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Genetic Variability in *Myracrodruon urundeuva* (Allemão) Engl. Progeny Tests

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Abstract

Aroeira (*Myracrodruon urundeuva*) is a widely spread tree species, but due to its excellent wood quality it is now part of the list of vulnerable trees for extinction. Thus, strategies for the conservation of the genetic variability of the remaining natural populations are needed. Therefore, this study aimed to evaluate the genetic variability in *M. urundeuva* progeny tests, from natural populations located in areas with and without human disturbance. Seeds of six natural populations of *M. urundeuva* were collected from two conditions, with and without anthropogenic disturbance, and nine progeny tests were installed in the Education, Research and Extension Farm, located in Selvíria, Mato Grosso do Sul State, Brazil. The overall height, average crown diameter (DMC) and the diameter at breast height (DBH) were assessed as phenotypic traits. Estimates of variance components and genetic parameters were obtained by REML/BLUP method (maximum restricted likelihood/best unbiased linear prediction). The results showed that natural population with human disturbance presented less genetic variability than populations originating from areas without human disturbance (CV_r until 0.87). The progeny tests evaluated had high accuracy (0.91 for DBH), which ensures the viability of the *ex situ* genetic conservation bank and its successful use in the breeding program, i.e., in the conversion of the progeny tests into *M. urundeuva* seed orchards. The most suitable character for selection was the DBH.

Keywords

Conservation, Improvement, Seed Orchard

1. Introduction

Myracrodruon urundeuva (Allemão) Engl., Anacardiaceae, popularly known as aroeira, backwoods aroeira or urundeuva, is a deciduous species, heliophytic and selective xerofita (Lorenzi, 1992). *M. urundeuva* occurs naturally in the extreme northwest of Argen-

tina, in the south and east of Bolivia and Paraguay. In Brazil, it occurs in the following states: Paraíba, Pernambuco, Piauí, Rio de Janeiro, Rio Grande do Norte, Sergipe, São Paulo, Tocantins, Federation District and Mato Grosso do Sul (Carvalho, 2003). It occurs also in different phytoecological regions, as semi deciduous forest; deciduous forest; scrubland and savanna; caatinga; kills drought; Mato Grosso do Sul and Mato Grosso Pantanal Chaco (Carvalho, 1994) and forest mono-dominated in Minas Gerais (Oliveira et al., 2015). The wide geographic distribution of a species is an indicator of high levels of genetic diversity, which can give it the ability to occupy different habitats (Kageyama et al., 2003).

The species has high-density wood, excellent mechanical performance and good chemical and physical defense, which explains the strength, hardness and durability. It is considered the toughest wood from Brazil. While one square centimeter concrete supports a load of 250 kgf wood, *M. urundeuva* can support 696 kgf, and it is registered at the Institute for Technological Research (IPT) in São Paulo, such as wood "durable" and put in select group of woods with secular durability, calls "imputrescible" (Ribeiro, 1989). Moreover, *M. urundeuva* was identified as the most potential species for research on phytochemicals (Pereira et al. 2014). Whereas *M. urundeuva* is endangered (BRASIL, 2008), Souza et al. (2012) reported a significant use of this species for timber purposes, due to the popularity and the timber and non-timber value of *M. urundeuva*, can lead to local extinction. Due to these facts, *M. urundeuva* is experiencing a strong exploration process, in a predatory way, causing the devastation of their natural populations. In addition, it should be noted that selective logging for use in the timber industry virtually wiped out the large individuals, therefore considered endangered and categorized as vulnerable (Brandão, 2000; Mendonça & Lins, 2000).

Studies to preserve and guarantee the genetic variability of these threatened populations have been intensified, and the tools used are the progeny tests, which is an *ex situ* strategy. Currently one of the major purposes of the progeny test is its transformation into an orchard, to provide seeds with genetic quality to restore the Legal Forest with superior material and adapted soil and climatic conditions associated with economic alternatives, to ensure the population's quality of life place. Thus, the aim of this study was to evaluate the genetic variability in nine *M. urundeuva* progeny tests.

