



## Estimates of genetic parameters in *Mimosa scabrella* populations by random and mixed reproduction models

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**ABSTRACT** - Heritabilities and expected selection gains were estimated in nine provenances of *Mimosa scabrella* Benth. by means of random and mixed reproduction models. In the random model, the relationship coefficient was considered as half-sibs, and in the mixed, relatedness was estimated based on parameters of the mating system. The trait height was measured six months after planting in the field and a progeny sample of each provenance was analyzed by isoenzyme electrophoresis to estimate parameters of the mating system. The mean inbreeding coefficient was 0.392, which is 56.8% higher than expected in half-sib progenies (0.25). The mean estimates of the additive genetic variance, heritability within progenies and gains expected with selection among and within progenies, calculated by the underlying random reproduction model were overestimated, respectively, by 36%, 48% and 41%, when compared to estimates obtained based on the mixed reproduction model.

**Key words:** Coancestry coefficient, parameter estimate, reproduction system, forest improvement.

### INTRODUCTION

*Mimosa scabrella* Benth. is a leguminous tree species of key socio-economic importance for the southern region of Brazil. The species, native to southern Brazil, has been grown in the surroundings of Curitiba, state of Paraná, since the beginning of the 20<sup>th</sup> century, representing the country's oldest agroforest system. Small holders and intermediate farmers of low net-worth, mainly, extract wood for firewood and carbon. The species could also be used in the recovery of degraded areas (Carvalho 1994), for animal feed (Nyang et al. 1994) or to shade crops as, for example, coffee (Carvalho 1994).

As most Mimosoideae, the small flowers are joined in inflorescences of the globose flower head type. These have green corolla gamopetal and free yellow pistil and

stamen (Catharino et al. 1982). The monoic flowers do not need specialized pollinators (Catharino et al. 1982). Some possible pollinators are already known, as for example, *Apis mellifera*, *Melipona marginata*, *M. quadrifasciata*, *Plebeia remota* (Pirani 1994) and *Trigona* sp (Catharino et al. 1982).

Many forestry traits of *M. scabrella* are known, but so far no studies on the genetics of the species, in terms of improvement as much as of conservation are available. The natural occurrence region of the species is one of the most degraded and fragmented of Brazil, thanks to intensive urbanization, industrialization and agricultural development. The risk of genetic drift is imminent, particularly because the remaining populations are found in forest fragments.

In natural populations the tree species usually has

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low yields. The use of techniques of genetic improvement could increase the yield considerably (Clement 2001). Genetic improvement of native tree species is similar to that of exotic species, but requires special care regarding experimental seed collection and installation (Resende et al. 1995). An important aspect in genetic improvement of tropical forest species is that many have mixed reproduction systems, combining reproduction predominantly by crossings with partial selfing (Bawa 1974). The improvement of species of mixed reproduction systems differs from improvement of perfectly autogamous or allogamous species, since the plants represent a mixture of individuals with different degrees of inbreeding and relatedness (Vencovsky et al. 2001).

Genetic improvement programs, based on open pollination-derived progenies have, in general, assumed that the crossings occur randomly and that each plant of a progeny receives pollen from a different parent, so the inbreeding coefficient among plants within progenies is equal to that of half-sibs (0.25). Additive genetic variance among plants within progenies therefore estimates  $\frac{1}{4}$  of the additive genetic variance (Sebbenn et al. 2002). Nevertheless, the application of the random reproduction model for tree species has been called into question (Namkoong 1966, Squillace 1974, Surlis et al. 1990, Sebbenn 2002), in view of the fact that natural populations often present spatial genetic structure and inbreeding while reproduction is not completely random, but rather combines random, biparental and inbred crossings and selfings (Sebbenn 2003).

