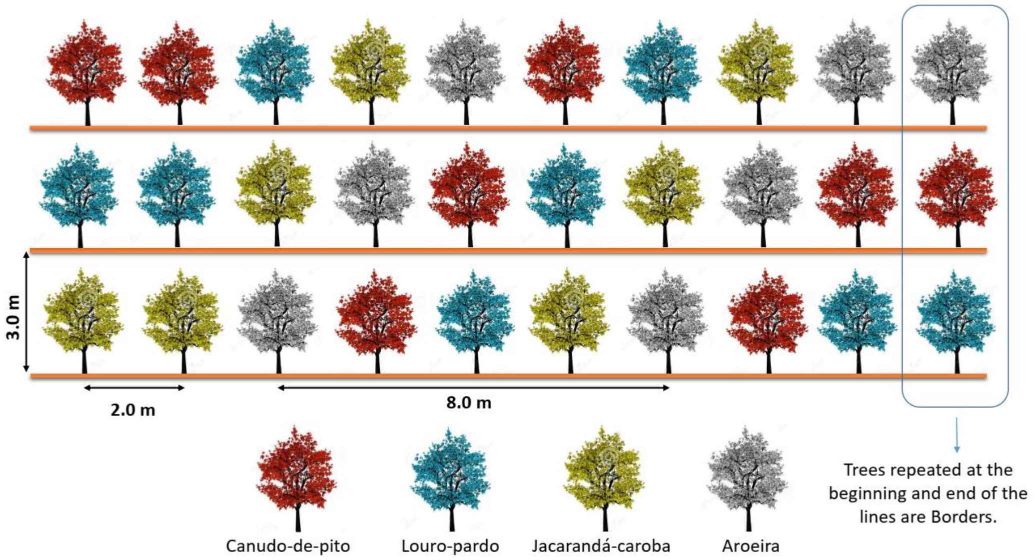

Figure 1. Scheme of arrangements of *Myracrodruon urundeuva* trees in the TP-MUE with the species *Jacaranda cuspidifolia*, *Cordia trichotoma* (louro-pardo) and *Mabea fistulifera* (canudo-de-pito).

Figura 1. Esquema das disposições das árvores de *Myracrodruon urundeuva* no TP-MUE com as espécies *Jacaranda cuspidifolia*, *Cordia trichotoma* (louro-pardo) e *Mabea fistulifera* (canudo-de-pito).

The TP-DES (progeny test in different spacing) was installed in October 2006, in the geographic coordinates 20°20'08” S and 51°24'23” O, in a systematic “fan” design, also known as Nelder design (Nelder, 1962), with 30 treatments (same progenies), nine replicates and one plant per plot.

The characters were evaluated at 12 years after planting. The data collected in the field were:

growth characters, height (H, m), diameter at breast height (DBH, cm) and average crown diameter (ACD, m); adaptive characters, survival (SUR, %) and phenological characters, number of males (Nm), number of females (Nf), monoecious (Mo) and without flowering (Wf). The sexing of trees in the progeny tests was carried out during the flowering months of the species in the region (July and August). The evaluation was performed visually with the aid of a binocular.

The estimates of genetic parameters were obtained using a mixed linear model (univariate additive) methodology, using the REML (Restricted Maximum Likelihood) / BLUP (Best Linear Unbiased Prediction) procedure, through SELEGEN software (Resende, 2016). For individual analysis, the "model 95" was used for the TP-MUE and the "model 19" (Equation 1) for the TP-DES (Resende 2007; Resende 2016). Both models are applied to evaluate open pollination progenies (considering half-sisters), complete block design, in one place, a single data evaluation and one observation per plot, according to the statistical model:

$$\mathbf{y = Xr + Za + e} \qquad (1)$$

where: ***y***, **r**, a and **e** refer to data vectors, replicate effects, additive genetic effects and errors, respectively. The incidence matrices for these effects are capital letters.

