

ORIGINAL ARTICLE

Agronomic Application of Genetic Resources

Genetic gain and yield performance of 42 genotypes of *Coffea canephora* in Brazil

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Abstract

Coffea canephora is a species of major economic and social importance, and the identification of superior genotypes is essential for sustainable crop improvement. This study evaluated the performance of 42 *C. canephora* genotypes over six consecutive harvests (2016–2021) to estimate genetic parameters and assess the efficiency of multi-harvest selection. The experiment was conducted in Nova Venécia, Espírito Santo, Brazil, using a randomized complete block design with three replications. Yield data were analyzed using restricted maximum likelihood/best linear unbiased prediction (REML/BLUP) mixed models. Significant genotypic, permanent environmental, and genotype $\times$ measurement interaction variance components were detected, supporting the use of repeated evaluations for reliable genetic inference. The broad-sense heritability of the genotype mean was 0.596, while repeatability (0.409) and the mean genotypic correlation across harvests (0.602) indicated moderate temporal consistency in genotype performance. Temporal selection accuracy exceeded 0.70 from the third harvest onward, demonstrating the feasibility of early selection. Predicted genetic gains reached 19.16 bags ha⁻¹ when selecting the single best genotype and remained substantial at 15.97, 14.11, and 12.49 bags ha⁻¹ when selecting the top three, five, and eight genotypes, respectively, confirming the effectiveness of the REML/BLUP approach for identifying superior materials and accelerating genetic progress in *C. canephora* breeding programs.

Abbreviations: BLUP, best linear unbiased prediction; GWS, genome-wide selection; LRT, likelihood ratio test; REML, restricted maximum likelihood.

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Plain Language Summary

Coffee is a major crop that supports millions of livelihoods worldwide, particularly in Brazil. Developing high-yielding and stable genetic materials is essential to sustain production under changing environmental conditions. In this study, 42 *Coffea canephora* genotypes were evaluated over six consecutive harvests to identify superior materials for productivity and long-term performance. The results revealed substantial genetic variability among genotypes, indicating strong potential for genetic improvement. Eight genotypes stood out, with predicted yields exceeding 100 bags ha⁻¹ and high performance across harvests. Selection of these superior genotypes resulted in significant expected genetic gains and high selection accuracy, demonstrating the effectiveness of the breeding approach. These materials represent valuable options for commercial cultivation and genetic resources for breeding programs aimed at increasing productivity, stability, and sustainability in coffee production.

1 | INTRODUCTION

Coffee is one of the most important agricultural crops worldwide, playing a key role in tropical economies by directly supporting more than 25 million families across over 80 countries (FAO, 2025). In Brazil, the *Coffea canephora* species is notable for its economic and social relevance, as it is fundamental to the livelihood of many smallholder farmers and increasingly cultivated using environmentally responsible agricultural practices (Loureço et al., 2022). Global coffee consumption considering both *Coffea arabica* L. and *C. canephora* Pierre ex A. Froehner exceeds 170 million bags per year, with Brazil standing as the world's leading producer and exporter (ICO, 2025). *Coffea canephora* has gained increasing prominence, raising its share of global production from approximately 30% in the 1990s to 42.5% in 2023 (ICO, 2025), and is primarily cultivated in Vietnam, Brazil, Indonesia, Uganda, and India (Salvador et al., 2024).

In Brazil, the cultivation of *C. canephora*, locally known as Conilon, is concentrated in a few states, most notably Espírito Santo, which is the largest national producer of this variety (CONAB, 2026). A growing demand for Conilon coffee has driven significant investments in research and innovation due to this species' genetic variability, hardiness, and high yield potential, attributes that are critical for addressing the climatic challenges faced in the region (Venancio et al., 2020).

The genetic variability of coffee species is a fundamental element for breeding programs, as it enables the selection of plants with higher productivity and resistance to adverse environmental conditions (Damatta et al., 2007; Partelli, da Silva, et al., 2022). *Coffea canephora* is an allogamous (cross-pollinating) species, a characteristic that naturally fosters a broader genetic diversity (Carvalho et al., 1991; V. A. Silva

et al., 2017). Such intra-specific diversity is essential for developing superior genotypes with high production rates and greater tolerance to biotic and abiotic stresses, traits that are indispensable for the sustainability of coffee farming in the face of modern cultivation challenges (Jordaim et al., 2025; Pamphile et al., 2024; A. N. R. Silva, Rocha, et al., 2025).

In this sense, several works have explored and characterized *C. canephora* germplasm through phenotypic and molecular studies; for instance, Zaidan et al. (2023) reported significant genetic divergence among genotypes, highlighting traits with high heritability, productivity, and stability (Martins et al., 2019, 2020; V. A. Silva et al., 2017). Selection and breeding programs have focused on harnessing the genetic variability of *C. canephora*, aiming to identify superior genotypes with desirable traits such as disease resistance, high productivity, bean quality (Gnapi et al., 2022; Rocha et al., 2021), and nutrient accumulation (C. A. Silva, Dalazen, et al., 2025). Furthermore, recent research has highlighted the relevance of investigating genotype × environment interactions and environmentally induced anatomical plasticity to support the identification and development of coffee cultivars better adapted to changing environmental conditions and future climate challenges (Senra et al., 2023; L. O. E. Silva et al., 2024). Genome-wide selection (GWS) and Bayesian approaches have improved selection efficiency by predicting phenotypes with greater accuracy, thereby increasing genetic gain per unit of time (Alkimim et al., 2020; Covre et al., 2022; Paixão et al., 2022).