Different models have been proposed to estimate genetic parameters in quantitative traits of species of mixed reproduction systems such as, e.g., the models of Ghai (1982), Cockerham and Weir (1984) and Ritland (1989). The model of Ghai (1982) has the drawback of not taking the linkage disequilibrium between loci into consideration and that additive genetic variance and variance of dominance vary with the selfing rate (Cockerham and Weir 1984). The model of Cockerham and Weir (1984) is based on the inbreeding equilibrium model of Wright, and assume that the progenies of open pollination are originated from mixtures of random and self crossings, thus, the relatedness within progenies includes mixtures of half and self sibs. The additive genetic variance is then estimated directly by the inbreeding coefficient. Nevertheless, since many natural populations of tree species presented spatial genetic structure and inbreeding and have mixed systems with random, biparental, inbred and self crossing, the model

of Cockerham and Weir (1984) is not the most adequate for such species (Sebbenn 2002). The model of Ritland (1989) estimates the additive genetic variance with the inbreeding coefficient among plants within progenies ( $\tau_{xy}$ ) calculated by parameters of the reproduction system such as: outcrossing rate, selfing rate, inbreeding coefficient in the parent generation, correlation of selfing, and correlation of paternity. This is therefore currently the most complete and appropriate model to estimate genetic parameters in species with mixed reproduction systems.

The objective of this study was to estimate and compare genetic parameters for the trait plant height in *M. scabrella* provenances, calculated with random and mixed reproduction models.

## MATERIAL AND METHODS

### Sample collection

This study was developed with plant material derived from eight natural provenances (Itararé, SP; Piraí do Sul, PR; Turvo, PR; Lapa, PR; Mandirituba, PR; Honório Serpa, PR; Caçador, SC; Ituporanga, SC) and a commercial one (Ituporanga, SC) selected across and throughout the geographical distribution of *M. scabrella*. One natural provenance was localized in each county, with exception of Ituporanga, with one natural and one commercial provenance. The identification of the provenances and seed collection were realized by technicians of the EMBRAPA/CNPQ between 1997 and 1999. The localization of provenances, trial site and the number of sampled progenies per provenance are shown in Table 1.

Ten to 20 mother trees of each provenance were sampled and enough seeds collected for the production of 50 plantlets per progeny. The seeds were germinated separately per progeny and in May 2003 the test of provenances and progenies was installed at the Experimental Station of Itatinga (ESALQ, USP). The trial was installed in a compact family block (Wright 1978) design with nine provenances, 10 to 20 progenies per provenance, six plants per subplot, in five replications. Spacing was 3.0 x 1.5 m and the trial was protected by three external border rows.

### Data collected

The evaluated quantitative trait was the total tree height, six months after planting. Additionally, to estimate the parameters of the reproduction system of *M. scabrella* and calculate the inbreeding coefficient among plants

within progenies, a random sample of progenies and plants per progeny was taken from the trial (Table 1). Approximately 50 trees per provenance were sampled, making up a total of 450 trees in the trial. The leaves were collected, wrapped in plastic bags and labeled accordingly with the number of the tree of origin and sent to the Laboratory of Reproduction and Genetics of Tree Species (ESALQ, USP) and immediately subjected to analyses of isoenzyme electrophoresis.

### Isoenzyme electrophoresis

For the isoenzyme extraction from leaf tissue we used extraction buffer number one, cited by Alfenas (1998). The following enzymes were identified: phosphoglucosomerase (PGI-EC 5.3.1.9), glucose-6-phosphate dehydrogenase (G6PDH-EC 1.1.1.49), leucine aminopeptidase (LAP-EC 3.4.11.1), malate dehydrogenase (MDH-EC 1.1.1.37), Isocitrate Dehydrogenase (IDH-EC 1.1.1.42), menadione reductase (MR-EC 1.6.99.2), and 6-phosphoglucuronate dehydrogenase (6PGDH-EC 1.1.1.44), all with morpholine citrate gel/electrode buffer. The isoenzymatic reactions were realized according to Alfenas (1998) but to improve the resolution of enzyme phosphoglucosomerase (PGI), the quantity of glucose-6-phosphate dehydrogenase enzyme was raised from 6 µL to 7.5 µL.

### Statistical analysis

The reproduction system of *M. scabrella* was characterized for each provenance and the set of provenances with the mixed reproduction model (Ritland and Jain 1981) and model of correlated crossings (Ritland 1989) on software Multiloci MLTR (Ritland 1997). The mixed model presupposes that progenies are result of a mixture of selfing and crossing, and the model of correlated

crossings assumes that progenies originated by crossings are generated by random and biparental crossings. The following parameters were estimated: multilocus outcrossing rate ( $\hat{i}_m$ ), mean unilocus outcrossing rate ( $\hat{i}_s$ ) outcrossing rate among relatives ( $\hat{i}_m - \hat{i}_s$ ), correlation of selfing ( $\hat{r}_s$ ), paternity correlation ( $\hat{r}_p$ ), and inbreeding coefficient in the parent generation ( $\hat{F}$ ).

