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PLANT BREEDING - Article

Genetic parameters estimates and visual selection for leaves production in *Ilex paraguariensis*

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ABSTRACT: The selection of yerba mate superior genotypes, based on each plant leaf weight, is based on genetic parameters obtained from experimental plantations and it is practically impossible from the fourth year of age. Therefore, we estimate genetic parameters and check the feasibility of selection through notes and weight estimates of each tree at 18.5 years of age. The genetic material consists of a combined trial of provenances and progenies of half-sibs with 140 progenies from 7 provenances, installed in Ivaí, Paraná, Brazil, in a randomized block design with 10 repetitions. The genetic control of leaf production is of low magnitude ($\hat{h}_a^2 = 0.175042 \pm 0.0393$) revealing high influence of the environment. The additive genetic correlations between the real weight of leaves × notes and real weight of leaves × visually estimated weight were of high magnitude (higher than 88%). Thus, the selection based on the leaves weight can be carried out without major losses in genetic gains by both methodologies when the purpose is the sexual selection, in which case the sort order has no importance. In the case of vegetative propagation, aiming clonal plantations, in which only the plants with the highest genotypic values should be selected, the selection by means of notes and leaves weight estimates proved to be inefficient.

Key words: genetic correlations, yerba mate, silviculture, progeny trial.

INTRODUCTION

In the 1990s the breeding programs of yerba mate (*Ilex paraguariensis var. Paraguariensis St.* Hill.) were started in Brazil in order to obtain clones and genetically superior seeds with emphasis on silvicultural variables relating to adaptation, leaf mass production, resistance to pests and diseases, defoliation and branch type. Such programs, conducted by Embrapa and Epagri (Sturion and Resende 2010), rely on the evaluation of provenances and half-sibs progenies in various locations, thus constituting the base populations for genetic improvement. Today, we seek to include in the breeding programs of the species characteristics related to the quality of their derived products. Among these, the content of chemical compounds has relevance to influence directly the characteristics of the commercial products and their biological effects (Cardozo Junior et al. 2010).

The evaluation of genetic materials in field trials aims to infer on their genotypic values and based on that to sort them. There is no interest in estimating the phenotypic means of the genetic material in the trials but in estimating its genetic means (or genotypic values), or its future means when planted again in commercial plantations. The genotypic values are the real values of cultivation and use (VCU) (Borges et al. 2010; Pompeu Junior et al. 2013).

In perennial plants like yerba mate, selection should be made by individual, based on their additive genetic value when the objective is the production of improved seeds and on the genotypic value when the purpose is clonal plantations (Barros Rocha et al. 2006). The additive genetic variance is the most important component of the variance, it is the principal cause of similarity between relatives and determining the genetic properties of the population and the response of the population to the selection (Neves et al. 2011).

The heritability in the narrow sense becomes important in sexually propagated species and species of long cycles, such as yerba mate. The heritability allows estimating the gain possibilities for a given feature. Estimates of genetic parameters in perennial species are particularly interesting for breeding due to the great responsibility of the selection, the difficulty of accomplishing it in a short time and the almost total lack of knowledge lack of the response to a selection made for the various characteristics of a tree. In mixed models, the candidates' trees for selection are unobservable random variables belonging to more than one population and the selection also depends on unknown fixed effects (Resende 2007).

The tree selection, especially for clonal plantations, must be extremely precise and held in ages closest as possible to the exploitation age for ranking the trees with the largest genotypic values. However, the selection of yerba mate trees based on its leaves weight is extremely laborious, mainly from the fourth year. This activity includes pruning each tree, removing leaves and thin branches (up to 7 mm) and its weighing (Santin et al. 2015).

The use of indirect methods for assessing the production of yerba mate plants can be an alternative for the species breeding, especially for the possibility of reduction in the evaluation time and consequently reduction of the expenses generated by the activity. However, there is no description in the literature about visual estimation methodologies developed for forest species.

