ARTICLE

Performance of yerba mate progenies in Southern Brazil

Crop Breeding and Applied Biotechnology
25(4): e536525410, 2025
Brazilian Society of Plant Breeding.
Printed in Brazil
http://dx.doi.org/10.1590/1984-70332025v25n4a55

Débora Caroline Defensor Benedito[1*], Cristiane Aparecida Fioravante Reis[2], Paulo Alfonso Floss[3] and Ivar Wendling[2]

Abstract: *The study evaluated the performance of yerba mate progenies in southern Brazil. It assessed the commercial biomass yield (in kilograms per plant) of 58 open-pollinated progenies. The experimental design followed a randomized block structure, with 10 replications, three plants per plot, and spacing of 3 m × 1.5 m. Data were collected at 18-month intervals from 2019 to 2023. In the individual deviance analyses, significant progeny effects were observed using the Likelihood Ratio Test at a 5% probability level. These individual analyses indicated satisfactory performance of the yerba mate progenies, and the selection of superior trees led to substantial gains for the breeding of the species. However, in the joint analysis across sites and harvests, none of the effects were statistically significant.*

Keywords: Ilex paraguariensis*, commercial biomass, REML/BLUP, selection gains, tree breeding*

INTRODUCTION

Yerba mate (*Ilex paraguariensis* A. St.-Hil.) plays an important role in the development of various localities in the southern region of Brazil. It is the primary non-timber forest product in this region and the second most significant at the national level (Viana et al. 2018). Its leaves are traditionally consumed in various beverages, including mate tea, chimarrão, and tereré (Paiva et al. 2020). Furthermore, yerba mate possesses significant potential for the development of a wide range of products, such as cosmetics, personal hygiene products, nutraceuticals, functional foods, natural dyes, antioxidants, and food preservatives (Cardozo Junior and Morand 2016).

In 2024, the production of cultivated yerba mate in Brazil reached 841,255 tons, with a production value around 1 billion reais, and an average yield of 9.325 tons per hectare (IBGE 2024). Despite its economic and cultural importance, the use of outdated technologies and seeds of low genetic and physiological quality has limited the yield of the species for decades (Simeão et al. 2002, Sturion and Resende 2010a). According to Penteado Junior and Goulart (2019), the yield of yerba mate plantations could be significantly increased to 20 tons per hectare if the production system were based on advanced techniques, such as those proposed by the Erva 20 System and the use of high-yield cultivars.

The pursuit of more productive cultivars adapted to cultivation environments has led to the establishment of yerba mate genetic breeding programs. These programs are based on recurrent selection, a process characterized by

***Corresponding author:**
E-mail: debora.defensor@ufpr.br

Received: 04 September 2025
Accepted: 06 November 2025
Published: 13 November 2025

[1] Universidade Federal do Paraná, Silvicultura,
Avenida Prefeito Lothário Meissner, 632,
80060-000, Curitiba, PR, Brazil
[2] Embrapa, Avenida W3 Norte (Final), s/n,
70770-901, Brasília, DF, Brazil
[3] EPAGRI, Servidão Ferdinando Ricieri Tusset,
s/n, 89803-904, Chapecó, SC, Brazil

successive selective cycles of field evaluations, selection of the most suitable trees, and recombination (Resende et al. 1995), followed by cloning of the best trees for recommendation of future cultivars. Consequently, the establishment of open-pollinated progeny trials in multiple locations constitutes an important step in this cycle to assess whether genotype-by-environment interaction (G×E) occurs (Sturion and Resende 2010a). Therefore, this study aims to evaluate the performance of yerba mate progenies across different locations in southern Brazil and select the best trees for cloning and recombination.

MATERIAL AND METHODS

Germplasm and experimental environmental conditions

This study is part of the Brazilian Agricultural Research Corporation (Embrapa) Yerba Mate Breeding Program. The program involves an extensive experimental network, which makes it possible to deepen knowledge about the germplasm in the southern region of Brazil.

The germplasm utilized in the experimental network currently under evaluation consists of 58 open-pollinated progenies of yerba mate (*Ilex paraguariensis* A. St.-Hil.), and nine clones were used as controls, and also included in the statistical analysis. The seeds of the progenies were collected from first-, second-, and third-generation parent trees originating from 19 different provenances. The seeds of the nine first-generation progenies were collected from superior native yerba mate parent trees in the states of Mato Grosso do Sul (MS), Paraná (PR), Santa Catarina (SC), and Rio Grande do Sul (RS). The seeds of the 46 second-generation progenies were collected from superior parent trees selected in first-generation progeny trials established in 1997 in Chapecó, SC, and Ponta Grossa, PR. The three third-generation progenies were derived from superior parent trees collected in a second-generation progeny trial established in Ponta Grossa, PR (1997) (originating from a first-generation trial established in Colombo, PR (1988)).