Based on the parameters of the reproduction system, the correlation coefficient of relatedness ( $\hat{r}_{xy}$ ) was estimated among plants within progenies, based on the model of Ritland (1989), and later used in the adjustment of the estimate of the additive genetic variance  $\sigma_A^2$ :  $r_{xy} = 0,25 (1 + \hat{F}) [4\hat{s} + (\hat{i}_m + \hat{s}\hat{i}_m - \hat{r}_s)(1 + \hat{r}_p)]$ .

The analysis of variance for the trait height was obtained on software SAS (SAS 2000) based on the following statistical model:  $Y_{ijk} = m + r_i + s_j + ps_{k(i)} + pr_{ij} + psr_{k(i)j} + e_{(ijk)}$ ; where:  $Y_{ijk}$  = value of the measured trait in the  $l^{th}$  plant of the  $k^{th}$  progeny, of the  $j^{th}$  provenance, of the  $i^{th}$  replication;  $m$  = overall trait mean;  $r_i$  = effect of the replication  $i$ ;  $s_j$  = effect of the provenance  $j$ ;  $ps_{k(i)}$  = effect of the  $k^{th}$  progeny within the  $j^{th}$  provenance;  $pr_{ij}$  = effect of the interaction of the  $j^{th}$  provenance with the  $i^{th}$  replication;  $psr_{k(i)j}$  = effect of the interaction of the  $k^{th}$  progeny with the  $j^{th}$  provenance in the  $i^{th}$  replication;  $e_{(ijk)}$  = effect of the  $l^{th}$  plant within the  $k^{th}$  progeny of the  $j^{th}$  provenance, in the  $i^{th}$  replication.

The components of variance were obtained in the analysis of variance by VARCOMP in combination with the routine procedure REML, due to the unequal number of progenies per provenance and the different mortality among subplots. The genetic parameters were estimated based on the components of variance.

The additive genetic variance ( $\sigma_A^2$ ) was estimated by two models: the random and mixed model of reproduction. The random reproduction model assumes

**Table 1.** Number of progenies sampled per provenance ( $m$ ) and for the study of isoenzymes ( $m_{iso}$ ), and geographical coordinates of the locations of origin of the provenances and the trial site

County/State	$m$	$m_{iso}$	Latitude (south)	Longitude (west)	Altitude(m)
Itararé/SP	20	10	24° 10'	49° 16'	1000
Pirai do Sul/PR	19	7	24° 50'	49° 56'	1250
Mandirituba/PR	20	12	25° 48'	49° 18'	-
Lapa/PR	20	9	25° 48'	49° 41'	910
Honório Serpa/PR	20	11	26° 11'	52° 26'	-
Turvo/PR	20	12	25° 03'	51° 33'	1200
Caçador/SC	20	9	27° 45'	51° 00'	1000
Ituporanga, native/SC	10	10	27° 24'	49° 36'	370
Ituporanga commercial/SC	19	9	27° 24'	49° 36'	370
Experimental station of Itatinga/SP	-	-	23° 02'	48° 38'	830

absence of relatedness and inbreeding in the parent population and that crossings in the populations occur randomly, so that each plant of a progeny would be generated by a different parent and the inbreeding coefficient among plants within progenies would be equal to that expected in half-sibs (0.25). So, the additive genetic variance can be estimated by:  $\hat{\sigma}_d^2 = 4\hat{\sigma}_p^2$ . The mixed reproduction model assumes that plants of a progeny may have been generated by different forms of reproduction, such as selfing, random and biparental crossings. The degrees of relatedness among progenies can be: half-sibs (MI), full-sibs (IC) and self-sibs (IA). In this model the additive genetic variance is obtained by:  $\hat{\sigma}_d^2 = \frac{\hat{\sigma}_p^2}{r_{xy}}$ .