However, the effectiveness of these methods may still be constrained by the low heritability of some important traits, such as fruit ripening time and yield per plant, which reduce the accuracy of predictions (Alkimim et al., 2020; Correia et al., 2024). Overcoming these limitations requires

integrating advanced molecular tools to obtain a deeper understanding of the species' genetic diversity and its interactions with the environment, namely to single stress factor, but also to multi-stress situations, since the resilience responses to a combination of stresses cannot be directly predicted from the responses to individual stresses alone, considering the impacts both on vegetative and reproductive structures (Marques et al., 2025).

Still, the use of mixed models in coffee breeding allows significant advances, providing a robust statistical framework for estimating genetic parameters and selecting superior progenies (Deon Vilela de Resende & Silva Alves, 2020). Procedures such as restricted maximum likelihood/best linear unbiased prediction (REML/BLUP) have been widely used to evaluate key agronomic traits, such as production, yield per plant, vegetative vigor, and plant height, across different harvests (Resende, 2016). Moreover, these models account for crucial factors such as biennial production and environmental effects, enhancing the accuracy of selection by isolating true genetic effects from confounding variables (Dias et al., 2020).

Therefore, this study aimed to evaluate the performance of 42 coffee genotypes over six harvests using a REML/BLUP approach model to identify superior genotypes as regards high yield potential and phenotypic stability, maximizing genetic gain and resilience of coffee cultivars.

2 | MATERIALS AND METHODS

2.1 | Plant material, experimental design, and environmental conditions

The experiment consisted in the evaluation of 42 genotypes of *C. canephora* Pierre ex A. Froehner (Table 1), propagated through cuttings and established in April 2014 in the municipality of Nova Venécia, Espírito Santo, Brazil, at an altitude of approximately 200 m. The site is located at Latitude: 18°39'43" S and Longitude: 40°25'52" W. The region is characterized by a climate classified as Aw: tropical with dry winters and rainy summers (Alvares et al., 2013). Average minimum temperatures remain above 16°C in July and August, while maximum temperatures reach up to 32°C in January and February. Occasionally, temperatures may drop below 13°C or exceed 36°C (Figure 1). The soil is classified as dystic Red-Yellow Latosol, with a clayey texture and undulating topography (Santos et al., 2018).

A randomized complete block design was adopted with three field replications, each consisting of seven plants. The experiment was established at a spacing of 3 × 1 m, corresponding to 3 m² per plant. Crop management followed the technical recommendations for *C. canephora* cultivation (Ferrão et al., 2019). Pruning was performed to control excessive branching and maintain a standard density of

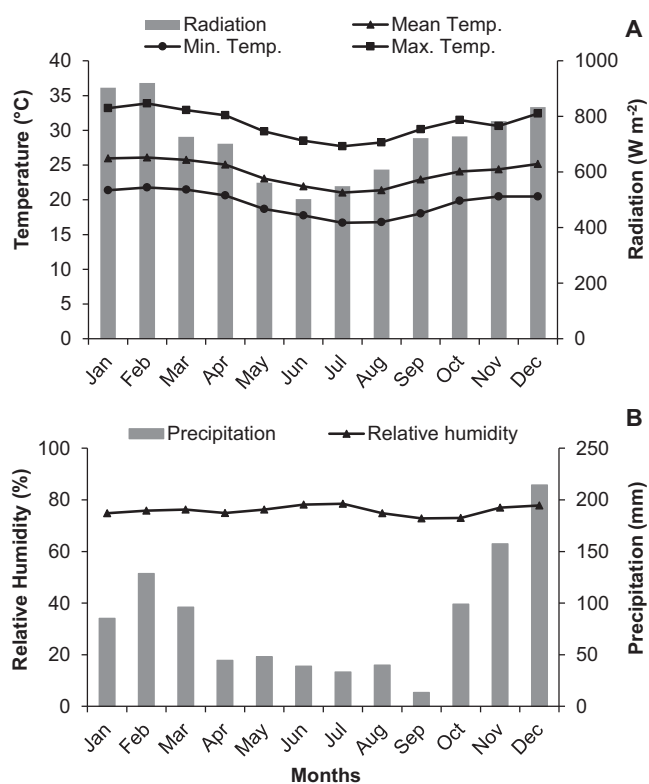


FIGURE 1 Mean values of solar radiation and maximum, mean, and minimum air temperature (A) and relative air humidity and precipitation (B) in the years 2014–2022, recorded at the meteorological station of Nova Venécia, Espírito Santo, Brazil.

12,000–15,000 stems ha⁻¹, while fertilization was based on soil analysis. Weed management included manual weeding within the canopy projection, mechanical mowing between rows, and complementary chemical control when necessary. Insecticides, fungicides, and nutrient applications were carried out according to integrated pest and nutrient management recommendations for conilon coffee (Ferrão et al., 2019). Supplemental irrigation was provided throughout the experimental period whenever rainfall was insufficient to meet crop water requirements. Yield was determined from the harvest of ripe fruits collected separately from each experimental plot on a genotype-by-genotype basis.