2. Materials and Methods

Seeds of six natural populations of *M. urundeuva* were collected in two situations, without human disturbance (natural forest) and with human disturbance (modified areas with agriculture and grazing) (Table 1). Which were seedlings produced and installed in nine progeny tests in Education, Research and Extension Farm, located in Selvíria, Mato Grosso do Sul State, Brazil, thus, constituting the *M. urundeuva ex situ* bank.

With the seeds from natural populations of *M. urundeuva* without human disturbance of Paulo de Faria, four progeny tests were installed. The other populations been installed in only one provenance and progeny test. All experiments were conducted, using the randomized block design. The number of replications; the number of progenies and the number of plants per plot are presented in Table 2.

Table 1. Geographical Location of natural populations of *Myracrodruon urundeuva* with human disturbance (CPA) and without human disturbance (SPA).

Type	Population	Latitude	Longitude	Altitude (m)
SPA	Paulo de Faria-SP	19˚58'S	49˚32'W	495
	Seridó-RN	06˚66'S	37˚40'W	160
	Bauru-SP	22˚19'S	49˚04'W	526
CPA	Selvíria-MS	20˚19'S	51˚26'W	372
	Petrolina-PE	09˚09'S	40˚22'W	365
	Itarumã-GO	18˚44'S	51˚13'W	480

Table 2. Characteristics of Progeny Tests (TP) of *Myracrodruon urundeuva* installed in Selvíria, Mato Grosso do Sul.

Population	TP	Planting date	Planting spacing (m)	R	P	N
Paulo de Faria-SP	1	18/03/97	3.0 × 3.0	3	30	10
Paulo de Faria-SP	2	19/03/97	3.0 × 1.5	3	30	10
Paulo de Faria-SP	3	23/04/97	3.0 × 1.6	3	30	10
Seridó-RN	4	23/04/97	3.0 × 1.6	6	12	10
Paulo de Faria-SP	5	12/05/97	3.0 × 6.0	3	30	10
Selvíria-MS	6	14/12/87	3.0 × 3.0	3	28	10
Bauru-SP	7	14/12/87	3.0 × 3.0	3	28	10
Petrolina-PE	8	07/12/92	3.0 × 6.0	21	10	6
Itarumã-GO	9	28/06/04	3.0 × 6.0	3	30	12

R: number of replications; P: number of progeny; N: number of plants by progenies.

In the test 1, 3, 4, 5, 8 and 9, *M. urundeuva* was planted in consortium with other species: 1-*Anadenthera falcata* and *Guazuma ulmifolia*; 3 and 4-*Ricinus communis*, *Zea mays* and *Cajanus cajan*; 5-*Eucalyptus* spp; 8-*Trema micranta*, *Peltophorum dubium* and *Eucalyptus* spp, 9-*Cordia trichotoma*, because *M. urundeuva* needs shade in early development. The progeny tests 2, 6 and 7 were planted only using *M. urundeuva*. All trials were measured in 2007 for the quantitative traits: total tree height (H); average crown diameter (DMC) and diameter at breast height (DBH).

Quantitative variables were analyzed by the method of linear mixed model (univariate additive)-REML/BLUP, applied to progeny tests in randomized block design, many plants per plot, one site and a single population, following the procedure proposed by Resende (2002a): $y = Xb + Za + Wc + e$; where: y = data vectors; b = vector of the effects of blocks (fixed); a = vector of additive genetic effects (random); c = vectors of the effects of plot (random); e = vector of random errors effects. X, Z e W = incidence matrices for b, a and c, respectively. Estimates of variance components and genetic parameters were obtained by REML/BLUP method (restricted maximum/best linear prediction likelihood untainted), using genetic-statistical software SELEGEN-REML/BLUP (Resende, 2002b). The estimated parameters were the coefficients: heritability in individual, strict sensus ($\hat{h}_a^2$), average among progenies ($\hat{h}_m^2$) and additive

within plot ($\hat{h}_d^2$); genetic variation at the individual level ($CVgi$) and plot level ($CVgp$); relative variation (CVr) and accuracy (Ac) to the traits H, DMC and DBH.