The joint analysis of the progeny tests to verify the effect of the planting systems was carried out by SELEGEN's "model 5" (Equation 2), according to the statistical model:

$$\mathbf{y = Xr + Za + Wp + Ts + e} \qquad (2)$$

where: **y** is the vector of data, **r** is the vector of repetition effects (assumed to be fixed) plus the general average, **a** is the vector of individual additive genetic effects (assumed to be random), **p** is the vector of the effects of plot (assumed to be random), **s** is the vector of population effects (random) and **e** is the vector of errors or residuals (random). The capital letters represent the incidence matrices for the respective effects.

From these analyzes, the following genetic parameters were estimated: individual heritability in the strict sense ($\hat{h}_a^2$), that is, the additive effects; individual additive genetic variation coefficient (CV_{gi}); coefficient of genotypic variation between progenies (CV_{gp}); residual variation coefficient ($r_{\hat{a}a}$);accuracy (CV_e) and general mean of the experiment. Differences between treatments were obtained by the LRT test by deviance analysis. The sex ratio ($\hat{r}$) was calculated according to Vencovsky et al. (2012) (Equation 3):

$$\hat{r} = \frac{N_f}{N_f + N_m} \qquad (3)$$

where: N_f and N_m correspond to the total number of female and male flowering plants, respectively. The effective population size ($\hat{N}_e$) (Equation 4) for dioic species was calculated by:

$$\hat{N}_e = \frac{4t}{D_5} \qquad (4)$$

on what: $t = N_f + N_m$ and $D_5 = \frac{1}{r(1-r)} + \frac{(1-u)t-1}{F} + \frac{(1-v)t-1}{M}$ being that: $1-r = \frac{N_m}{N_f + N_m}$; $u = \frac{F}{N_f}(0 < u \leq 1)$; $v = \frac{M}{N_m}(0 < v \leq 1)$ *F* and *M* correspond to the number of plants with female flowering (*F*) and male flowering (*M*) in a 1: 1 ratio that effectively participate in the reproductive event. Statistical analyzes were performed based on the chi-square test (χ^2), based on the hypothesis that the expected frequency was 1♂: 1♀. Monoic individuals were included in the male parent (Vencovsky et al., 2012).

3 RESULTS AND DISCUSSION

The survival rate (SOB) was high (>80%) for both *M. urundeuva* progeny tests at 12 years after planting (82% for TP-MUE and 85% for TP-DES). Otsubo et al. (2015) found an average survival higher than 90% in progeny tests of *M. urundeuva* and *Astronium fraxinifolium* in the same planting site, which characterizes an excellent adaptation of species in Selvíria. Bertonha et al. (2016) found high survival for the same species in a homogeneous planting test and also for the *M. urundeuva* test intercropped with *Corymbia citriodora*, both with survival higher than 90%, emphasizing progenies adaptation to the site where the progeny tests were installed and planting systems.

The averages for silvicultural traits of *M. urundeuva* progenies at 12 years of age for TP-MUE and TP-DES, respectively, were: 7.58 m and 10.02 m for H (total plant height); 8.24 cm and 10.91 cm for DBH (diameter at breast height) and 3.82 m and 4.60 m for DMC (average crown diameter), indicating that the growth of the progenies in homogeneous planting was higher (between 17 % to 24 %) than the mixed planting system (Table 1). Analyzing the genetic parameters and growth traits, Tung et al. (2010) reported in a *M. urundeuva* progenies test the following averages for silvicultural characters at 12 years of age (3 m x 3 m spacing): 9.81 m in total height for the cut trees; 11.35 cm for the DAP; 2.96 m for stem height. Cornacini et al. (2017) obtained averages of 9.54 m and 8.62 m (H); 11.45 cm and 10.78 cm (DAP); 4.14 m and 4.10 m (DMC), in progenies of *Astronium fraxinifolium* in the mixed planting system at age 18, a species that belongs to the same botanical family as *M. urundeuva* (Anacardiaceae), coming from Selvíria (MS) and Ilha Solteira (SP), respectively, values similar to TP-DES at 12 years of age.