2.2 | Statistical analysis

Yield data collected over six consecutive harvests (2016–2021) were used to evaluate the temporal stability and adaptability of the 42 *C. canephora* genotypes. The analyses were performed using the REML/BLUP methodology implemented in the Selegen-REML/BLUP software, according to the procedures described by Resende (2016).

TABLE 1 Identification of 42 genotypes of *Coffea canephora* cultivated in Nova Venécia, Espírito Santo, Brazil.

ID	Name	Origin	ID	Name	Origin
1	Verdim R	Tributun (Partelli et al., 2020)	22	Z38	Selected from a farmer's seed-derived plantation
2	B01	Selected from a farmer's seed-derived plantation	23	Z18	Selected from a farmer's seed-derived plantation
3	Bicudo	Plena (Oliosi et al., 2025)	24	Z37	Salutar (Partelli, Olioso, et al., 2022)
4	Alecrim	Selected from a farmer's seed-derived plantation	25	Z21	Selected from a farmer's seed-derived plantation
5	700	Selected from a farmer's seed-derived plantation	26	Z36	Selected from a farmer's seed-derived plantation
6	CH1	Selected from a farmer's seed-derived plantation	27	Ouro Negro	Magnus grano (Sousa et al., 2024)
7	Imbigudinho	Monte Pascoal (Partelli et al., 2021)	28	18	Selected from a farmer's seed-derived plantation
8	AD1	Plena (Oliosi et al., 2025)	29	Tardio C	Salutar (Partelli, Olioso, et al., 2022)
9	Graudão HP	Salutar (Partelli, Oliosi, et al., 2022)	30	A1	Plena (Oliosi et al., 2025)
10	Valcir P	Selected from a farmer's seed-derived plantation	31	Cheique	Selected from a farmer's seed-derived plantation
11	Beira Rio (8)	Tributun (Partelli et al., 2020)	32	P2	Monte Pascoal (Partelli et al., 2021)
12	Tardio V	Salutar (Partelli, Olioso, et al., 2022)	33	02	Emcapa 8111 (Bragança et al., 2001)
13	AP	Monte Pascoal (Partelli et al., 2021)	34	153	Emcapa 8131 (Bragança et al., 2001)
14	L80	Plena (Oliosi et al., 2025)	35	P1	Andina (Partelli et al., 2019)
15	Bamburral	Tributun (Partelli et al., 2020)	36	LB1	Plena (Oliosi et al., 2025)
16	Pirata	Tributun (Partelli et al., 2020)	37	122	Selected from a farmer's seed-derived plantation
17	Peneirão	Plena (Oliosi et al., 2025)	38	Verdim D	Selected from a farmer's seed-derived plantation
18	Z39	Selected from a farmer's seed-derived plantation	39	143	Emcapa 8131 (Bragança et al., 2001)
19	Z35	Selected from a farmer's seed-derived plantation	40	Ouro Negro 1	Selected from a farmer's seed-derived plantation
20	Z40	Selected from a farmer's seed-derived plantation	41	Ouro Negro 3	Selected from a farmer's seed-derived plantation
21	Z29	Selected from a farmer's seed-derived plantation	42	Clementino	Tributun (Partelli et al., 2020)

Note: Origin refers to the cultivar from which the genotype was derived or, when applicable, to its identification as a farmer-selected genotype collected from local seed-derived plantations.

The analysis was based on the following mixed linear model:

$$y = X_m + Z_g + W_p + T_i + e$$

where y is the vector of observed data (yield), m is the vector of fixed effects for the measurement $\times$ replicate combinations added to the overall mean, g is the vector of genotypic effects (random), p is the vector of permanent environmental effects (random), i is the vector of genotype $\times$ measurement

interaction effects (harvests, random), and e is the vector of residual errors (random).

The uppercase letters X , Z , W , and T represent the incidence matrices for the respective effects. A likelihood ratio test (LRT) was performed to assess the significance of the effects of the model mentioned above.

The defining feature of repeated-measures models is the need to specify an appropriate variance-covariance structure for the residuals. Because repeated observations are collected from the same experimental unit over successive harvests,

measurements within a unit are temporally correlated, and their residuals cannot be assumed to be independent. In contrast, residuals associated with different experimental units are assumed to be independent.

$$\text{Cov} [e_{mg'p'i} e_{mgpi'}] = 0$$

If $m \neq m'$, $g \neq g'$, or $p \neq p'$

Furthermore, because repeated assessments were obtained from the same plant over successive harvests, observations are expected to exhibit temporal dependence, with the strength of the correlation varying according to the interval between measurements. Accordingly, repeated observations on the same individual were assumed to be correlated across harvests, and this dependence was accounted for through an appropriate residual variance-covariance structure.

$$\text{Var} [e_{mgpi}] = \sigma_i^e$$

$$\text{Cov} [e_{mgpi}, e_{mgpi'}] = \sigma_{ii'}$$

The following variances and genetic parameters were estimated:

- genotypic variance (σ_g^2);
- permanent environmental variance (σ_{perm}^2);
- genotype $\times$ measurement interaction variance (σ_{gm}^2);
- residual variance (σ_e^2);
- total phenotypic variance (σ_p^2);
- individual broad-sense heritability (H^2);
- broad-sense heritability of the genotype mean (h_{mg}^2);
- plot-level repeatability coefficient (r), calculated as $r = (\sigma_g^2 + \sigma_{\text{perm}}^2) / \sigma_p^2$
- mean genotypic correlation across harvests (r_{gmean});
- coefficient of determination of permanent environmental effects (c_{perm}^2); and
- coefficient of determination of the genotype $\times$ measurement interaction (c_{gm}^2).