Based on these considerations, this study aimed to estimate genetic parameters and check the feasibility of selection through notes and weight estimates of each tree.

MATERIAL AND METHODS

The genetic material consists of a combined trial of provenances and progenies of half-sibs, installed in Ivaí, state of Paraná, Brazil, in March 1997, as detailed in Cardozo Junior et al. (2010) and Sturion and Resende (2010). Briefly, it is composed of provenances from Antônio Olinto (PR), Barão de Cotegipe (RS), Cascavel (PR), Colombo (PR), Ivaí (PR), Pinhão (PR) and Quedas do Iguaçu (PR).

On-site testing predominantly occurs Dark-red Moderate Alic Oxisol A class soils, clayey, undulated relief (Sturion and Resende 2010). The area is under the influence of the climate type CFA — mesothermal humid subtropical climate with hot summers and infrequent frosts, with a tendency of rainfall concentration in the summer months without dry season.

The real weight of leaf biomass (leaves and branches up to 7 mm) was obtained by weighing them with a dynamometer at 18.5 years of age of the plants. This pruning was made in August 2015, 2 years after the previous one. Additionally, the weight of the leaf biomass was evaluated by visual estimates and score assigned by 1 to 10, based on the authors' experience, by 5 trained evaluators.

Targeting the use of optimal techniques of genetic evaluation involving both the prediction of genetic values and the estimation of variance components under statistical models at the level of individuals, estimates of genetic and phenotypic parameters were performed by the genetic-statistical program SELEGEN-REML/BLUP (Resende 2007). We used model 5 of the software that includes experiments in blocks of half-sibs progenies, several plants per plot and several populations. When the origins are considered both as fixed or random genetic effects, for individuals' selection, it must be added the individual genetic values predicted to the effects of provenances. Thus, individuals from different provenances can be compared directly for their new breeding values. In this case there are estimators and predictors models described below (mixed linear model, univariate additive model, multi-populations) according to Resende (2007).

$$y = Xb + Za + Wc_1 + Qr + e,$$

where: y, b, a, c_1, r, and e are data vectors, fixed effects (blocks), random additive genetic effects, random effects relating to progeny plots (subplots), populations (or race), the random effects of plots for the provenances and random errors, respectively; X, Z, W, and Q are the incidence matrices for b, a, c, and r, respectively.

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_{c_1}^2 + \sigma_r^2 + \sigma_e^2}$$

where h^2 is the individual heritability in the narrow sense.

$$c^2 = \frac{\sigma_c^2}{\sigma_a^2 + \sigma_c^2 + \sigma_r^2 + \sigma_e^2}$$

where c^2 is the correlation between individuals due to the common environment of the plot concerning to progenies (subplots).

$$r^2 = \frac{\sigma_r^2}{\sigma_a^2 + \sigma_c^2 + \sigma_r^2 + \sigma_e^2}$$

where r^2 is the phenotypic intraclass correlation between individuals of the same origin in different blocks.

The iterative estimators of variance components by REML via EM algorithm are:

$$\hat{\sigma}_e^2 = [y'y - \hat{b}'X'y - \hat{a}'Z'y - \hat{c}'\ W'y - \hat{r}'Q'y]/[N - r(x)];$$

$$\hat{\sigma}_a^2 = [\hat{a}'A^{-1}\hat{a} + \hat{\sigma}_e^2\ tr\ (A^{-1}\ C^{22})]/q;$$

$$\hat{\sigma}_c^2 = [\hat{c}'\hat{c} + \hat{\sigma}_e^2\ tr\ C^{33}]/s_1;$$

$$\hat{\sigma}_r^2 = [\hat{r}'\hat{r} + \hat{\sigma}_e^2\ tr\ C^{44}]/t.$$

where: s and t represent the number of plots relating to progenies and the number of provenances, respectively; C^{22}, C^{33}, and C^{44} come from the matrix inverse coefficient of the mixed model equations.