The narrow-sense heritability coefficients at the individual plant level ( $\hat{h}_i$ ), mean among progenies ( $\hat{h}_m$ ) and within progenies ( $\hat{h}_d$ ) were estimated according to Namkoong (1979):

$$\hat{h}_i = \frac{\hat{\sigma}_A^2}{\hat{\sigma}_p^2 + \hat{\sigma}_{eb}^2 + \hat{\sigma}_d^2}, \hat{h}_m = \frac{\hat{\sigma}_p^2}{\hat{\sigma}_p^2 + \frac{\hat{\sigma}_{eb}^2}{J} + \frac{\hat{\sigma}_d^2}{nJ}}, \hat{h}_d = \frac{(-r_{xy})\hat{\sigma}_A^2}{\hat{\sigma}_d^2}$$

The expected selection gains were predicted according to Namkoong (1979):

- i) Expected selection gains among progenies:  $G_{Se} = i_c \hat{\sigma}_p \hat{h}_m$
  - ii) Expected selection gains within progenies:  $G_{Sd} = i_d \hat{\sigma}_d \hat{h}_d$
  - iii) Expected selection gains among and within progenies:  $G_{Se+d} = i_c \hat{\sigma}_p \hat{h}_m + i_d \hat{\sigma}_d \hat{h}_d$ .
- The selection indices we used aimed to select 25% of the progenies of best performance ( $i_c = 1.271$ ) and the three best trees within the best progeny ( $i_d = 1.673$ ) (Hallauer and Miranda Filho 1988).

## RESULTS AND DISCUSSION

The analysis of the reproduction system of the provenances of *M. scabrella* indicated that the species presents a mixed reproduction system with predominance of crossings ( $\hat{t}_m$  varying from 0.859 – Turvo – to 1.00 – Piraí do Sul, Mandirituba, Lapa and Ituporanga, native) (Table 2). The difference between the multilocus and unilocus outcrossing rate (varying from 0.012 – Caçador – to 0.105 – Ituporanga, commercial) demonstrated that part of the crossings occurred among related trees. In turn, the estimate of the paternity correlation suggests that part of the progenies of crossings are relatives in the degree of full-sibs (varying from 0.153 – Lapa – to 0.694 – Caçador). In agreement, the mean estimate of the inbreeding coefficient among plants within progenies was 0.392, varying from the expected values in progenies of half-sibs (0.25) to full-sibs (0.50). Hence, it becomes clear that the assumption that open pollinated progenies of *M. scabrella* are half-sibs would strongly overestimate the additive genetic variance and the parameters dependent thereof, such as heritability at the individual plant level, heritability within progenies, expected selection gains within progenies and expected selection gains among and within progenies.

The F test of the analysis of variance demonstrated significant differences (at 95% probability) in tree height among provenances (provenance MS = 0.7726, F test = 4.75, CV<sub>E</sub> = 25.44%; Mean = 0.84 m), demonstrating the possibility of obtaining selection gains among these. Nevertheless, no significant differences were detected among progenies within provenances (progeny/provenance

**Table 2.** Estimate of the parameters of the reproduction system for *Mimosa scabrella* Bentham

Parame- -ters	Provenances									Mean perspecies
	Itararé	Piraí do Sul	Mandi- rituba	Lapa	Honório Sarpa	Turvo	Caçador	Itupor. (nat.)	Itupor. (com.)	
$\hat{F}$	0	0	0	0.004	0.004	0	0	0.004	0	0.012
$\hat{t}_m$	0.949	1.000	1.000	1.000	0.979	0.859	0.945	1.000	0.958	0.971
$\hat{t}_s$	0.877	0.985	0.923	0.913	0.917	0.801	0.933	0.926	0.853	0.895
$\hat{t}_m - \hat{t}_s$	0.072	0.015	0.077	0.087	0.062	0.058	0.012	0.074	0.105	0.076
$\hat{r}_s$	0.026	0.109	0.109	0.113	0.095	0.013	0.310	0.107	0.052	0.091
$\hat{r}_p$	0.521	0.449	0.477	0.153	0.244	0.476	0.694	0.495	0.529	0.513
$\hat{r}_{xy}$	0.396	0.362	0.370	0.290	0.320	0.414	0.440	0.376	0.394	0.392

$\hat{F}$  = Fixation Index in the mother trees;  $\hat{t}_m$  = Multilocus outcrossing rate;  $\hat{t}_s$  = Unilocus outcrossing rate;  $\hat{t}_m - \hat{t}_s$  = Outcrossing rate among relatives;  $\hat{r}_s$  = Correlation of selfing;  $\hat{r}_p$  = Correlation of paternity;  $\hat{r}_{xy}$  = Inbreeding coefficient among plants within progenies, in nine *Mimosa scabrella* provenances

MS = 0.1633, F test = 1.03). The absence of differences among progenies within provenances can be associated to the precocity of the plants, considering that an evaluation at six months is preliminary, and the trial should be measured anew at more advanced development stages.