Based on the predicted genetic values (BLUPs), the expected genetic gains from selection and the new population means were estimated, enabling the identification of superior genotypes in terms of yield and genotypic stability across the evaluated harvests.

The estimates of mean heritability, accuracy, coefficient of determination, and efficiency for different numbers of measurements (n) were obtained based on the repeatability coefficient (r), using the expression:

$$h_{\text{mg}}^2 = \frac{n \cdot r}{1 + (n - 1) \cdot r}$$

TABLE 2 Likelihood ratio tests (LRTs) for assessing the significance of random effects by comparing reduced and full mixed models.

Effect	Deviance	LRT
Null model ($y \sim 1$)	791,787.80	6.7862***
Permanent environmental effect	616,604.50	2.6886***
Genotype $\times$ measurement	604,569.60	86.5833***
Genotype + permanent environmental effect	437,919.30	6.7929***
Full model	400,987.50	–

***Significance level $<0.01\%$.

From this, the accuracy was calculated as follows:

$$r_{\text{gg}} = \sqrt{h_{\text{mg}}^2}$$

The coefficient of determination (R_y^2) and the selection efficiency index (η) were subsequently estimated to evaluate the effect of the number of repeated measurements on the reliability of genotype selection and to project the expected gains associated with successive harvest evaluations.

Simultaneous selection for productivity, temporal adaptability, and stability was performed using the Harmonic Mean of the Relative Performance of Genotypic Values (HMRPGV), calculated as follows:

$$\text{HMRPGV}_i = n / \left(\sum_{j=1}^n (1/V_{\text{gij}}) \right)$$

where n is the number of repeated evaluations (harvests) for genotype i , and V_{gij} is the predicted genotypic value of genotype i in the j th harvest, expressed relative to the mean of that harvest. In single-location experiments, this statistic combines mean performance with consistency across successive evaluations, allowing the identification of genotypes with superior productivity and stable performance over time.

3 | RESULTS

The inference about the existence of genetic variability among genotypes was confirmed by the LRT, obtained from the deviance analysis (Table 2). In this procedure, the deviance of the full model was compared with that of reduced models obtained by sequentially removing the genotypic effect, the permanent environmental effect, or the genotype $\times$ measurement interaction, allowing the significance of each random component to be assessed through the LRT.

The first analysis estimated the variance components for the yield of 42 *C. canephora* genotypes evaluated over six harvests (Table 3). The genotypic variance (σ_g^2) was estimated at 144.4, while the permanent environmental variance

TABLE 3 Estimates of variance components and genetic and non-genetic parameters were obtained from the analysis of variance for production traits over six harvests (from 2016 to 2021) for 42 genotypes of *Coffea canephora* cropped in northern Espírito Santo.

Component	Estimate	Proportion (σ^2/σ_p^2)	Component	Estimate
σ_g^2	144.357	0.181	c_{gm}^2	0.119
σ_{perm}^2	182.905	0.229	r_{gmean}	0.602
σ_{gm}^2	95.407	0.119	h_{mg}^2	0.596
σ_e^2	376.173	0.471	m	87.425
σ_p^2	798.843	1	CV_g (%)	13.743
H^2	0.180	–	CV_e (%)	22.185
r	0.409		CV_r	0.619
c_{perm}^2	0.228			

Note: σ_g^2 : genotypic variance; σ_{perm}^2 : permanent environmental variance; σ_{gm}^2 : variance of the genotype $\times$ measurement interaction; σ_e^2 : residual variance; σ_p^2 : individual phenotypic variance; H^2 : heritability of the total genotypic effects; r : repeatability coefficient; c_{perm}^2 : coefficient of determination of permanent environmental effects; c_{gm}^2 : coefficient of determination of genotype $\times$ measurement interaction effects; r_{gmean} : genotypic correlation across measurements; h_{mg}^2 : heritability of the genotype mean; m : overall mean; CV_g (%) coefficient of genetic variation; CV_e (%) coefficient of residual variation; CV_r : coefficient of relative variation; Proportion (σ^2/σ_p^2): ratio between each variance component and the total phenotypic variance (σ_p^2).

(σ_{perm}^2) was even higher, at 182.9, exceeding the variance attributed to the genotype $\times$ measurement interaction, which totaled 95.4. The residual variance (σ_e^2) reached 376.2, and the individual phenotypic variance (σ_p^2) was 798.8. The broad-sense heritability for individual plots (H^2) was estimated at 0.18, while the heritability of genotype means (h_{mg}^2) reached 0.60, indicating greater precision of selection when based on means. Repeatability was 0.41, and the mean genotypic correlation between measurements (r_{gmean}) was estimated at 0.60, reflecting moderate consistency across evaluation cycles. The overall mean yield in the experiment was 87.4 bags ha⁻¹.

An increase in the number of measurements led to higher estimates for genetic parameters (Table 4). Mean heritability rose from 0.339 (one measurement) to 0.635 (ten measurements), and the coefficient of determination increased from 0.410 to 0.874. Prediction accuracy also improved progressively, from 0.582 to 0.797, as did selection efficiency that reached 1.461 with ten measurements.