The experimental network was established in eight locations across the states of Paraná (municipalities of Cruz Machado and São Mateus do Sul), Santa Catarina (Catanduvas, Chapecó/Guatambu, and Major Vieira), Rio Grande do Sul (Áurea and Ilópolis), and Mato Grosso do Sul (Dourados).

The environmental conditions of the experimental sites are presented in Table 1. The mean values for rainfall and temperatures were calculated based on data collected by the National Institute of Meteorology (INMET) between 2016 and 2023. The climate type was defined according to the Köppen-Geiger classification. Soil classification was conducted in accordance with the methodology outlined by Santos et al. (2018). The experiments were established in July 2016, employing a completely randomized block design, with 10 replications of three plants per plot, spaced at 3.0 m x 1.5 m. Due to technical constraints, the experiment established in Ilópolis, RS, comprised six replications.

The production of yerba mate seedlings and the experiments were established according to the standard protocol for yerba mate plantations (Penteado Junior and Goulart 2019). Based on soil analysis from each location, planting and maintenance fertilization were carried out according to Wendling and Santin (2015).

Table 1. Environmental conditions of the sites where the yerba mate progeny trial network was established in the states of Rio Grande do Sul, Santa Catarina, Paraná, and Mato Grosso do Sul

Location	Latitude South	Longitude West	Altitude (m)	Average annual precipitation (mm)	Average annual temperature (°C)			Climate type [1]	Soil classification
					Max	Mean	Min		
Áurea, RS	27° 38’ 1.85’’	51° 59’ 59.61’’	562	1160	22.6	18.0	12.6	Cfa	Entisols
Ilópolis, RS	28° 53’ 31.37’’	52° 7’ 15.42’’	575	1554	22.7	17.5	12.2	Cfa	Inceptisols
Catanduvas, SC	27° 3’ 46.50’’	51° 44’ 3.60’’	915	1138	22.6	19.3	15.6	Cfb	Inceptisols
Chapecó/Guatambu, SC	27° 05’ 16.46’’	52° 37’ 54.40’’	676	1692	23.9	19.6	14.4	Cfa	Oxisols
Major Vieira, SC	26° 18’ 20.33’’	50° 21’ 23.72’’	810	1129	21.8	17.3	11.6	Cfb	Inceptisols
Cruz Machado, PR	25° 57’ 24.39’’	51° 1’ 57.64’’	980	1252	20.9	16.5	10.9	Cfb	Inceptisols
São Mateus Sul, PR	25° 54’ 40.00’’	50° 26’ 34.00’’	835	1152	22.0	17.6	12.2	Cfa	Inceptisols
Dourados, MS	22° 16’ 50.00’’	54° 48’ 58.00’’	568	734	25.9	23.7	20.1	Cwa	-

[1] Climate type: Cfa = Subtropical climate with hot summer; Cfb = Temperate climate with mild summer; Cwa: Humid subtropical climate with dry winter and hot summer.

In each experimental site, seedling survival was measured, and replanting was carried out 30 days after planting, when the mortality rate exceeded 5%. From 3 years of age, survival was assessed every 18 months.

Data collection and analysis

The collection of data commenced three years after the initiation of the experiments and continued until the seventh year, with intervals of 18 months, thus encompassing four harvests (2019, 2021, 2022, and 2023) evaluated for each experiment. Harvest 1: conducted at 3 years of age (winter); harvest 2: 4.5 years (summer); harvest 3: 6.1 years (winter); harvest 4: 7.6 years (summer). At each harvest, the commercial biomass yield of yerba mate (leaves and fine branches smaller than 7 mm) was evaluated in kg plant^{-1}, following the methodology developed by Wendling et al. (2016). Data analyses were conducted using the mixed model procedure, Restricted Maximum Likelihood/Best Linear Unbiased Prediction (REML/BLUP), according to the protocol established by Resende (2007a), and implemented through the Statistical System and Computerized Genetic Selection (SELEGEN - REML/BLUP) (Resende 2007b).

For the individual analyses, performed separately by harvest and location, the statistical model described in Equation 1 of the SELEGEN - REML/BLUP software was applied, considering open-pollinated progenies of allogamous species (Resende 2007b).

$$y = Xr + Za + Wp + e \qquad (1)$$

where *y*: represents the data vector, *r*: the vector of fixed effects for replication added to the overall mean, a: the vector of random individual additive genetic effects, *p*: the vector of random plot effects, and e: the vector of random residual effects or errors. The uppercase letters represent the incidence matrices for the respective effects.