The estimate of the coefficient of genetic variance among provenances ( $CV_g$ ; mean = 2.38%) (Table 3), varied from 2.35% (Turvo - PR) to 8.30% (Caçador - SC), suggesting that higher genetic gains can be capitalized on in the selection within the provenance from Caçador. Compared with the value obtained by Farias Neto and Castro (1999) reported for the *Sclerolobium paniculatum*, (4.60%), suggest that, in mean terms, the genetic variation in *M. scabrella* provenances is low, compared to other native species. The coefficient of phenotypic variation within progenies ( $CV_d$ ) (Table 3) estimated for the mean of *M. scabrella* provenances (25.34%) was higher than found for the *S. paniculatum* (18.80%), cited by Farias Neto and Castro (1999). This piece of information is important since in species of crossings, as the tree species, a great part of the additive genetic variance is found within progenies (up to 75%) and genetic gains can be capitalized on by sequential selection of best plants of best progenies. Generally speaking, the magnitude of both coefficients of genetic variation indicate that higher selection gains can be expected in the provenance from Caçador.

The estimate of additive genetic variance and the genetic parameters for the random (MI) and mixed models of reproduction (MS) detected overestimates when the random model was used instead of the mixed reproduction model (Table 3). The provenance from Lapa presented the lowest overestimate in all parameters and the one from Caçador the highest. The reason is the reproduction system. The provenance from Lapa had an outcrossing rate estimated at 1.00, the lowest paternity correlation (0.153) and consequently, the inbreeding coefficient among plants within progenies (0.290) closest to the one expected in half-sib progenies (0.25). On the other hand, the outcrossing rate of the provenance from Caçador was under the unit (0.945) and had the highest estimate of paternity correlation (0.694), indicating that approximately 70% of the progenies generated by crossings were relatives in the degree of full-sibs. Consequently, the inbreeding coefficient among plants within progenies (0.440) had a value near the expected in full-sib progenies (0.5). The error in the supposition of the reproduction mode in the provenance of Caçador and, consequently, in the mean degree of relatedness among plants within progenies resulted in an overestimated additive genetic variance by 54.55%.

Other genetic parameters dependent on the additive genetic variance such as heritability at the individual plant level and among plants within progenies performed

**Table 3.** Estimates of the genetics parameters for *Mimosa scabrella* Bentham

Parameter	Provenances									Mean perspecies
	Itararé	Pirai do Sul	Mandi-rituba	Lapa	Honório Serpa	Turvo	Caçador	Itupor. (nat.)	Itupor. (com.)	
$CV_g$ (%)	4.12	3.35	6.17	5.92	5.71	2.35	8.30	3.61	7.43	2.38
$CV_d$ (%)	21.98	29.47	25.63	27.55	24.37	24.31	28.13	20.83	27.84	25.34
$\hat{\sigma}_A^2$ HS	0.0048	0.0028	0.0100	0.0092	0.0092	0.0016	0.0172	0.0048	0.0156	0.0016
$\hat{\sigma}_A^2$ MR	0.0030	0.0019	0.0068	0.0079	0.0072	0.0010	0.0078	0.0032	0.0099	0.0010
$\hat{\sigma}_A^2$ Dif. (%)	36.87	30.94	32.43	13.79	21.88	39.61	54.55	33.51	36.55	36.22
$\hat{h}_m^2$	0.2083	0.1126	0.3414	0.3076	0.3244	0.0775	0.4561	0.2045	0.4229	0.0068
$\hat{h}_i^2$ HS	0.0876	0.0376	0.1536	0.1285	0.1444	0.0255	0.2350	0.0791	0.1997	0.0245
$\hat{h}_i^2$ MR	0.0553	0.0260	0.1038	0.1108	0.1128	0.0154	0.1068	0.0526	0.1267	0.0157
$\hat{h}_i^2$ Dif. (%)	36.87	30.94	32.43	13.79	21.88	39.61	54.55	33.51	36.55	336.22
$\hat{h}_d^2$ HS	0.1056	0.0387	0.1740	0.1385	0.1647	0.0281	0.2611	0.0900	0.2139	0.0265
$\hat{h}_d^2$ MR	0.0537	0.0228	0.0988	0.1131	0.1166	0.0133	0.0712	0.0498	0.1097	0.0137
$\hat{h}_d^2$ Dif. (%)	49.16	41.25	43.24	18.39	29.17	52.82	72.73	44.68	48.73	48.30