The analysis of predicted genotypic values using REML/BLUP approach revealed significant variability among the genotypes (Table 5). Genotype LB1 exhibited the highest predicted genetic value ($g = 19.16$), followed by Bicudo ($g = 14.55$), AD1 ($g = 14.18$), and Z21 ($g = 11.72$). Among the ten best-performing genotypes, the adjusted means ($\mu + g$) ranged from 93.97 to 106.59 bags ha⁻¹, with genetic gains between 11.48 and 19.16 bags ha⁻¹ and estimated new population means above 98.91 bags ha⁻¹. On the other hand, low-performing genotypes such as Alecrim

and B01 showed negative genetic values and predicted yields below 67 bags ha⁻¹.

Genotypes were classified into four descriptive groups according to the distribution of predicted yield values relative to the overall mean (87.43 bags ha⁻¹) and standard deviation (Figure 2). The classification comprised genotypes with yields above the mean plus one standard deviation, above the mean, below the mean, and below the mean minus one standard deviation.

Group I included genotypes LB1, Bicudo, AD1, Z21, Peneirão, Z39, A1, and 143, with predicted yields ranging from 98 to 109 bags ha⁻¹. Group II comprised L80, P1, 02, Pirata, Clementino, Bamburral, CH1, Z36, P2, 700, Verdim D, Z37, Graudão HP, Imbigudinho, and Ouro Negro, with predicted yields between 88 and 97 bags ha⁻¹. Group III consisted of genotypes 122, AP, Verdim R, Z18, 153, Ouro Negro 3, Z35, Z40, Ouro Negro 1, Z38, Z29, Valcir P, Tardio V, Cheique, and Tardio C, with predicted yields ranging from 78 to 87 bags ha⁻¹. Group IV comprised Beira Rio 8, 18, Alecrim, and B01, which exhibited the lowest predicted yields, ranging from 60 to 72 bags ha⁻¹ (Figure 2).

The predicted genetic gain obtained by selecting the single best genotype was 19.16 bags ha⁻¹. When selection intensity was expanded to include the top three, five, and eight genotypes, the expected genetic gains were 15.97; 14.11; and 12.49 bags ha⁻¹, respectively.

4 | DISCUSSION

The genotypic variance ($\sigma_g^2 = 144.36$) was statistically significant according to the LRT from the deviance analysis (Table 2), providing robust evidence of the existence of genetic differences among the evaluated genotypes for annual yield. This result confirms that a relevant proportion of the observed phenotypic variation is attributable to heritable genetic effects rather than solely to environmental influences, thereby validating the assumptions required for effective genetic selection. The significance of the genotypic variance, together with the estimated heritability of the genotype mean ($h_{mg}^2 = 0.596$), indicates that selection based on multi-harvest performance is expected to produce consistent genetic gains, reinforcing the suitability of this population for breeding purposes (Deon Vilela de Resende & Silva Alves, 2020; D. O. Silva et al., 2018).

The permanent environmental variance (σ_{perm}^2) was also statistically significant (Table 2), indicating that stable, non-genetic environmental factors consistently influenced genotype performance across successive harvests. This result demonstrates that a portion of the observed phenotypic variation originated from persistent environmental conditions, such as local soil characteristics and microclimatic effects, which remained relatively constant over time. Consequently,

TABLE 4 Mean heritability, accuracy, efficiency, and coefficient of determination for the yield over six harvests (from 2016 to 2021), obtained from the 42 genotypes of *Coffea canephora*, cropped in northern Espírito Santo.

Measurement	Mean heritability (h^2_{mg})	Determination (R^2_y)	Accuracy (r_{gg})	Efficiency (η)
1	0.339	0.410	0.582	1.000
2	0.457	0.581	0.676	1.191
3	0.518	0.676	0.719	1.284
4	0.554	0.735	0.744	1.340
5	0.579	0.776	0.761	1.377
6	0.596	0.806	0.772	1.403
7 ^a	0.609	0.829	0.781	1.423
8 ^a	0.620	0.847	0.787	1.438
9 ^a	0.628	0.862	0.792	1.451
10 ^a	0.635	0.874	0.797	1.461

^aValues refer to theoretical projections based on the repeatability coefficient (r).

repeated measurements are essential to disentangle permanent environmental effects from genetic effects and to ensure unbiased prediction of genotypic values, thereby increasing the reliability of selection decisions (Dias et al., 2020). The significance of this variance component further highlights the importance of employing mixed-model approaches capable of appropriately partitioning long-term environmental influences when evaluating perennial crops such as *C. canephora*.

The estimated permanent environmental determination coefficient ($c^2_{perm} = 0.228$) indicates that persistent non-genetic factors exerted a moderate influence on yield expression across harvests. This finding reinforces the importance of explicitly modeling permanent environmental effects in repeated-measures analyses of perennial crops, as failure to partition this source of variation may confound long-term environmental influences with genetic effects and compromise the prediction of genotypic values. Similar considerations have been emphasized in studies on repeated measurements in coffee breeding, in which accounting for permanent environmental variation is essential to improve the reliability of genetic parameter estimation and selection decisions (Fonseca et al., 2004; Resende & Alves, 2020).