Progeny tests are differentiated by the planting system. TP-MUE is intercropped with other native species, while TP-DES was installed without intercropping. The greater development of TP-DES in relation to TP-MUE, probably occurred due to the influence of larger spacing, which allowed for greater development of silvicultural characters. On the other hand, the competition for space, nutrients and light from other species on the growth of *M. urundeuva* in TP-MUE must have been more intense, besides to the weed competition, which occurs in certain experiment places. Bertoni e Dickfeldt (2007) observed a good development of *M. urundeuva* based on the mean DAP (8.25 cm) and H (7.20 m) and a high survival rate (90 %) at 10 years, despite the competition for light, water and nutrients with other species, especially pioneers, which had greater occurrence and distribution in the area of natural regeneration.

The coefficient of experimental variation (CV_e) was higher in the TP-MUE for H, DAP and DMC, and in both progeny tests and ranged from 21.90 to 40.51% (Table 1). The highest coefficients of experimental variation (CV_e) were found in the TP-MUE. This indicates a greater influence of the environmental effect on the progenies, probably due to the competition with the species intercropped by the test and with regenerants that occur in the area, in addition to the greater influence weed competition that occurs in certain experiment blocks, instead to what occurs in TP-DES. Tung et al. (2010) found a CV_e of 11.7 to 19.0% for a progeny test of *M. urundeuva* at 19 years old. Canuto et al. (2015), studying the genetic characterization of a progeny test of *Dipteryx alata* from forest remnants, found an experimental variation ranging from low to high, from 8.80% to 52.36%.

The deviance analysis was performed using the likelihood ratio test (LRT) and presented significant values at 1% with a degree of freedom for H in both tests and for DMC in TP-MUE; for DAP the significance was obtained at 5% with a degree of freedom and for DMC it was significant only in TP-MUE.

The highest accuracy ($r_{\hat{a}a}$) was for the H character in the TP-DES (85%) and considered as high. But in general, the accuracy varied from moderate to high for the characters evaluated in the progenies of *M. urundeuva*. In general, the accuracy varied from moderate to high for the characters evaluated in *M. urundeuva* progenies. Individual heritability in the narrow sense ($r_{\hat{a}a}$) was higher for the H character in the TP-DES (0.61 ± 0.24). Resende e Duarte (2007) reported the accuracy classes as very high for accuracy from 0.90 to 0.99; high from 0.70 to 0.85; moderate from 0.50 to 0.65; and low from 0.10 to 0.40.

All intervals of $\hat{h}_a^2$ were different from zero, indicating genetic differences between individuals. The DAP and H vary according to the age of the plant, planting location and planting system, due to competition for water, light and nutrients. The average heritability of progenies $\hat{h}_m^2$ was higher for H in the TP-DES. The $\hat{h}_a^2$ was considered high for DAP compared to other studies with the same species, such as: 0.00 and 0.27 (Guerra et al., 2009); 0.001 to 0.59 (Freitas et al., 2006); 0.15 (Freitas et al., 2007) 0.12 and 0.31 (Bertonha et al., 2016). The values (0.55 TP-MUE and 0.72 TP-DES) were higher than that obtained by Sebbenn and Ettori (2001) for the same species, which was 0.15 for H.

The highest coefficients of genetic variation (CV_{gi} e CV_{gp}) e were for H and DAP in the TP-DES, as well as the coefficient of relative variation (CV_r). For Sebbenn et al. (1998) a coefficient of genetic variation (CV_{gi}) above 7% is considered high. Thus, it can be said that the coefficients of genetic variation were high for silvicultural traits.

The CV_r was higher for all characters in the TP-MUE, indicating a greater influence of the environmental effect on the progenies, in particular, by competition with regenerants, and due to a greater influence of bush, unlike the TP-DES.

Table 1. Estimates of genetic parameters for the TP-MUE (multi-species progeny test) and TP-DES (progeny test in different spacing) tests for total height (H, m), diameter at breast height (DBH, cm) and average crown diameter (DMC, m), at 12 years old, in Selvíra (MS).