3. Results and Discussion

The highest average annual increment (IMA) for the height (Table 3) for populations without human disturbance was found in the TP-3 (0.89 m) and the lowest in TP-4 (0.58 m), and for the population with human disturbance, the highest was in TP-9 (1.20 m) and the lowest was in TP-8 (0.43 m). Sebbenn and Etorri (2001), studying a progeny

Table 3. Average estimates $(\hat{m})$, mean annual increment (IMA), experimental variation coefficient (CV_{exp}), change index (IV), F-test (F) and correlation due to the common environment of the plot $(\hat{C}^2)$, for traits height (H), DMC and DBH.

Character	TP	$\hat{m}$	IMA	CV_{exp}	IV	F	$\hat{C}^2$
Height (m)	1	6.31	0.63	16.9	5.62	1.06^{ns}	0.20
	2	8.47	0.85	11.8	3.94	1.11^{ns}	0.20
	3	8.89	0.89	11.5	3.83	1.03^{ns}	0.16
	4	5.77	0.58	14.8	2.46	4.19**	0.07
	5	6.02	0.60	12.1	4.02	2.23^{ns}	0.13
	6	9.13	0.46	11.5	3.83	1.24^{ns}	0.21
	7	10.47	0.52	9.5	3.18	1.97^{ns}	0.16
	8	6.28	0.42	17.7	0.84	1.42^{ns}	0.07
	9	3.61	1.20	30.6	2.55	1.72^{ns}	0.11
DMC (m)	1	2.39	0.24	22.8	7.60	1.01^{ns}	0.42
	2	3.25	0.33	9.5	3.17	1.75^{ns}	0.07
	3	3.12	0.31	14.3	4.78	1.54^{ns}	0.21
	4	2.88	0.29	15.7	2.62	2.81*	0.21
	5	3.96	0.40	9.6	3.20	1.93^{ns}	0.13
	6	4.60	0.23	8.4	2.81	3.07*	0.03
	7	4.78	0.24	13.6	4.53	1.06^{ns}	0.20
	8	3.59	0.24	14.7	0.70	3.48*	0.12
	9	3.17	1.06	19.5	1.63	1.74^{ns}	0.25
DBH (cm)	1	5.36	0.54	27.0	9.01	1.11^{ns}	0.11
	2	8.52	0.85	10.0	3.32	1.45^{ns}	0.01
	3	4.82	0.48	13.9	4.63	1.03^{ns}	0.07
	4	5.90	0.59	16.2	2.69	5.53**	0.09
	5	6.55	0.66	13.1	4.36	2.13^{ns}	0.14
	6	11.38	0.57	18.1	6.04	1.23^{ns}	0.08
	7	12.94	0.65	15.8	5.25	1.50^{ns}	0.07
	8	7.06	0.47	18.3	0.87	1.07^{ns}	0.16
	9	-	-	-	-	-	-

test of *M. urundeuva* consortium with *Peltophorum dubium* and *Esenbechia leiocarpa* found IMA H of 0.89 m. Bertoni and Dickfeldt (2007) evaluating *M. urundeuva* planted in alternating areas in the State Park of Porto Ferreira, Sao Paulo State, Brazil, found for H an IMA 0.72 m.

In general, environmental control was good for all trials ($CV_{exp} < 20\%$, Pimentel Gomes (1985)). But the variation index (IV) showed a lower percentage because the value depends only on CV_{exp}, as a proportion of the residual variation of experimental medium (Pimentel Gomes, 1987) and the variation index proposed by Pimentel Gomes (1991) or experimental precision coefficient Storck et al. (2000) consider the number of replications used in the trial, apart from a residual nature variation.

The TP-4 showed significant difference at 1% of probability among progenies, indicating genetic variation among the progeny for the traits height; in other progeny tests occurred homogeneity of values, which was acquired with the development of the progeny, as in earlier ages had differences. When the TP-8 and the TP-3 were evaluated at younger ages, Fonseca (2003); Freitas, Moraes and Buzetti (2002) and Freitas et al. (2006) detected significant differences at 5% of probability for height.