The experimental coefficient of variation ($CV_e = 22.19\%$) indicates satisfactory experimental precision for a perennial crop evaluated under field conditions over multiple harvests and exposed to substantial seasonal environmental variation. Values within this range are commonly reported for *C. canephora* productivity trials conducted under tropical conditions, reflecting the inherent complexity of yield expression in long-cycle species influenced by climatic and management fluctuations (Akpertey et al., 2022; Camargo, 2010). The estimated genetic coefficient of variation ($CV_g = 13.74\%$) and the resulting CV_g/CV_e ratio of approximately 0.62 further demonstrate that, despite considerable environmental variation, sufficient genetic variability was present to support

effective selection. This level of experimental precision is consistent with the moderate heritability estimates obtained and provides a reliable basis for the prediction of genotypic values, particularly when repeated measurements across harvests are incorporated into the mixed-model analysis.

The genotype $\times$ measurement interaction ($\sigma^2_{gm} = 95.41$) was statistically significant according to the LRT (Table 2), demonstrating that genotype performance was not completely consistent across successive harvests. This finding provides strong statistical support for the adoption of a multi-harvest evaluation strategy, as selection based on a single cropping cycle would likely capture transient genotype-specific responses rather than stable genetic merit. By accounting for temporal variation in genotype performance, repeated assessments improve the reliability of genotypic value prediction and reduce the risk of biased selection decisions. The observed interaction is consistent with previous reports in *C. canephora*, where genotype performance has been shown to vary across years due to fluctuations in environmental conditions, reinforcing the importance of longitudinal evaluations for breeding programs (Martins et al., 2019; Resende & Alves, 2020).

The estimated broad-sense heritability at the individual level ($H^2 = 0.18$) indicates that a relatively small proportion of the phenotypic variation in yield was attributable to genetic differences among genotypes, with the remaining variation largely influenced by environmental factors and genotype $\times$ measurement interactions. This result suggests that selection based on a single observation would have limited effectiveness, reinforcing the importance of repeated evaluations to improve the reliability of genetic inference. Similar patterns have been reported for *C. canephora*, where heritability estimates vary substantially among traits and populations. For example, Adunola et al. (2023) reported values ranging from 0.15 for the proportion of ripe and green fruits to 0.92 for bean size, highlighting the strong trait