Tabela 1. Estimativas de parâmetros genéticos para os testes TP-MUE (teste de progênie multiespécies) e TP-DES (teste de progênie em diferentes espaçamentos) para altura total (H, m), diâmetro à altura do peito (DAP, cm) e diâmetro médio da copa (DMC, m), aos 12 anos, em Selvíra (MS).

Estimates	TP-MUE DAP			TP-DES DAP		
	H	DBH	DMC	H	DBH	DMC
$\hat{h}^2_a$	0.32 ± 0.17	0.27 ± 0.16	0.32 ± 0.17	0.61 ± 0.24	0.40 ± 0.23	0.26 ± 0.19
$\hat{h}^2_m$	0.55	0.50	0.55	0.72	0.50	0.39
$r_{\hat{a}a}$	0.74	0.70	0.74	0.85	0.70	0.62
CV_{gi} (%)	18.25	21.81	16.72	27.07	24.20	13.97
CV_{gp} (%)	9.12	10.90	8.36	11.85	12.10	6.98
CV_e (%)	30.52	40.51	28.28	21.90	36.03	26.05
CV_r	0.29	0.26	0.29	0.53	0.33	0.26
$\hat{m}$	7.58	8.24	3.82	10.02	10.91	4.60
LRT	7.73**	5.14*	7.33**	22.8**	4.61*	2.95^{ns}

$\hat{h}^2_a$: individual heritability in the narrow sense; $\hat{h}^2_m$: heritability of the average of progenies; $r_{\hat{a}a}$: accuracy; CV_{gi}: coefficient of individual additive genetic variation; CV_{gp}: coefficient of genetic variation between progenies; CV_e: coefficient of experimental variation; CV_r: coefficient of relative variation; $\hat{m}$: general average; LRT - likelihood ratio test. ** Significant at 1% probability with one degree of freedom; * Significant at 5% probability with one degree of freedom; ^{ns} not significant.

$\hat{h}^2_a$: herdabilidade individual no sentido restrito; $\hat{h}^2_m$: herdabilidade da média de progênies; $r_{\hat{a}a}$: acurácia; CV_{gi}: coeficiente de variação genética aditiva individual; CV_{gp}: coeficiente de variação genética entre progênies; CV_e: coeficiente de variação experimental; CV_r: coeficiente de variação relativa; $\hat{m}$: média geral; LRT: teste de razão de verossimilhança; ** Significativo a 1% com um grau de liberdade; *Significativo a 5% com um grau liberdade; ^{ns} não significativo.

No significant results were obtained for the LRT test for the planting system. The progeny effect was significant for H, DAP and DMC, (Table 2) showing that this planting system did not influence the character development.

Table 2. Deviance analysis (LRT) for total height (H, m), diameter at breast height (DBH, cm) and average crown diameter (DMC, m) in the progenies tests of *Myracrodruon urundeuva*, in two planting systems, at 12 years old, in Selvíria (MS).

Tabela 2. Análise de deviance (LRT) para altura total (ALT, m), diâmetro a altura do peito (DAP, cm), diâmetro médio da copa (DMC, m) nos testes de progênies de *Myracrodruon urundeuva*, em dois sistemas de plantio, aos 12 anos de idade, em Selvíria- MS.

LRT	H	DBH	DMC
Progeny	5.52**	5.23**	2.81*
Planting system	2.29^{ns}	0.16^{ns}	0.61^{ns}

** Significant at 1% probability with a degree of freedom (6.63); ^{ns} not significant.

**Significativo a 1% com um grau de liberdade (6.63); ^{ns} não significativo.

At 12 years after planting, from July to September 2018, sexing of *M. urundeuva* trees was evaluated. The percentage of Nm was 41.6 %; Nf=27.1%; Mo=2.9% and Sf=28.3 % in TP-MUE. For the TP-DES the observed values were: Nm=30.6%; Nf=7.9%; Mo=2.2% and Sf=59.4%. Thus, trees with male flowering prevailed in TP-MUE, in the approximate proportion of 2♂: 1♀ and, individuals without flowering, in TP-DES, in the approximate proportion of 4♂: 1♀, which may be related, also to the different spacing of the last experiment. From the analysis of the chi-square test, it was observed that there were significant differences between plants with male and female. In a population of *M. urundeuva*, from the State of Paraíba (Caatinga vegetation), it was also established in the same location, whose proportion found was 1♂: 1♀ (Leite e Machado, 2010). Vencovsky et al. (2012) pointed out important factors that change the effective population size, being the size of the population and its fluctuations, unequal proportion between sexes, number of descendants sampled flowering, in the two tests (Table 3).