The joint analysis was performed only for the experiments in which treatment effects were significant in the individual deviance analyses. In this case, the statistical model presented in Equation 2 of SELEGEN - REML/BLUP was employed, which allows the simultaneous consideration of multiple sites and harvests.

$$y = Xm + Za + Wp + Ts + Qi + e \qquad (2)$$

where *y*: represents the data vector; *m*: represents the vector of fixed effects for the measurement-repetition-site combinations added to the overall mean; *a*: is the vector of random individual additive genetic effects; *p*: is the vector of random plot effects; *s*: is the vector of random permanent environment effects; *i*: is the vector of random genotype-by-environment interaction effects; and *e*: is the vector of random error or residual effects. The uppercase letters denote the incidence matrices for the respective effects.

The significance of the effects was evaluated using the likelihood ratio test (LRT) in both the individual and combined analyses. Breeding values ($u + g$) and additive breeding values ($u + a$) at the individual level were estimated using Best Linear Unbiased Prediction (BLUP). Based on these estimates, the best clone and parent tree candidates were selected using a selection intensity of 1%, totaling 10 individuals of each. From the two equation models used to perform the analyses several genetic parameters were estimated.

RESULTS AND DISCUSSION

The highest survival rates across the different harvests were observed in the trials located in Rio Grande do Sul (Áurea > 89% and Ilópolis > 92%) (Figure 1). Within the domain of forestry trials, a survival rate is high when it exceeds 90% (Floss et al. 2022), indicating adaptation to the experimental climatic conditions.

However, most survival rates obtained across locations and harvests were less than 90%. It is imperative to acknowledge that certain trials were confronted with extreme weather conditions and operational constraints, which were recorded descriptively. The trial in Áurea, RS, was impacted by a fire in 2021, which compromised replicates 9 and 10. In the subsequent year, this trial was confronted with a severe drought, during which several adult plants experienced complete desiccation, resulting in an apparent decline in survival (78%) during the third harvest conducted in 2022. Nevertheless, despite the absence of replanting, survival rates exhibited an increase in the fourth harvest (89%), attributable to the natural regeneration of some individuals previously classified as dead in the preceding harvest. In 2023, the progenies cultivated in Major Vieira, SC, experienced an infestation by the yerba mate borer (*Hedypathes betulinus*). Despite the

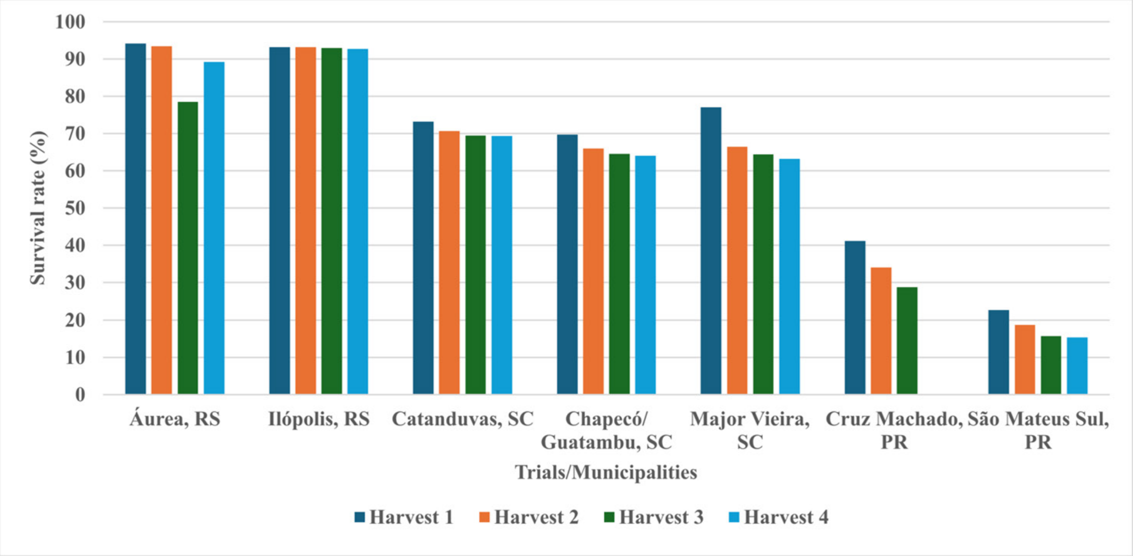

Figure 1. Estimates of survival rates in five open-pollinated progeny trials of *Ilex paraguariensis* (yerba mate) in Santa Catarina and Rio Grande do Sul, Brazil.

implementation of pest control measures, the infestation had a deleterious effect on the survival rate of the fourth harvest (63%).