The following genetic correlations were estimated by the model 102 of SELEGEM REML/BLUP Program: real weight of leaves × notes; leaves real weight × leaves estimated weight.

RESULTS AND DISCUSSION

The individual heritabilities in a narrow sense, obtained for leaves weight at 18.5 years of age, was of low magnitude ($\hat{h}_a^2 = 0.175042 \pm 0.0393$). However, such heritability is associated with a standard deviation of a small magnitude compared to the magnitude of heritability, ensuring that it does not reach the 0 via confidence interval lower limit (given by approximately 2 times the standard deviation), which denotes lack of genetic variability (Table 1).

We had the presence of significant genetic variability among progenies for the real weight of leaf biomass as demonstrated by individual genetic variation coefficients (CVi%) of 37%. The greater the amount of genetic variation, the easier is to find individuals who will provide higher gains with the selection. However, this genetic variability is associated with high values of experimental variation coefficient (CVe%), providing individual heritability of low magnitude, revealing high influence of the environment for this feature. Despite high magnitude (43%), the experimental variation coefficient value is consistent with the values obtained for the character evaluated in field conditions for yerba mate (Sturion and Resende 2010). However, the relative variation coefficient that expresses the ratio of genetic variation coefficient and experimental coefficient of variation was above 86%. This value associated with the 10 repetitions used in this work demonstrates good genetic gain possibilities with the selection.

Table 1. Estimates of genetic parameters for leaf biomass weight of yerba mate at 18.5 years of age (REML Single).

Parameters	Real weight	Weight 1	Score 1	Weight 2	Score 2	Weight 3	Score 3	Weight 4	Score 4	Weight 5	Score 5
$\hat{\sigma}^2_a$	6.8771	2.9690	0.4405	1.3674	0.5298	1.2824	0.3955	2.1358	0.9932	2.0419	0.8917
$\hat{\sigma}^2_{parc}$	4.7289	4.0065	0.5213	1.0968	0.3986	1.0622	0.5357	1.8253	0.8219	2.3372	0.8763
$\hat{\sigma}^2_{proc}$	5.7118	2.7991	0.5042	1.2108	0.5919	1.5337	0.6778	1.8232	0.9867	2.5425	0.8888
$\hat{\sigma}^2_e$	21.9706	13.7287	1.9660	4.4531	1.8540	4.9906	1.9606	8.0119	3.2576	10.2732	4.1659
$\hat{\sigma}^2_f$	39.2884	23.5033	3.4320	8.1280	3.3743	8.8688	3.5697	13.7961	6.0594	17.1948	6.8227
$\hat{h}^2_a$	0.175042 ± 0.0393	0.126324 ± 0.0335	0.128343 ± 0.0337	0.168229 ± 0.0386	0.157011 ± 0.0373	0.144592 ± 0.0358	0.110803 ± 0.0313	0.154811 ± 0.0370	0.163905 ± 0.0380	0.118753 ± 0.0324	0.130697 ± 0.0340
c^2_{parc}	0.1204	0.1705	0.1519	0.1349	0.1181	0.1198	0.1501	0.1323	0.1356	0.1359	0.1284
c^2_{prov}	0.1454	0.1191	0.1469	0.1490	0.1754	0.1729	0.1899	0.1322	0.1628	0.1479	0.1303
CVgi%	37.2513	27.1610	22.7432	25.9816	20.3640	18.8041	14.2784	22.5915	20.9198	24.0316	23.7841
Vgp%	18.6257	13.5805	11.3716	12.9908	10.1820	9.4020	7.1392	11.2958	10.4599	12.0158	11.8920
CVe%	43.2032	40.6971	32.5822	31.4997	24.6108	23.7996	21.6806	28.6193	25.6148	34.8923	32.6662
OA	7.0398	6.3440	2.9182	4.5007	3.5743	6.0222	4.4047	6.4690	4.7638	5.9462	3.9703