Table 3. Observed (FO) and expected (FE) frequencies for individuals of *Myracrodruon urundeuva*, with female♀ and male-flowering in multi-species progeny tests (TP-MUE) and progeny test in different spacings (TP-DES), in Selvíria (MS).

Tabela 3. Frequências observadas (FO) e esperadas (FE) para indivíduos de *Myracrodruon urundeuva*, com florescimento feminino♀ e masculino♂ nos testes de progênies multi-espécie (TP-MUE) e teste de progênies em diferentes espaçamentos (TP-DES), em Selvíria-MS.

Flowering	TP-DES			TP-MUE		
	FO	FE	χ^2	FO	FE	χ^2
♂	75	46.50	17.5**	151	121.50	7.2**
♀	18	46.50	17.5**	92	121.50	7.2**
Total	93	93	34.94**	243	243	14.33**

χ2: chi-square table (6.63) for the 1% probability. **: significant at 1% probability.

χ^2: qui quadrado tabelado (6,63) para a probabilidade de 1%. **: significativo a 1% de significância.

The effective size (*Ne*) for the sample of the natural population of Ribeirão Preto was expected to be 120 (30 free-pollinating trees x 4 Ne arv^{-1}), assuming the ratio of 1♀:1♀, in this population, in absence of sexual selection. Therefore, the Ne of TP-MUE represents 38% of the expected *Ne*, and the *Ne* of TP-DES represents 12% of the expected *Ne* (Table 4), considering that the effective size is below 50% for both tests, it is not recommended the transformation of the progeny tests in a seed orchard by seedlings, mainly in the TP-DES, which had its representativeness much lower than expected, because only few individuals bloomed during the evaluation of this reproductive event. However, it is necessary to evaluate future reproductive events of individuals with flowering, to obtain a larger sample.

Souza (2017) working with 34 progenies from four fragmented natural populations of *M. urundeuva*, found that, in order to obtain seed lots with a *Ne* of 150 (long-term genetic conservation), it was necessary to collect seeds from at least 55 trees matrices, because *Ne* indicates how many non-related and non-inbreeding individuals the population has. The number of trees sampled for seed collection in a population is fundamental for long-term *ex situ* genetic conservation. Thus, as seeds were collected from 30 trees, *ex situ* genetic conservation will be in the short term. To reduce the genetic risk inherent to populations conserved *ex situ*, to preserve representative levels of genetic diversity and to minimize deleterious genetic alterations, it is recommended to practice a more efficient sampling (Potter et al., 2017) and, for that, a new collection of seeds from parent trees at this location could be carried out. However, as this is an environment heavily anthropized by the expansion of the municipality, the number of available specimens may not reach a minimum size of 50 trees. Thus, it is additionally recommended to expand the region for seed collection as long as climate and soil conditions are maintained.

Table 4. Effective size (Ne), sex ratio (r), total number of plants that contribute to gametes in the reproductive event (t), total number of male plants which flowered in that reproductive event (M), total number of female plants, which bloomed in that reproductive event (F), total number of male plants (Nm) and total number of female plants (Nf) in two *Myracrodruon urundeuva* progenies tests: TP-MUE and TP-DES, installed in 2006 in the region of Selvíria (MS).