$CV_g$  = Genetic variation coefficient among provenances;  $CV_d$  = Phenotypic variation coefficient within provenances;  $\hat{\sigma}_A^2$  = Additive genetic variation;  $\hat{h}_m^2$  = Coefficient of mean heritability among provenances;  $\hat{h}_i^2$  = Coefficient of heritability at the individual plant level;  $\hat{h}_d^2$  = Coefficient of heritability within provenances; and their respective overestimates (Dif. %), in nine *Mimosa scabrella* provenances assuming progenies of half-sibs (HS) and progenies of mixed reproduction (MR)

similarly to the additive genetic variance, with overestimated values when the random reproduction model was employed instead of the mixed model. The heritability coefficients at the individual plant level and within progenies estimated for the mixed reproduction model were similar among the same provenances and varied from low (0.0154, provenance Turvo) to moderate (0.1267, commercial provenance from Ituporanga). In turn, the coefficient of heritability among plants within progenies varied from low (0.0775, provenance Turvo) to high (0.4561, provenance Caçador). Heritability at the mean level did not differ between the two systems, since the additive genetic variance is not taken into consideration to estimate it. These results indicate that the provenances present different potentials for selection, in other words, some present higher genetic control over the phenotype, and therefore, greater chances of genetic progress through selection. The results further demonstrate that greater gains can be obtained by selection among progenies, relatively to among plants in the experiment (mass selection) and among plants within progenies (mass selection within progenies). The use of sequential selection among and within progenies is doubtlessly the most appropriate method or otherwise, selection based on genetic values from selection indices, such as the multi-effect index (Resende and Higa 1994).

The provenances that presented highest coefficients of genetic variation and heritability (Caçador, Ituporanga - commercial, and Mandirituba), also obtained the best perspectives of selection gains. Expected gains, even with

the correction based on the mixed reproduction model, were high, reaching up to 8.89% (Ituporanga - commercial) (Table 4). Nevertheless, these estimates are preliminary. To capitalize on genetic gains, selection in the middle of the rotation cycle of the species is ideal (Zobel and Talbert 1984), which is about four to five years for *M. scabrella*.

Other studies also mention overestimates of genetic parameters in tree species when using the random instead of the mixed reproduction model. Surles et al. (1990) detected overestimates in the expected selection gains in *Robinia pseudoacacia* of up to 38% when using the random instead of the mixed model. Askew and El-kassaby (1994) corrected the estimate of the heritability coefficient at the level of individual plants in Western Red Cedar by the model of Cockerham and Weir (1984). The authors observed a 29% overestimate in heritability when the progenies were considered half-sibs. Using the same model to estimate the inbreeding coefficient among plants within progenies of *Hevea brasiliensis*, Costa et al. (2000) detected overestimates in the expected selection gains of up to 30.5%, when the random model was used instead of the mixed reproduction model. Sebbenn and Etori (2001) compared the estimates of genetic parameters in a combined progeny test with *Esenbeckia leiocarpa*, *Myracrodruon urundeuva* and *Peltophorum dubium* and detected overestimates in the additive genetic variance between 40% and 50%. Sebbenn et al. (2002) compared the estimate of genetic parameters in *Cariniana legalis* obtained by the underlying random model and the mixed reproduction model of Ritland (1989) and detected

**Table 4.** Estimate of expected gains with selection among ( $GS_e$ ), within ( $GS_d$ ), among and within sequentially ( $GS_{e+d}$ ) and their respective overestimates (Dif. %), in nine *Mimosa scabrella* provenances, considering progenies of half-sibs (HS) and mixed system (MR)