$\hat{\sigma}^2_a$ = Additive genetic variance; $\hat{\sigma}^2_{parc}$ = Environmental variance between plots; $\hat{\sigma}^2_{proc}$ = Genetic variance among provenances; $\hat{\sigma}^2_e$ = Residual variance within plots; $\hat{\sigma}^2_f$ = Individual phenotypic variance; h^2_a = Individual heritability in the narrow sense of the block; c^2_{parc} = Determination coefficient of plot effects; c^2_{prov} = Determination coefficient of provenance effects; CVgi% = Individual additive genetic variation coefficient; Vgp% = Genotypic coefficient of variation between progenies; CVe% = Experimental coefficient of variation; OA = Overall average.

The individual heritability in the narrow sense of the block, estimated for the real weight of leaf biomass was 17% at 18.5 years of age of the plantation, a value considered of low magnitude. This means that much of the phenotypic variability of this character is due to environmental variation. Thus, the selection based on the phenotype can be inefficient. For 5 distinct populations of yerba mate, Sturion and Resende (2005) detected individual heritability in the narrow sense of the block, from low (around 20%) to average magnitude (around 40%), estimated for the leaf mass weight, at the second harvest by the 6-year-old combined provenance and progeny test.

The coefficients of determination of the plots effects (c^2_{parc}) were 12%, indicating that 12% of the total variability was due to environmental variation between plots; this variation is mainly due to soil variation between plots. According to Sturion and Resende (2010), c^2_{parc} values observed in good experiments on perennial plants are approximately around 0.10 (where the estimated heritability is around 0.30), or 10% of the total variation in block. Thus, for an individual heritability around 0.30, $c^2 \leq 0.10$ can be classified as low and $c^2 > 0.10$ can be classified as high, allowing to infer the spatial variability within the blocks. In this case, a 12% value is very close to the 10% one, indicating that the spatial variability within the block is relatively small.

For calculation of the genetic gains, 2 situations should be considered: (i) when the selected genetic material is vegetatively propagated for planting; (ii) when it is propagated through seeds. In the first situation, with the component $\hat{\sigma}^2_a$, the selection will explore $\hat{\sigma}^2_a + \hat{\sigma}^2_d$. In the second situation, the selection will only explore the component $\hat{\sigma}^2_a$, since that in propagation by seed the genotypic combinations of selected plants crumble and the dominance effects manifest themselves only at the level of genotypes and therefore are not passed through gametes as in the case of average effects of the genes (Sturion and Resende 2010). In the case of sexual strategy and considering the installation of a seed orchard with yerba mate seedlings from the 100 trees with larger additive genetic values it is predicted a gain of 5.84 kg·tree⁻¹, raising the average settlement for 12.8 kg·tree⁻¹, which led to the production of 20 thousand kg·ha⁻¹, taking into account a stocking of 1,666 plants·ha⁻¹ (Table 2).

The smaller the number of selected individuals, the greater the genetic gain. However, to determine the genetic gain, we should take into account the effective population size appropriate for have security in the selection, considering the inbreeding in planting generation. Considering the selection of 100 individuals, the corresponding effective population size is 50. In this

Table 2. Additive genetic values predicted for the 31 best individuals selected (including individual of order 100) for leaf production of yerba mate plantation with 18.5 years of age.