Tabela 4. Tamanho efetivo (Ne), razão sexual (r), número total de plantas que contribuem com gametas, no evento reprodutivo (t), Número total de plantas masculinas, que floresceram, naquele evento reprodutivo (M), Número total de plantas femininas, que floresceram, naquele evento reprodutivo (F), Número total de plantas masculinas (Nm) e Número total de plantas femininas (Nf) em dois testes de progênies de *Myracrodruon urundeuva*: teste de progênies multi-espécie (TP-MUE) e teste de progênies em diferentes espaçamentos (TP-DES), instalados em 2006 na região de Selvíria-MS.

EXP	Nm	Nf	M	F	v	u	t	r	D_5	Ne	Ne (%)
TP-MUE*	210	210	210	210	1.0000	1.0000	420	0.50	3.9905	421	-
TP-MUE**	210	210	151	92	0.7190	0.4381	243	0.38	6.1694	158	38

EXP	Nm	Nf	M	F	v	u	t	r	D_5	Ne	Ne (%)
TP-DES*	135	135	135	135	1.0000	1.0000	270	0.50	3.9852	271	-
TP-DES**	135	135	75	18	0.5556	0.1333	93	0.19	11.3667	33	12

*When installing the experiment (EXP), assuming 1♂:1♀ and **Evaluation at the 2018 reproductive event.

*Na instalação do experimento (EXP), supondo 1♂:1♀ e **Avaliação no evento reprodutivo de 2018.

Souza (2017) working with 34 progenies from four fragmented natural populations of *M. urundeuva*, found that, in order to obtain seed lots with a *Ne* of 150 (long-term genetic conservation), it was necessary to collect seeds from at least 55 trees matrices, because *Ne* indicates how many non-related and non-inbreeding individuals the population has. The number of trees sampled for seed collection in a population is fundamental for long-term *ex situ* genetic conservation. Thus, as seeds were collected from 30 trees, *ex situ* genetic conservation will be in the short term. To reduce the genetic risk inherent to populations conserved *ex situ*, to preserve representative levels of genetic diversity and to minimize deleterious genetic alterations, it is recommended to practice a more efficient sampling (Potter et al., 2017) and, for that, a new collection of seeds from parent trees at this location could be carried out. However, as this is an environment heavily anthropized by the expansion of the municipality, the number of available specimens may not reach a minimum size of 50 trees. Thus, it is additionally recommended to expand the region for seed collection as long as climate and soil conditions are maintained.

4 CONCLUSIONS

The survival of *Myracroduon urundeuva* is high for both progeny tests, indicating good adaptation of the species to the site.

The population has sufficient genetic variability for *ex situ* genetic conservation and expresses this, both in TP-MUE and TP-DES.

The planting system does not influence the development of individuals, and is independent for genetic conservation, as long as the spacing is the same.

The tendency to lose genetic basis in the two progeny tests is similar and Ne indicates conditions for *ex situ* genetic conservation in the short term, by the number of progenies present in the test.

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REFERENCES

BALDONI, A.B. et al. Contemporary pollen and seed dispersal in natural populations of *Bertholletia excelsa* (Bonpl.). **Genetics and Molecular Research**, v. 16, n. 3, p. 1-14, 2017.

BERTI, C.L.F. et al. Diversidade genética de populações naturais de *Dipteryx alata* localizadas nos municípios de Brasilândia/MS, Indiara/GO e Ituramã/GO estimada por marcadores microssatélites. **Cultura Agronômica**, v. 26, n. 2, p. 203-216, 2017.

BERTONHA, L.J. et al. Seleção de progênies de *Myracrodruon urundeuva* baseada em caracteres fenológicos e de crescimento para reconstituição de áreas de reserva legal**. Scientia Forestalis**, v. 44, n. 109, p. 95-104, 2016.

BERTONI, J.E.A.; DICKFELDT, E.P. Plantio de *Myracrodruon urundeuva* Fr. All. (aroeira) em área alterada de floresta: desenvolvimento das mudas e restauração florestal. **Revista do Instituto Florestal**, v.19, n.1, p.31-38, 2007.

CANUTO, D.S.O. et al. Genetic Variability in *Myracrodruon urundeuva* (Allemão) Engl. Progeny Tests. **Open Journal of Forestry**, v. 7, p. 1-10, 2016.