Parame- -ter (%)	Provenances									Mean perspecies
	Itararé	Pirai do Sul	Mandi- rituba	Lapa	Honório Serpa	Turvo	Caçador	Itupor. (nat.)	Itupor. (com.)	
$GS_e$	1.09	0.48	2.68	2.31	2.35	0.23	4.81	0.94	4.00	0.20
$GS_d$ HS	3.88	1.91	7.46	6.39	6.71	1.14	12.29	3.14	9.96	1.20
$GS_d$ MR	1.97	1.12	4.23	5.21	4.76	0.54	3.35	1.73	5.11	0.53
$GS_d$ Dif.	49.16	41.25	43.24	18.39	29.17	52.82	72.73	44.68	48.73	48.30
$GS_{e+d}$ HS	4.97	2.39	10.14	8.70	9.07	1.37	17.10	4.07	13.96	1.20
$GS_{e+d}$ MR	2.97	1.58	6.71	7.38	6.92	0.74	7.90	2.58	8.89	0.71
$GS_{e+d}$ Dif.	39.13	33.30	32.49	13.73	22.05	44.77	53.07	35.22	35.33	41.11

$CV_g$  = Genetic variation coefficient among progenies;  $CV_d$  = Phenotypic variation coefficient within progenies;  $\sigma_A^2$  = Additive genetic variation;  $\hat{h}_m^2$  = Coefficient of mean heritability among progenies;  $\hat{h}_i^2$  = Coefficient of heritability at the individual plant level;  $\hat{h}_w^2$  = Coefficient of heritability within progenies; and their respective overestimates (Dif. %), in nine *Mimosa scabrella* provenances assuming progenies of half-sibs (HS) and progenies of mixed reproduction (MR)

overestimates in the expected selection gains of up to 33%. Interesting in the results of this species is that, although the outcrossing rate was practically 1.0 there was interference with the estimate of the additive genetic variance, because the model used by the authors not only takes selfing into consideration, but also admits biparental crossings in its analyses (Sebbenn et al. 2002).

The overestimates of additive genetic variance, heritabilities and expected selection gains occur based on the assumption that progenies of open pollination retain ¼ of the additive genetic variance and that the coefficient of correlation of relatedness is 0.25. This presupposition is only valid when there is no inbreeding and relatedness in the parental generation, if the species is perfectly allogamous, no biparental crossings occur, and when a large number of pollinators participate in the reproduction. If one of the above-mentioned conditions is not fulfilled, the additive genetic variance is redistributed among and

within progenies and part of the genetic variance of dominance is incorporated, resulting in an overestimation of additive variance (Sebbenn et al. 2002).

Summing up, the random model of reproduction is not adequate to describe the heritability of quantitative traits in *M. scabrella*. For an enhanced reliability in the estimates of the genetic parameters used in the improvement one should use models that take the deviations of the mixed reproduction system into account.

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## Estimativas de parâmetros genéticos em populações de *Mimosa scabrella* Bentham usando os modelos aleatório e misto de reprodução

**RESUMO** - Herdabilidades e ganhos esperados na seleção foram estimados em nove procedências de *Mimosa scabrella* Bentham, usando os modelos aleatório e misto de reprodução. No modelo aleatório, o coeficiente de parentesco foi assumido como de meios-irmãos, e no misto, o parentesco foi estimado de parâmetros do sistema de reprodução. O caráter altura foi mensurado seis meses após o plantio no campo, e uma amostra de progênies de cada procedência foi analisada por eletroforese de isoenzimas, visando estimar parâmetros do sistema de reprodução. O coeficiente médio de parentesco foi de 0,392, portanto, 56,8% superior ao esperado em progênies de meios-irmãos (0,25). As estimativas médias da variância genética aditiva, herdabilidade dentro de progênies e ganhos esperados na seleção entre e dentro de progênies, calculadas com base no modelo aleatório de reprodução foram respectivamente superestimadas, em 36%, 48% e 41%, quando comparadas com as estimativas obtidas com base no modelo misto de reprodução.

**Palavras-chave:** Coeficiente de coancestria, estimativa de parâmetros, sistema de reprodução, melhoramento florestal.

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