Yield estimates

Classified yield average in above/below one standard deviation

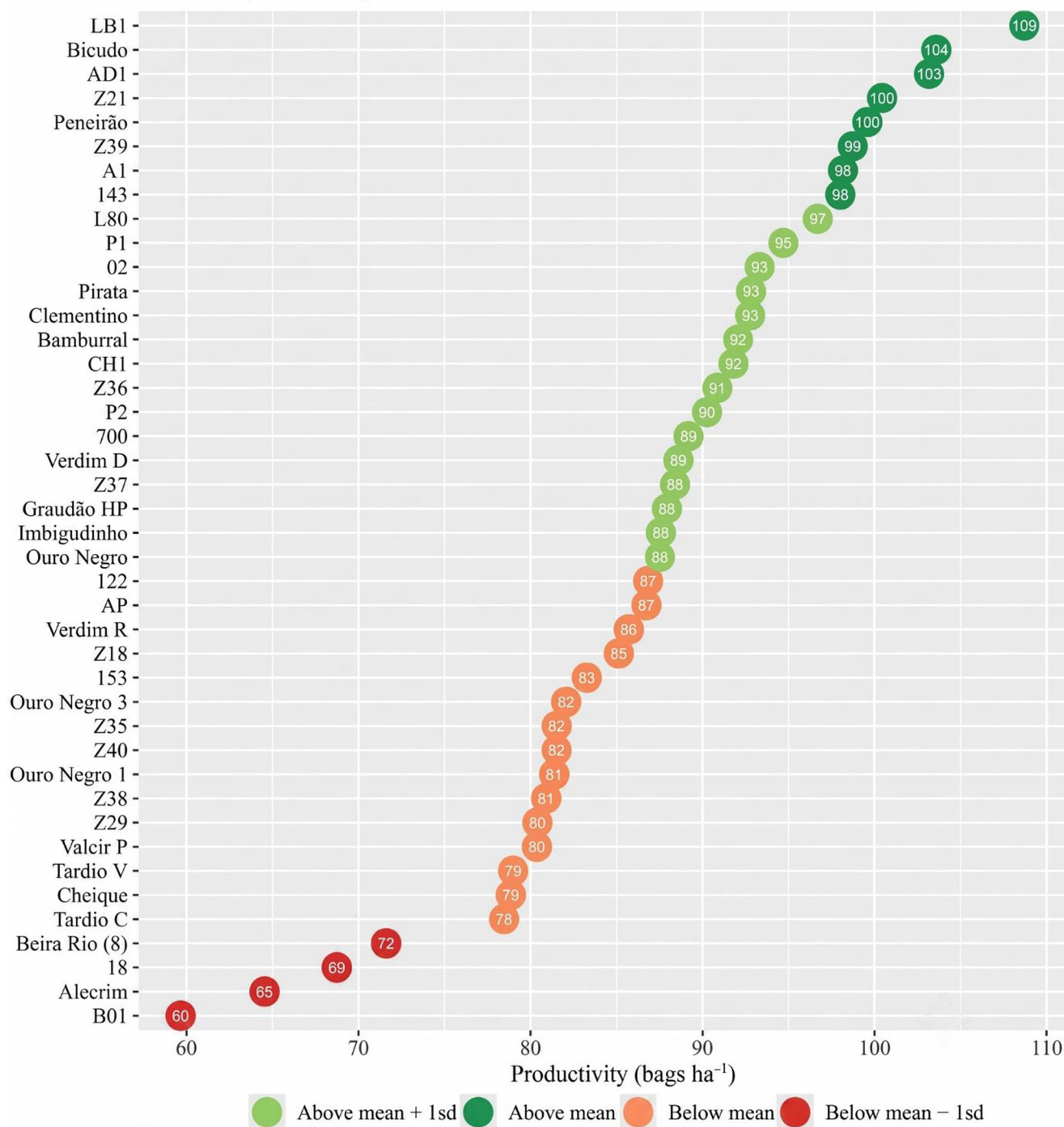


FIGURE 2 Yield estimates for the 42 genotypes of *Coffea canephora* cropped in northern Espírito Santo, based on six harvests, grouped based on the overall mean. Group I: estimates 1 standard deviation above the overall annual mean; Group II: estimates above the overall annual mean; Group III: estimates below the overall annual mean; Group IV: estimates 1 standard deviation below the overall mean.

dependence of genetic control. In agreement with Falconer and Mackay (1996), the relatively low heritability observed for yield reflects the substantial contribution of non-genetic sources of variation to phenotypic expression and underscores the need for breeding strategies based on repeated measure-

ments and mixed-model approaches to maximize selection efficiency.

Estimates of genetic parameters, such as heritability, are essential for designing effective selection strategies in Conilon coffee breeding. Alkimim et al. (2021) argued

TABLE 5 Estimates of genotypic values for the yield over six harvests (from 2016 to 2021), obtained from the 42 genotypes of *Coffea canephora*, cropped in northern Espírito Santo.

Ranking	Genotype	g	u + g	Gain	New mean
1	LB1	19.16	106.59	19.16	106.59
2	Bicudo	14.55	101.98	16.86	104.28
3	AD1	14.18	101.61	15.97	103.39
4	Z21	11.72	99.14	14.90	102.33
5	Peneirão	10.95	98.37	14.11	101.54
6	Z39	10.18	97.61	13.46	100.88
7	A1	9.67	97.09	12.92	100.34
8	143	9.53	96.96	12.49	99.92
9	L80	8.35	95.78	12.03	99.46
10	P1	6.55	93.97	11.48	98.91
11	02	5.30	92.73	10.92	98.35
12	Pirata	4.86	92.29	10.42	97.84
13	Clementino	4.81	92.24	9.99	97.41
14	Bamburral	4.18	91.61	9.57	97.00
15	CH1	3.94	91.36	9.20	96.62
16	Z36	3.10	90.52	8.82	96.24
17	P2	2.56	89.98	8.45	95.87
18	700	1.59	89.01	8.07	95.49
19	Verdim D	1.05	88.48	7.70	95.12
20	Z37	0.88	88.31	7.36	94.78
21	Graudão HP	0.45	87.88	7.03	94.45
22	Imbigudinho	0.13	87.56	6.71	94.14
23	Ouro Negro	0.09	87.51	6.43	93.85
24	122	−0.53	86.89	6.14	93.56
25	AP	−0.62	86.81	5.87	93.29
26	Verdim R	−1.54	85.88	5.58	93.01
27	Z18	−2.06	85.36	5.30	92.72
28	153	−3.74	83.69	4.97	92.40
29	Ouro Negro 3	−4.82	82.60	4.64	92.06
30	Z35	−5.06	82.11	4.00	91.43
31	Z40	−5.32	82.11	4.00	91.43
32	Ouro Negro 1	−5.45	81.97	3.71	91.13
33	Z38	−5.87	81.56	3.42	90.84
34	Z29	−6.33	81.10	3.13	90.56
35	Valcir P	−6.36	81.07	2.86	90.29
36	Tardio V	−7.59	79.83	2.57	90.00
37	Cheique	−7.72	79.71	2.29	89.72
38	Tardio C	−8.08	79.35	2.02	89.44
39	Beira Rio (8)	−14.25	73.18	1.60	89.03
40	18	−16.83	70.60	1.14	88.57
41	Alecrim	−20.61	66.81	0.61	88.04
42	B01	−25.01	62.41	0.00	87.43

Note: Predicted genotypic effects (g), predicted genotypic values (u + g).

that accurate estimates of parameters like heritability and repeatability are crucial for defining effective selection strategies and guiding breeding efforts, which directly contribute to the success of Conilon coffee breeding programs.

The estimated repeatability coefficient ($r = 0.409$) indicates a moderate level of consistency in genotype performance across successive harvests, implying that a single evaluation is insufficient to reliably discriminate superior genotypes. Consequently, repeated measurements are required to increase the precision of genotypic value prediction and support robust selection decisions. This pattern is clearly reflected in the progressive increase in the heritability of genotype means (h_{mg}^2), which rises from 0.339 based on a single harvest to 0.596 after six harvests and is projected to reach 0.635 with ten harvests (Table 3). These results indicate that four to six consecutive evaluations provide a practical minimum for achieving satisfactory selection efficiency in *C. canephora*, with additional harvests yielding comparatively smaller gains in precision. Similar conclusions have been reported by Martins et al. (2019), who emphasized the importance of multi-year evaluations for improving the reliability of genotype selection in this species.