_____. et al. Caracterização genética de um teste de progênies de *Dipteryx alata* Vog. proveniente de remanescente florestal da Estação Ecológica de Paulo de Faria, SP, Brasil. **Hoehnea**, v. 42, n. 4, p. 641-648, 2015.

CARVALHO, P.E.R. **Espécies Arbóreas Brasileiras**. Colombo: Empresa Brasileira de Pesquisa Agropecuária. Centro Nacional de Pesquisas Florestais, 2003. 179 p.

CORNACINI, M.R. et al. Desbaste em teste de procedências e progênies de *Astronium fraxinifolium* Schott com base na variabilidade genética. **Scientia Forestalis**, v. 45, n. 115, p. 581-591, 2017.

FREITAS, M.L.M. et al. Variação genética em progênies de *Myracrodruon urundeuva* F.F. & M.F. Allemão em três sistemas de cultivo. **Revista Árvore**, v. 30, n. 3, p. 319-329, 2006.

_____. et al. Formação de pomar de sementes a partir da seleção dentro de teste progênies de *Myracrodruon urundeuva*. **Revista do Instituto Florestal**, v. 19, n. 2, p. 65-72, 2007.

FLORES, T.B. et al. **Eucalyptus no Brasil**: zoneamento climático e guia para identificação. Piracicaba: Instituto de Pesquisas Florestais, 2016. 447 p.

GUERRA, C.R.S.B. et al. Estratégias de seleção em duas populações de *Myracrodruon urundeuva* Fr. All. **Scientia Forestalis**, v. 37, v. 81, p. 79-87, 2009.

LEITE, A.V.L.; MACHADO, I.C. Reproductive biology of woody species in Caatinga, a dry forest of northeastern Brazil. **Journal of Arid Environments**, v. 74, n. 11, p. 374-1380, 2010.

LENZA, E.; OLIVEIRA, P.O. Biologia reprodutiva de *Tapirira guianensis* Aubl. (Anacardiaceae), uma espécie dioica em mata de galeria do Triângulo Mineiro, Brasil. **Revista Brasileira de Botânica**, v. 28, n.1, p. 179-190, 2005.

LORENZI, H. **Árvores brasileiras**: manual de identificação e cultivo de plantas arbóreas nativas do Brasil. 6 ed. Nova Odessa: Instituto Plantarum, 2014. v. 1, 384 p.

MORAES, M.A. et al. Estimating coancestry within open-pollinated progenies of a dioecious species: the case study of *Myracrodruon urundeuva*. **Silvae Genetica**, v. 61, n. 6, p. 256-264, 2012.

NELDER, J.A. New kinds of systematic designs for spacing experiments. **Biometrics**, n. 18, p. 283-307, 1962.

NUNES, Y.R.F. et al. Aspectos ecológicos da aroeira (*Myracroduon urundeuva* Allemão – Anacardiaceae): fenologia e germinação de sementes. **Revista Árvore**, v. 32, n. 2. p. 233-243, 2008.

OLIVEIRA, P.E.; GIBBS, P.E. Reproductive biology of wood plants in a Cerrado community of central Brazil. **Flora**, v. 195, p. 311-329, 2000.

OTSUBO, H.C.B. et al. Variação genética para caracteres silviculturais em três espécies arbóreas da região do bolsão sul-mato-grossense. **Cerne**, v. 21, n. 4, p. 535-544, 2015.

PALUDZYSZYN FILHO, E. et al. Avaliação e seleção precoce para crescimento de *Pinus taeda*. **Pesquisa Agropecuária Brasileira**, v. 37, n. 12, p. 1719-1726, 2002.

POTTER, K.M. et al. Banking on the future: progress, challenges and opportunities for the genetic conservation of forest trees. **New Forests**, v. 48, p. 153-180, 2017.