In contrast to the trials in Rio Grande do Sul, the trials conducted in Paraná (Cruz Machado (survival = 0%) and São Mateus do Sul (15%)) and Mato Grosso do Sul (Dourados 0%) showed the lowest survival rates. The experiment in Cruz Machado, PR, was severely affected by frost following replanting in the first year, resulting in a high mortality rate and low average commercial biomass. The trials implemented in São Mateus do Sul, PR, and Dourados, MS, were significantly affected by inadequate seedling maintenance due to management and operational problems. These trials were excluded from deviance analysis and the selection of superior trees due to the substantial loss of individuals.

A variety of factors have been demonstrated to exert a direct influence on the initial establishment of yerba mate plantations, including frost, drought, weed competition, and pest infestations. The most critical phase for the survival of yerba mate seedlings in the field occurs in the initial months after planting (Santin et al. 2015). Furthermore, the species exhibits sensitivity to direct sunlight during the seedling stage, necessitating immediate protection after planting (Sturion and Resende 2010a).

The mean commercial biomass across diverse harvests and locations ranged from 0.57 kg plant^{-1} (or 1.27 tons ha^{-1}: Cruz Machado, PR – Harvest 1) to 9.18 kg plant^{-1} (or 20.4 tons ha^{-1}: Chapecó/Guatambu, SC – Harvest 3), with a consistently rising trend observed in each successive harvest (Figure 2). The yield of 20.4 tons ha^{-1} is similar to the value recommended in Erva 20 System (Penteado Junior and Goulart 2019) and much higher than the average Brazilian yield of 9.325 tons ha^{-1} (IBGE 2024). The trial in Chapecó/Guatambu exhibited the highest averages in nearly all harvests, except for the second harvest, while Cruz Machado had the lowest averages. It is important to emphasize that the commercial biomass yield of yerba mate with future selected cultivars has the potential to further increase the yield stipulated by Yerba 20.

Individual deviance analyses were conducted for the five trials (Áurea, RS; Ilópolis, RS; Catanduvas, SC; Chapecó / Guatambu, SC; and Major Vieira, SC) with survival rates above 63.21% and across all four harvests. There were significant progeny effects (5% probability) for all harvests in the Áurea, RS, Catanduvas, SC, and Chapecó/Guatambu, SC, trials, suggesting that at least one treatment differs in performance from the others. There were no significant progeny effects in harvest 1 in Ilópolis, RS, and harvests 1, 2 and 3 in Major Vieira, SC (Table 2). Non-significant progeny effects may be related to biotic/abiotic stresses or operational failures responsible for masking genetic differences, highlighting the importance of greater experimental control or additional future trials.

Accuracy estimates ranged from 0.77 to 0.86 in Áurea, RS, 0.20 to 0.74 in Ilópolis, RS, 0.77 to 0.81 in Catanduvas, SC, 0.63 to 0.72 in Chapecó/Guatambu, SC, and 0.48 to 0.75 in Major Vieira, SC. The occurrence of fire and severe drought between harvests 2 and 3 in the Áurea, RS, trial, as well as the yerba mate borer infestation during harvest 4