Order	Block	Family	Provenance	Tree	f	a	u + a	Gain	N. mean	Ne	d	G	u + g
1	7	61	3	3	41.80	8.53	15.57	8.53	15.57	1.00	3.47	12.00	19.04
2	7	3	1	2	35.70	8.02	15.06	8.27	15.31	2.00	3.25	11.27	18.31
3	5	10	1	3	37.00	7.75	14.79	8.10	15.14	3.00	2.35	10.10	17.14
4	5	53	3	6	32.00	7.69	14.73	8.00	15.04	4.00	2.23	9.92	16.96
5	3	53	3	3	28.75	7.47	14.51	7.89	14.93	4.50	2.08	9.55	16.59
6	5	10	1	1	35.40	7.44	14.48	7.82	14.86	5.10	2.15	9.59	16.63
7	4	25	1	5	35.80	7.42	14.46	7.76	14.80	6.10	3.14	10.56	17.60
8	6	5	1	4	31.10	7.20	14.24	7.69	14.73	7.10	2.28	9.48	16.52
9	4	53	3	1	32.10	7.20	14.24	7.64	14.68	7.20	1.90	9.10	16.14
10	7	14	1	2	32.95	7.12	14.16	7.58	14.62	8.20	2.71	9.83	16.87
11	4	15	1	2	33.65	7.07	14.11	7.54	14.58	9.20	2.60	9.67	16.71
12	6	69	3	4	35.15	6.98	14.02	7.49	14.53	10.20	3.01	9.99	17.03
13	6	93	4	3	27.80	6.98	14.02	7.45	14.49	11.20	1.97	8.95	15.99
14	4	10	1	4	25.30	6.95	13.99	7.42	14.46	11.40	1.82	8.77	15.81
15	5	4	1	3	38.30	6.86	13.90	7.38	14.42	12.40	2.76	9.62	16.66
16	6	21	1	2	33.00	6.74	13.78	7.34	14.38	13.40	2.61	9.35	16.39
17	6	10	1	5	24.25	6.68	13.72	7.30	14.34	13.30	1.64	8.32	15.36
18	7	64	3	2	28.80	6.44	13.48	7.25	14.29	14.20	2.22	8.65	15.69
19	5	79	4	5	27.00	6.39	13.43	7.21	14.25	15.20	1.84	8.23	15.27
20	7	93	4	1	24.55	6.39	13.43	7.17	14.21	15.80	1.58	7.97	15.01
21	7	10	1	4	24.80	6.39	13.43	7.13	14.17	15.90	1.45	7.83	14.87
22	5	8	1	5	28.20	6.37	13.41	7.09	14.13	16.50	1.99	8.36	15.40
23	4	53	3	5	27.60	6.35	13.39	7.06	14.10	16.60	1.33	7.68	14.72
24	6	5	1	2	26.30	6.29	13.33	7.03	14.07	17.20	1.67	7.96	15.00
25	5	10	1	2	29.00	6.22	13.26	7.00	14.04	16.90	1.34	7.56	14.60
26	6	65	3	5	27.85	6.21	13.25	6.97	14.01	17.80	1.97	8.18	15.22
27	5	93	4	3	24.20	6.20	13.24	6.94	13.98	18.20	1.45	7.65	14.69
28	4	53	3	6	26.50	6.14	13.18	6.91	13.95	18.30	1.19	7.33	14.37
29	7	96	4	1	23.00	6.07	13.11	6.88	13.92	19.10	1.65	7.72	14.76
30	7	96	4	6	23.00	6.07	13.11	6.85	13.89	19.70	1.65	7.72	14.76
...	...	...	...	...	...	...	...	...	...	...	...	...	...
100	3	79	4	5	19.90	5.02	12.01	5.84	12.87	45.99	0.92	5.94	12.98

f = Individual phenotypic value or field measurement; a = Predicted additive genetic effect; u + a = Predicted additive genetic value; Ne = Effective population size; d = Predicted genetic effect of dominance (assuming a certain average degree of dominance in the case of half-sib progenies); G = a + d = Predicted genotypic effect; u + g = Predicted genotypic value; N. mean = New mean.

case, the effective population size should be analyzed in 2 ways: (i) if the selection aims to seed production in one generation; and (ii) if the selection aims to seed production and continuous improvement of the material in the future generations. In the first case, the only concern is to avoid inbreeding depression in individuals who will be part of the plantations, while in the second, the biggest problems are the inbreeding that is being accumulated through generations due to the crossing between related individuals and the risk of not achieving the selective limit, due to a loss of favorable alleles by genetic drift (Sturion and Resende 2010). In the case of an effective size around 80, alleles with more than 5% of frequency are retained in the sample and therefore only the rare ones are not retained (Raposo et al. 2007). Effective size of 40 presents no problem if the objective is seeds production in one generation. However, when the goal is a continuous improvement, we should monitor the new effective population size obtained, in this case, by the recombination of individuals from different provenances. Note that there will be a cross between individuals of different populations, a fact that will contribute to the increase of the genetic basis and consequently to reduce inbreeding levels (Labate et al. 2009).