QUEIROZ, C.R.A.A.; MORAIS, S.A.L.; NASCIMENTO, E.A. Caracterização dos taninos da aroeira-preta (*Myracrodruon urundeuva*). **Revista Árvore**, v. 26, n. 4, p. 485-492, 2002.

RAMOS, S.L.F. et al. Spatial genetic structure, genetic diversity and pollen dispersal in a harvested population of Astrocaryum aculeatum in the Brasilian Amazon. **BMC Genetics**, v. 17, n. 63, 2016.

RESENDE, M.D.V. Software Selegen – REML/BLUP: a useful tool for plant breeding. **Crop Breeding and Applied Biotechnology**, v. 16, n. 4, p. 330-339, 2016.

_____. **Matemática e estatística na análise de experimentos e no melhoramento genético**. Colombo: Embrapa Florestas, 2007. 362 p.

_____.; DUARTE, J.B. Precisão e controle experimental de qualidade em experimentos de avaliação de cultivares. **Pesquisa Agropecuária Tropical**, v. 37, n. 3, p. 182-194, 2007.

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

SANT'ANA, V.Z. **Proporção sexual em populações de *Myracrodruon urundeuva* para fins de formação de pomares de sementes por mudas**. 2017. 54 f. Dissertação (Mestrado em Agronomia) – Faculdade de engenharia de Ilha Solteira, Universidade Estadual Paulista Júlio de Mesquita Filho.

SANTOS, H.G. et al. **Sistema brasileiro de classificação de solos**. 5 ed. Brasília, DF: Embrapa, 2018. 353 p.

SEBBENN, A.M.; ETTORI, L.C. Conservação genética *ex situ* de *Esenbeckia leiocarpa*, *Myracrodruon urundeuva* e *Peltophorum dubium* em teste de progênies misto. **Revista do Instituto Florestal**, v. 13, n. 2, p. 201-211, 2001.

_____. et al. Parâmetros genéticos na conservação da cabreúva – *Myroxylon peruiferum* L.F. Allemão. *Scientia Forestalis,* n. 53, p. 31-38, 1998.

SOUZA, D.C.L. **Sistema de reprodução e distribuição da variabilidade genética de *Myracrodruon urundeuva* (F.F. & M.F. Allemão) em diferentes biomas**. 126 f. 2017. Tese (Doutorado em Ciência Florestal) - Faculdade de Ciências Agronômicas, Universidade Estadual Paulista..

SHIMIZU, J.Y.; KAGEYAMA, P.Y.; HIGA, A.R. **Procedimentos e recomendações para estudos de progênies de essências florestais**. Curitiba: EMBRAPA - URPFCS, 1982. 33p. (Série Documentos, 11).

SPOLADORE, J. et al. A.M. Genetic conservation of small populations of the endemic tree *Swartzia glazioviana* (Taub.) Glaz. (Leguminosae) in the Atlantic Forest. **Conservation Genetics**, v. 18, n. 5, p. 1105-1117, 2017.

TAMBARUSSI, E.V. et al. Inbreeding depression from selfing and mating between relatives in the Neotropical tree *Cariniana legalis* Mart. Kuntze. **Conservation Genetics**, v. 18, p. 225-234, 2017a.

_____. et al. *Dipteryx alata* Vogel (Fabaceae), a neotropical tree with high levels of selfing: implications for conservation and breeding programs. **Annals of Forest Research**, v. 60, n. 2, p. 243-261, 2017b.

TUNG, E.S.C. et al. Variação genética para caracteres silviculturais e anatômicos de madeira em progênies de *Myracrodruon urundeuva* (Engler) Fr. Allem. **Scientia Forestalis**, v. 38, n. 87, p. 499-508, 2010.

VENCOVSKY, R.; CHAVES, L.J.; CROSSA, J. Variance effective population size for dioecious species. **Crop Science**, v.52, n.1, p.79-90, 2012.

ZARUMA D.U.G. et al. Variabilidade genética em procedências e progênies de *Dipteryx alata* Vogel para fins de conservação genética e produção de sementes. **Scientia Forestalis**, v. 43, n. 107, p. 609-615, 2015.