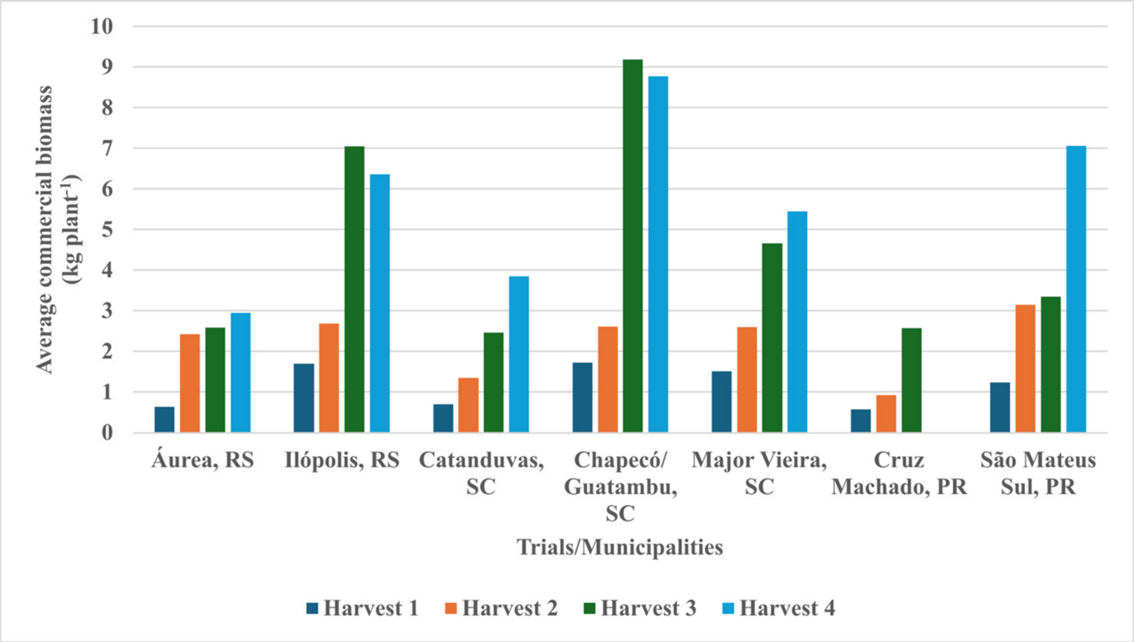

Figure 2. Estimates of average commercial biomass in five open-pollinated progeny trials of *Ilex paraguariensis* (yerba mate) in Santa Catarina and Rio Grande do Sul, Brazil.

Table 2. Deviance analyses for commercial biomass production (kg plant^{-1}) across four harvests in five open-pollinated progeny trials of *Ilex paraguariensis* (yerba mate), conducted in Santa Catarina and Rio Grande do Sul, Brazil

Sources of variation	Áurea, RS		Ilópolis, RS		Catanduvas, SC		Chapecó / Guatambu, SC		Major Vieira, SC	
	Harvest 1									
	Deviance	LRT[1]	Deviance	LRT[1]	Deviance	LRT[1]	Deviance	LRT[1]	Deviance	LRT[1]
Progenies	-660.70^{+}	21.76*	655.42^{+}	0.06	-342.78^{+}	22.95*	2150.95^{+}	11.63*	1009.17^{+}	2.83
Plots	-595.31^{+}	87.15*	836.18^{+}	180.82*	-328.29^{+}	37.44*	2186.90^{+}	47.58*	1095.91^{+}	89.57*
Complete model	-682.46		655.36		-365.73		2139.32		1006.34	
	Harvest 2									
	Deviance	LRT[1]	Deviance	LRT[1]	Deviance	LRT[1]	Deviance	LRT[1]	Deviance	LRT[1]
Progenies	1346.05^{+}	39.80*	998.41^{+}	5.22*	589.96^{+}	15.86*	1953.98^{+}	7.60*	1802.4^{+}	0.83
Plots	1402.83^{+}	96.58*	1242.56^{+}	249.37*	625.10^{+}	51.00*	1983.34^{+}	36.96*	1895.08^{+}	93.51
	1306.25		993.19		574.10		1946.38		1801.57	
Complete model	Harvest 3									
	Deviance	LRT[1]	Deviance	LRT[1]	Deviance	LRT[1]	Deviance	LRT[1]	Deviance	LRT[1]
Progenies	1955.58^{+}	28.19*	2835.52^{+}	16.77*	1719.28^{+}	18.00*	3773.12^{+}	4.58*	2547.17^{+}	2.46
Plots	2006.12^{+}	78.73*	2942.39^{+}	123.64*	1735.83^{+}	34.55*	3837.12^{+}	68.58*	2620.36^{+}	75.65*
Complete model	1927.39		2818.75		1701.28		3768.54		2544.71	
	Harvest 4									
	Deviance	LRT[1]	Deviance	LRT[1]	Deviance	LRT[1]	Deviance	LRT[1]	Deviance	LRT[1]
Progenies	2083.59^{+}	50.24*	2612.85^{+}	16.03*	2996.74^{+}	15.45*	3760.32^{+}	4.34*	3188^{+}	9.71*
Plots	2092.11^{+}	58.76*	2712.32^{+}	115.50*	3052.42^{+}	71.13*	3823.61^{+}	67.63*	3201^{+}	22.71*
Complete model	2033.35		2596.82		2981.29		3755.98		3178.29	

[1] Likelihood ratio test with 1 degree of freedom distribution; * Significant by the chi-square test, at 5% probability; + Deviation from the model adjusted without these effects.

in the Major Vieira, SC, trial, did not lead to a reduction in selection accuracy values and did not affect the significance of the treatment effects in these trials. In plant breeding experiments, accuracy values above 0.70 are desirable, as this estimate reflects how closely the actual values match those estimated from field data (Resende and Duarte 2007, Sturion and Resende 2010a).