Asexual strategy present advantages, mainly the standardization of crops and an increased productivity (Wendling et al. 2007; Reis et al. 2011; Baccarin et al. 2015; Kratz et al. 2015). If we seek to achieve maximum genetic gain by selecting the best clones, it is appropriate to make the selection, the closer to the age of commercial exploitation, or when the plantation stabilizes its production per tree. In general, it is recommended to use seven to 30 clones in a clonal forestry program (Xavier et al. 2013).

It is important to note that for the clonal strategy there is no concern about the effective population size in which the clones are being selected and that the degree of relatedness between individuals involved in the selection is not so important. The importance of the degree of relatedness is restricted only to the fact that the related clones could be more vulnerable to pests and pathogens and would not be related to inbreeding depression. To increase the chances of success in the clonal forestry programs we must maintain a continuous monitoring of the selected clones, selection of new clones and replacement of those with an income below expectations.

Most of the characters economically important are complex in their inheritance and may involve several related characters. When a desired character is difficult to be selected because of its identification difficulty, measurement or due to its low heritability, the use of a character correlated with high heritability and easily measurable, enables greater effectiveness in its selection (Goldenberg 1968). Another alternative would be to check through notes or other variable that represents the feature under selection. According Moraes et al. (2015), positive genetic correlations and a high magnitude among the characteristics show that they can be regarded as a single case in the selection, when the direction of the selection is the same, without much injury to any of the features. No significant correlations indicate independence between them. High negative correlations may impair simultaneous selection and therefore deserve a special care during the selection.

Anjos Cutrim et al. (1997) verified if the visual selection can identify differences in productive capacity between individuals of the F2 generation of rice (*Oryza sativa* L.) grains and if there are differences among the ability of selectors involved in 3 segregating populations coming from triple crosses. They used 11 selectors with different experience in culture, to visually identify productive plants in the F2 generation. The selectors differed in ability to visually identify the productive plants and this ability was not associated with the selector experience with the plant.

The additive genetic correlations obtained, all above 85%, between the weight of yerba mate leaves reached through the dynamometer with visual estimates of weights and the evaluation of the most productive trees by notes of 5 evaluators, showed high magnitude. This indicates that selection for yerba mate leaf weight, obtained at the population age of 18.5 years, can be performed without major damage indirectly by notes and through estimates of its weights, when the target is the sexual strategy (Table 3).

In the sexual strategy, the order of the selected individuals is not so important since the best ones are mostly contemplated in the sample. Nevertheless, when the goal is to select clones, in which the purpose is to select individuals of high leaf biomass production, the order of the selected individuals is crucial. In this case, the selection either by notes or by the real weight estimates was ineffective (Table 4).

Table 3. Additive (above diagonal) and phenotypic (below diagonal) genetic correlations among real weight of yerba mate leaf biomass with the weight visually estimated and the weight obtained by notes.