Correlation due to the common environment of the plot $\left(\hat{C}^2 \right)$ in TP-4 and TP-8 showed to be the most suitable trials for the selection for height, because there is little environmental influence on the variation observed in the plots. According to Sturion and Resende (2005), the values of around 0.10 are observed in experiments with perennials plants.

The highest means of DMC were found in the TP-5 and TP-7, the CV_{exp} ranged from 8.4 to 22.8%, which shows appropriate experimental environmental control in the trials. The variation rates (IV), which takes into account the number of replications, ranged from 0.70 to 7.60, these values can be considered low for experiments where there is competition (Pimentel Gomes and Garcia, 2002).

The F test indicated that there is genetic variability among progenies in TP-4, 6 and 8 for the DMC, with significant differences at the level of 1% and 5%. The TP-2 and 6 showed lowest value for the $\left(\hat{C}^2 \right)$, 0.07 and 0.03, respectively. The other progeny tests presented values higher than 10%.

For DBH the highest averages were found in TP-6 (7 cm) and 7 (12.94 cm). The highest IMA value was 0.85 cm for TP-2/ These values are superior to that found by Guerra et al. (2009), obtained average DBH of 6.87 cm and 5.98 cm for *M. urundeuva* originating from Aramina-SP and Selvíria-MS, at 15 years of age.

The CV_{exp} ranged from medium to high, but the IV indicated good environmental control. TP-4, 5 and 6 showed significant differences between progenies for DBH. The correlation due to the common environment of the plot revealed that the DBH is the most favorable trait for selecting.

The average heritability among progenies ($\hat{h}_m^2$) was greater than the individual heritability ($\hat{h}_a^2$) and additive within plots ($\hat{h}_d^2$) for all trait in all of progeny tests (Table 4). This results are in agreement with the results found by Siqueira et al. (2000), in *Balfourodendron riedelianum*, Sebbenn and Ettori (2001) in *M. urundeuva*, Sebbenn et al. (2003) in *Araucaria angustifolia*, Souza et al. (2003) in *Astronium fraxinifolium*, Costa et al. (2005) in *Ilex paraguariensis*, Moraes et al. (2007) in *Hevea brasiliensis*,

Table 4. Genetic parameter estimates for the traits height, DMC and DBH for testing progenies *Myracrodruon urundeuva* with and without human disturbance.

Trait	TP	$\hat{h}_a^2$	$\hat{h}_m^2$	$\hat{h}_d^2$	CV_{gi}	CV_{gp}	CV_r	Ac
	1	0.02	0.06	0.02	4.8	2.4	0.14	0.24
	2	0.04	0.10	0.04	4.4	2.2	0.19	0.31
	3	0.01	0.03	0.01	2.4	1.2	0.10	0.18
	4	0.34	0.76	0.30	21.5	10.8	0.73	0.87
Height (m)	5	0.43	0.55	0.42	15.5	7.7	0.64	0.74
	6	0.09	0.19	0.09	6.5	3.2	0.28	0.44
	7	0.30	0.49	0.30	10.8	5.4	0.57	0.70
	8	0.02	0.30	0.02	5.1	2.5	0.14	0.55
	9	0.10	0.42	0.08	15.0	7.5	0.25	0.65
	1	0.01	0.01	0.01	2.4	1.2	0.05	0.09
	2	0.16	0.43	0.13	9.5	4.8	0.50	0.66
	3	0.20	0.35	0.21	12.2	6.1	0.43	0.59
	4	0.34	0.64	0.36	17.3	8.6	0.55	0.80
DMC (m)	5	0.33	0.48	0.31	10.7	5.3	0.56	0.69
	6	0.32	0.67	0.27	14.0	7.0	0.83	0.82
	7	0.02	0.06	0.02	4.0	2.0	0.15	0.25
	8	0.11	0.69	0.09	9.5	4.7	0.32	0.89
	9	0.12	0.42	0.13	9.7	4.8	0.25	0.65
	1	0.03	0.10	0.02	10.2	5.1	0.19	0.31
	2	0.07	0.31	0.05	7.7	3.8	0.39	0.56
	3	0.01	0.03	0.01	2.8	1.4	0.10	0.17
	4	0.50	0.82	0.48	28.1	14.0	0.87	0.91
DBH (cm)	5	0.41	0.53	0.40	16.0	8.0	0.61	0.73
	6	0.05	0.19	0.05	10.1	5.1	0.28	0.44
	7	0.11	0.33	0.09	12.8	6.4	0.41	0.58
	8	0.00	0.06	0.00	2.1	1.0	0.06	0.25
	9	-	-	-	-	-	-	-