The estimates of the variance components by location and harvest, which exhibited significant treatment effects in the variance analysis, are presented in Table 3. A tendency for the additive genetic variance to increase over the harvests was observed, reflecting the release of genetic variability (Wendling et al. 2018). However, the residual variance (environmental + non-additive) exhibited a high magnitude in most of the trials, reaching values up to four times greater than the additive genetic variances. This result indicates that most of the data variations were not explained by the factors in the model used. This behavior reflects the occurrence of various environmental stresses that some of the trials suffered.

At the level of individual deviance analysis, the individual narrow-sense heritability indicates low to moderate genetic control for the leaf biomass trait. According to Resende et al. (1995), the heritability is considered low when it falls between 0.01 and 0.15, medium when it ranges between 0.15 and 0.50, and high when it exceeds 0.50.

These results are consistent with Sturion and Resende (2010b) and Sturion et al. (2017), who reported narrow-sense heritability values for leaf biomass of open-pollinated yerba mate progenies at 6 years ($h_r^2 = 0.22$) and 18.5 years ($h_r^2 = 0.17$), respectively. In contrast, Wendling et al. (2018) found high heritability values for commercial biomass in open-

Table 3. Variance components for commercial biomass production (kg plant^{-1}) in five open-pollinated progeny trials of *Ilex paraguariensis* (yerba mate) in Santa Catarina and Rio Grande do Sul, Brazil

Parameters	ÁUREA, RS				CATANDUVAS, SC			
	Harvest 1	**Harvest 2**	**Harvest 3**	**Harvest 4**	**Harvest 1**	**Harvest 2**	**Harvest 3**	**Harvest 4**
Additive genetic variance (V_a)	0.07	0.40	0.72	0.79	0.09	0.17	0.46	1.51
Environmental variance between plots (V_{plot})	0.06	0.25	0.46	0.33	0.05	0.14	0.33	1.48
Residual variance (environmental + non-additive) (V_e)	0.12	0.32	0.63	0.52	0.13	0.31	0.86	2.22
Individual phenotypic variance (V_p)	0.25	0.96	1.82	1.63	0.28	0.63	1.65	5.21
Individual narrow-sense heritability (h^2)	0.28 ±0.08	0.41± 0.09	0.40 ±0.09	0.48 ±0.10	0.33 ±0.09	0.27±0.09	0.28±0.09	0.29±0.09
Plot determination coefficient (c^2)	0.25	0.26	0.26	0.20	0.19	0.23	0.20	0.28
Average heritability of progenies (h^2_{mp})	0.59	0.69	0.68	0.74	0.65	0.60	0.61	0.59
Individual additive genetic variation coefficient (CV_{gi}%)	41.41	26.10	32.79	30.03	43.36	30.74	27.64	31.85
Genotypic variation between progenies coefficient (CV_{gp}%)	20.70	13.05	16.39	15.02	21.68	15.37	13.82	15.92
Residual variation coefficient (CV_e%)	54.15	27.79	35.64	28.29	50.06	39.91	34.66	41.78
Relative variation coefficient (CV_r)	0.38	0.47	0.46	0.53	0.43	0.39	0.40	0.38

Parameters	CHAPECÓ/GUATAMBU, SC				ILÓPOLIS, RS			MAJOR VIEIRA, SC
	Harvest 1	**Harvest 2**	**Harvest 3**	**Harvest 4**	**Harvest 2**	**Harvest 3**	**Harvest 4**	**Harvest 4**
Additive genetic variance (V_a)	0.42	0.31	1.26	1.17	0.35	3.49	2.74	1.86
Environmental variance between plots (V_{plot})	0.45	0.39	2.60	2.54	0.72	2.92	2.30	1.48
Residual variance (environmental + non-additive) (V_e)	1.16	1.14	4.94	5.05	0.29	1.48	1.27	4.83
Individual phenotypic variance (V_p)	2.03	1.84	8.80	8.76	1.37	7.89	6.30	8.16
Individual narrow-sense heritability (h^2)	0.21±0.07	0.17±0.07	0.14± 0.06	0.13±0.06	0.26 ±0.09	0.44±0.12	0.43±0.12	0.23±0.08
Plot determination coefficient (c^2)	0.22	0.21	0.30	0.29	0.53	0.37	0.36	0.18
Average heritability of progenies (h^2_{mp})	0.52	0.48	0.41	0.39	0.37	0.55	0.55	0.57
Individual additive genetic variation coefficient (CV_{gi}%)	37.61	21.23	12.21	12.32	22.18	26.52	26.00	25.01
Genotypic variation between progenies coefficient (CV_{gp}%)	18.80	10.61	6.11	6.16	11.09	13.26	13.00	12.50
Residual variation coefficient (CV_e%)	56.61	35.19	23.28	24.25	35.60	29.41	28.98	34.56
Relative variation coefficient (CV_r)	0.33	0.30	0.26	0.25	0.31	0.45	0.45	0.36

pollinated yerba mate progenies at 2.5 years (h^2_r = 0.59), 4.5 years (h^2_r = 0.79), 6.5 years (h^2_r = 0.88), and 18.7 years (h^2_r = 0.65). Narrow-sense heritability considers only the additive genetic variance fixed by selection, making it an essential parameter for selecting parents to produce improved seed (Ramalho et al. 2021).