Evaluator	Variable	Real weight	W1	N1	W2	N2	W3	N3	W4	N4	W5	N5
	Real weight score	1.00	0.94	0.92	0.90	0.89	0.90	0.88	0.95	0.93	0.91	0.90
1 (W1)	Estimated weight	0.87	1.00	0.94	0.90	0.86	0.89	0.87	0.93	0.91	0.91	0.88
1 (N1)	Score	0.86	0.90	1.00	0.89	0.88	0.90	0.88	0.91	0.92	0.90	0.89
2 (W2)	Estimated weight	0.82	0.80	0.81	1.00	0.96	0.90	0.86	0.93	0.92	0.88	0.88
2 (N2)	Score	0.81	0.77	0.81	0.93	1.00	0.88	0.88	0.90	0.92	0.87	0.88
3 (W3)	Estimated weight	0.73	0.71	0.71	0.69	0.64	1.00	0.96	0.92	0.92	0.91	0.89
3 (N3)	Score	0.72	0.71	0.73	0.70	0.68	0.93	1.00	0.89	0.91	0.87	0.88
4 (W4)	Estimated weight	0.84	0.83	0.80	0.79	0.74	0.88	0.84	1.00	0.97	0.92	0.92
4 (N4)	Score	0.80	0.77	0.79	0.76	0.74	0.88	0.88	0.94	1.00	0.91	0.93
5 (W5)	Estimated weight	0.71	0.69	0.70	0.67	0.62	0.87	0.82	0.84	0.84	1.00	0.95
5 (N5)	Score	0.70	0.66	0.70	0.66	0.63	0.83	0.81	0.82	0.85	0.93	1.00

W = Weight; N = Notes.

Table 4. Ordering of 30 trees with the largest predicted genotypic values according to real weight with the estimated weight and the weight measured by score (evaluator 1*).

Real weight (kg·tree⁻¹)				Weight 1				Score 1			
Order	Block	Family	Tree	Order	Block	Family	Tree	Order	Block	Family	Tree
1	7	61	3	1	5	10	3	1	7	93	6
2	7	3	2	2	7	14	2	2	5	79	4
3	5	10	3	3	7	3	2	3	5	79	5
4	5	53	6	4	7	61	3	4	7	3	2
5	3	53	3	5	7	61	4	5	7	96	1
6	5	10	1	6	5	10	1	6	3	93	6
7	4	25	5	7	5	10	2	7	3	82	1
8	6	5	4	8	7	93	6	8	6	70	1
9	4	53	1	9	5	100	1	9	3	79	2
10	7	14	2	10	6	165	4	10	4	79	1
11	4	15	2	11	5	79	4	11	4	79	2
12	6	69	4	12	5	79	5	12	6	93	3
13	6	93	3	13	7	153	5	13	7	57	4
14	4	10	4	14	5	8	5	14	6	5	2
15	5	4	3	15	6	10	5	15	6	79	2
16	6	21	2	16	4	25	5	16	6	79	3
17	6	10	5	17	6	93	3	17	5	70	3
18	7	64	2	18	7	96	1	18	7	93	1
19	5	79	5	19	6	69	4	19	7	93	2
20	7	93	1	20	7	10	1	20	3	53	2

Table 4. continuation...

Real weight (kg·tree⁻¹)				Weight 1				Score 1			
Order	Block	Family	Tree	Order	Block	Family	Tree	Order	Block	Family	Tree
21	7	10	4	21	7	10	4	21	5	100	1
22	5	8	5	22	5	53	6	22	7	8	3
23	4	53	5	23	3	93	6	23	6	57	3
24	6	5	2	24	7	64	2	24	4	81	6
25	5	10	2	25	5	71	4	25	4	10	4
26	6	65	5	26	7	57	5	26	6	21	2
27	5	93	3	27	3	64	6	27	5	8	5
28	4	53	6	28	6	5	2	28	3	96	6
29	7	96	1	29	6	21	2	29	3	88	2
30	7	96	6	30	5	93	3	30	7	81	2

*The correlations and ordering obtained by other evaluators were similar.

CONCLUSION

The genetic control of leaves weight is of low magnitude. The installation of combined provenance and progeny trials to select individuals based on their breeding values, using the individual values and family information, is appropriate to increase the yerba mate leaf mass production. The additive genetic correlations among the real weight of biomass and the visual estimates of weight and scores were of high magnitude. The selection based on leaf biomass weight can be used without major losses by both methodologies, only when the objective is the sexual strategy.

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