Missio et al. (2005) in *Pinus caribaea* var. *hondurensis*, and Oliveira et al. (2004) in *Spondias tuberosa*.

The $\hat{h}_m^2$ was higher in progeny tests originated from areas with human disturbance, except for the DBH. This results for all the traits studied indicate that the selection can be more effective by selection among progenies (Costa et al., 2010). According to Falconer (1987), small populations are expected to present lower heritability than large populations. The average heritability among progeny show great generic control of traits, indicating the possibility to obtain genetic gains by selecting the best families for seed production.

The highest heritability coefficients for height were obtained in TP-4 (Table 3). The TP-4 presented highest heritabilities in the first yea (0.8, 0.36 and 0.07, for $\hat{h}_a^2$, $\hat{h}_m^2$, $\hat{h}_d^2$, respectively) and in the second year (0.35, 0.75 and 0.28 to $\hat{h}_a^2$, $\hat{h}_m^2$, $\hat{h}_d^2$, respectively). According Ettori et al. (2006) the coefficient of heritability shows variation with age of the plant, because until there is full to the countryside and balance, there may be greater or lesser influence of the environment on the expression of growth traits.

In progeny tests derived from the Ecological Station of Paulo de Faria (TP-1, 2, 3 and 5) the $\hat{h}_m^2$) ranged from 0.03 to 0.55 for height, 0.01 to 0.48 for DMC and, 0.03 to 0.53 for DBH. Such variations show that heritability is a property not only of the traits, but also the population and environmental circumstances to which the progenies are subject of investigations (Falconer, 1987).

The presence of genetic variability can be confirmed and quantified by the coefficient of genetic variation, which expresses the magnitude of genetic variation relative to the nature of the medium (Resende et al., 1991). The greatest genetic variation values were found in the DMC and DBH in TP-4 (17.3 and 2.8, respectively), indicating that there is a greater amount of genetic variation among progenies from areas without human disturbance. Incontrast, occurred less genetic variation when compared to populations from forest fragments.

The coefficient of genetic variation in individual level (CV_{gi}) was in general twice time large than the CV_{gp} (Table 3) for height, DMC and DBH. According to Aguiar et al. (2010), the larger value for the greater ease to find individuals that may provide higher gains in the selection.

The CV_r indicates the most appropriate trait for selection, and the TP-5, 7 and 9 the height, the TP-2, 3, 6, 8 and 9 the DMC, the TP-1 and 4 DBH. According Vencovsky and Barriga (1992), traits that have values close to one are suitable for carrying out a selection.

The accuracy, which measures the confidence level of the estimates, was high in TP-4 for DBH, in TP-4, 5 and 7 for height and TP-4, 6 and 8 for the DMC, according with the magnitude criterion of Resende and Duarte (2007). Thus, the *M. urundeuva* progeny tests provide genetic variability among progenies enough to conduct genetic conservation and breeding programs.

4. Conclusion

The evaluations of silvicultural traits in the nine *M. urundeuva* progeny tests allowed the observation that the trees had a satisfactory development.

Genetic variation of the populations with human disturbance is lower than populations originated from areas without human disturbance.

The progeny tests showed a high accuracy, which ensures the viability of the genetic conservation bank *ex situ* and success in the breeding programs, by the transformation of trials seed orchards. The most appropriate trait for selection is the diameter at breast height.

Acknowledgements

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