As expected, the heritabilities based on progeny means were higher than those obtained for individual narrow-sense heritability, reaching moderate to high values at the level of individual deviance analysis. Similarly, the study conducted by Floss et al. (2022) also reported a moderate heritability value (h^2_{mp} = 0.51) for commercial biomass yield in open-pollinated yerba mate in Guatambu, SC, at three years of age. Although heritability in the mean of clones is not calculated in progenies trials, it is inferred that it is higher than in the mean of progenies, as all genetic variance is capitalized in cloning.

The joint analysis performed using the SELEGEN - REML/BLUP 65 model did not reveal significant effects of treatments, permanent environment, or genotype-by-environment interaction (G × E). These non-significant effects may be related to generational heterogeneity (first-, second-, and third-generation progenies evaluated) and sample sizes, mortality, environmental contrasts between sites, and possible limited statistical power for certain components. However, individual selection within each site remains useful for advancing generations at the environmental level. Due to the tendency for additive genetic variance to increase over time, it was decided to select the best trees based on their classification at the fourth harvest in each site, as this provided a greater prospect of genetic gain at the level of individual analysis.

The breeding mean of the top 10 selected parents ($u + a$) in the Áurea, RS, experiment resulted in a genetic gain of 68.8% compared to the original population mean, with a selection intensity of 1%. For the selection of the top 10 clone candidates ($u + g$), the genetic gain reached 105.1%. In Ilópolis, the additive selection gain was 49.4% and the genotypic selection gain was 70.7%. In Catanduvas, the additive selection gain was 67.1% and the genotypic selection gain was 100.3%. In Chapecó, the additive selection gain was 14.0% and the genotypic selection gain was 19.3%. In Major Vieira, the additive selection gain was 41.1% and the genotypic selection gain was 58.2%. This estimate of selection gain supports the production of improved seeds and superior genetic material, contributing to the advancement of generations and the progress of the Yerba Mate Breeding Program.

At the level of individual analysis, the gains from selecting individuals (clones) based on genotypic values were higher than those from selecting based on additive genetic values (parent). This result is explained by the fact that genotypic values capture not only additive genetic effects, but also dominance effects and epistatic interactions (Resende and Barbosa 2005).

At the level of individual analysis, in the selection of the best 10 individuals from each experiment, the progenies of the second generation stood out. These progenies, having undergone a higher degree of breeding than the first generation, naturally tend to perform better. In addition, 67% of the germplasm consisted of progenies from this generation, while the remaining material was used in smaller quantities.

A similar trend was observed with provenances from municipalities in Paraná, which represented 78% of the germplasm and appeared more frequently in the selection of individuals. However, no specific provenance stood out in the trials. Provenances from Rio Grande do Sul, which represented 16% of the germplasm, stood out only in the trial set up in Major Vieira, SC.

In this study, different genetic materials from different breeding generations (first, second and third) and with different numbers of treatments were evaluated in experimental sites with contrasting environmental conditions, with the aim of optimizing the use of germplasm. This large diversity, sample sizes, mortality, and environmental contrasts between sites may have contributed to the lack of significant genotype-by-environment interaction (G × E), despite differences in the ranking of the best trees/progenies between sites and harvests. However, in future trials, it is advisable to use genotypes from the same generation in each trial to achieve more balanced experiments and to maximize the gains from improved seed, as maximizing genetic gain is one of the main objectives of plant breeding programs.

CONCLUSION

At the level of individual analysis, the selection of superior trees confirms substantial gains in commercial biomass yield, allowing the advancement of generations in the Embrapa Yerba Mate Breeding Program through the recombination of the best genitors, as well as the production of improved seeds and the selection of clone candidates.

The establishment of new clone trials in contrasting environments is essential to consolidate the results of this work, with the aim of recommending new clonal cultivars adapted to the climatic and soil conditions of southern Brazil in the future.

ACKNOWLEDGEMENTS

We would like to express our profound gratitude to the rural producers and public and private partner organizations that facilitated this study. We are also indebted to the Coordination for the Improvement of Higher Education Personnel (CAPES) for awarding the doctoral scholarship and to the Brazilian Agricultural Research Corporation (Embrapa) for the financial and operational support.

DATA AVAILABILITY

The datasets generated and/or analyzed during the current research are available from the corresponding author upon reasonable request.

REFERENCES

Cardozo Junior EL and Morand C (2016) Interest of mate (*Ilex paraguariensis* A. St.-Hil.) as a new natural functional food to preserve human cardiovascular health - A review. **Journal of Functional Foods 21**: 440-454.

Floss PA, Stuepp CA, Wendling I, Cipriani VB and Reis CAF (2022) Genetic improvement of *Ilex paraguariensis* in western Santa Catarina State: estimate of phenotypic and genetic parameters. **Research, Society and Development 11**: e1711326084.

IBGE – Instituto Brasileiro de Geografia e Estatística (2024) Produção de erva-mate (cultivo). Available at <https://www.ibge.gov.br/explica/producao-agropecuaria/erva-mate-cultivo/br>. Accessed on October 2, 2025.

Paiva DI, Cascales J, Rosetti MEN, Scherer RA, Gauchat ME and Gottlieb AM (2020) Unraveling the genetic complexity of a cultivated breeding population of "yerba mate" (*Ilex paraguariensis* St. Hil.). **Academia Brasileira de Ciências 92**: e20190113.

Penteado Junior JF and Goulart ICGR (2019) **Erva 20: Sistema de produção de erva-mate**. Embrapa, Brasília, 152p.

Ramalho MAP, Santos JB, Pinto CABP, Souza EA, Gonçalves, FMA and Souza JC (2021) **Genética na Agropecuária**. Editora UFLA, Lavras, 508p.

Resende MD, Sturion JA and Mendes S (1995) **Genética e melhoramento da erva-mate (*Ilex paraguariensis* St. Hil.)**. Embrapa**,** Colombo, 33p.

Resende MDV (2007a) **Matemática e estatística na análise de experimentos e no melhoramento genético**. Embrapa Florestas, Colombo, 560p.

Resende MDV (2007b) **Software SELEGEN-REML/BLUP: sistema estatístico e seleção genética computadorizada via modelos lineares mistos**. Embrapa Florestas, Colombo**,** 359p.

Resende MDV and Barbosa MHP (2005) **Melhoramento genético de plantas de propagação assexuada**. Embrapa Florestas, Colombo, 130p.

Resende MDV and Duarte JB (2007) Precisão e controle de qualidade em experimentos de avaliação de cultivares. **Pesquisa Agropecuária Tropical 37**: 182-194.

Santin D, Wendling I, Benedetti EL, Morandi D and Domingos DM (2015) Sobrevivência, crescimento e produtividade de plantas de erva-mate produzidas por miniestacas juvenis e por sementes. **Ciência Florestal 25**: 571-579.

Santos HG, Jacomine PKT, Anjos LHC, Oliveira VA, Lumbreras JF, Coelho MR, Almeida JA, Araujo Filho JC, Oliveira JB and Cunha TJF (2018) **Sistema brasileiro de classificação de solos**. Embrapa, Brasília, 356p.

Simeão RM, Sturion JA, Resende MDV, Fernandes JSC, Neivert DD and Ulbrich AL (2002) Avaliação genética em erva-mate pelo procedimento BLUP individual multivariado sob interação genótipo x ambiente. **Pesquisa Agropecuária Brasileira 37**: 1589-1596.

Sturion AJ and Resende MDV (2010a) **Melhoramento genético de erva-mate**. Embrapa Florestas, Colombo 274p.

Sturion JA and Resende MDV (2010b) Avaliação genética e análise de deviance em um teste desbalanceado de procedência e progênie de *Ilex paraguariensis*. **Pesquisa Florestal Brasileira 30**: 157-160.

Sturion JA, Stuepp CA and Wendling I (2017) Genetic parameters estimates and visual selection for leaves production in *Ilex paraguariensis*. **Bragantia 76**: 492-500.

Viana G, Hoeflich VA, Santos AJ, Schwans A and Macedo JJ (2018) A contribuição dos produtos florestais não-madeireiros - Erva-mate e

Pinhão - ao setor florestal e agropecuário do Paraná. **Revista Ciência da Madeira 9**: 181-190.

Wendling I and Santin D (2015) **Propagação e nutrição de erva-mate**. Embrapa, Brasília, 195p.

Wendling I, Sturion JA, Reis CAF, Stuepp CA and Peña MLP (2016) Indirect and expedite assessment of *Ilex paraguariensis* commercial yield. **Cerne 22**: 241-248.

Wendling I, Sturion JA, Stuepp CA, Reis CAF, Ramalho MAP and Resende MDVD (2018) Early selection and classification of yerba mate progenies. **Pesquisa Agropecuária Brasileira 53**: 279-**286.**