The genotypic correlation across measurements ($r_{gmean} = 0.602$) indicates a moderate degree of temporal stability in genotype performance across the six consecutive harvests. In single-location repeated-measures experiments such as the present study, this parameter reflects the consistency of genotypic rankings over time rather than across environments and is therefore closely associated with the repeatability coefficient. The moderate value observed is consistent with the estimated repeatability ($r = 0.409$), indicating that although genotypes tend to maintain their relative performance across harvests, changes in ranking still occur as a result of the statistically significant genotype $\times$ measurement interaction detected by the deviance analysis (Table 2). According to Resende and Alves (2020), repeatability coefficients between 0.30 and 0.60 are classified as medium magnitude, providing acceptable predictability for permanent phenotypic selection in perennial crops. Thus, the estimate obtained here suggests that early evaluations can provide useful information on long-term genotype performance, although repeated harvests remain necessary to improve the reliability of selection decisions and accurately identify superior genotypes (Dias et al., 2020; Fonseca et al., 2004).

The overall mean yield of 87.43 bags ha^{−1} observed in the present study highlights the high yield potential of the evaluated germplasm under the edaphoclimatic conditions of northern Espírito Santo. This value substantially exceeds the mean yields of 58–60 bags ha^{−1} reported for the first clonal cultivars released in the state (Bragança et al., 2001), reflecting the considerable genetic progress achieved through

successive breeding cycles over recent decades. Moreover, the observed mean is markedly higher than the 61.86 bags ha^{-1} reported by Colodetti et al. (2026) for 27 *C. canephora* genotypes evaluated over eight harvests at 650 m altitude under contrasting irrigation regimes in Espírito Santo. Collectively, these comparisons demonstrate that the productivity achieved in the present study is consistent with that of elite breeding materials and further confirms the effectiveness of recent genetic improvement efforts aimed at increasing yield potential in *C. canephora*.

The broad-sense heritability of the genotype mean ($h_m^2 = 0.596$) indicates that selection based on multi-harvest averages can effectively discriminate superior genotypes by capturing a substantial proportion of the genetic variation underlying yield performance. This estimate is higher than the moderate heritability reported by Akperter et al. (2022) for coffee yield (0.34) and falls within or above the range described by other studies evaluating productivity in *C. canephora*. For example, Bergo et al. (2020) reported heritabilities ranging from 0.10 to 0.44 for yield, whereas D. O. Silva et al. (2018) obtained estimates between 0.47 and 0.77. Likewise, Adunola et al. (2023) reported medium to high heritabilities for bean-related traits and moderate values for yield and disease resistance, while Senra et al. (2023) observed the highest heritability for plant height. Collectively, these findings demonstrate that, despite the substantial influence of environmental factors on coffee performance, sufficient genetic variability exists to support meaningful selection gains.

The relatively high heritability estimated in the present study is largely attributable to the use of repeated measurements across successive harvests, which reduces the influence of seasonal environmental variation on genotype evaluation and improves the prediction of genetic values. This interpretation is consistent with the recommendations of Resende (2016), who emphasized that repeated evaluations are particularly important for perennial crops because they increase selection accuracy by averaging transient environmental effects. Similarly, Alkimim et al. (2021) highlighted that accurate estimation of genetic parameters, especially heritability, is fundamental for designing efficient breeding strategies and maximizing the expected response to selection.

The results presented in Table 3 quantitatively illustrate the benefits of increasing the number of harvest evaluations for genetic selection in *C. canephora*. The heritability of genotype means increased from 0.339 based on a single harvest to 0.596 after six harvests and was projected to reach 0.635 with ten harvests, demonstrating the substantial gains in selection precision achieved through repeated assessments. A similar pattern was observed for the coefficient of determination, which increased from 0.410 to 0.874 as additional harvests were incorporated into the analysis, reflecting progressively greater reliability in the prediction of

genotypic values. However, the relatively modest increase in heritability beyond six harvests suggests diminishing returns from additional evaluations, indicating that approximately four to six consecutive harvests provide a practical balance between selection accuracy and experimental cost in breeding programs. This interpretation agrees with the general relationship between heritability and expected selection response discussed by Petek et al. (2008).

In experiments with *C. canephora*, Correia et al. (2024) reported broad-sense heritability above 0.96 for grain traits, while Bergo et al. (2020) indicated that mean progeny heritabilities across multiple harvests reached 0.64 for yield, demonstrating the advantages of multi-year evaluations. Selection accuracy also increased from 0.582 to 0.797, highlighting the importance of this parameter as an indicator of the precision of genetic predictions.

According to Resende and Alves (2020), selection accuracy values above 0.70 are generally considered acceptable for the early stages of breeding, allowing reliable identification of promising genotypes, whereas values exceeding 0.90 are desirable for final recommendations and cultivar release decisions. In the present study, the 0.70 threshold was surpassed from the third measurement onward (Table 4), indicating that preliminary selection could be performed with satisfactory reliability at this stage. Nevertheless, accuracy continued to increase with additional harvests, thereby reducing the risk of incorrect genotype ranking. This finding is particularly relevant because it demonstrates the possibility of accelerating breeding progress through early identification of superior materials while maintaining confidence in selection decisions. In parallel, selection efficiency increased progressively, reaching 1.403 with six measurements, confirming the advantages of predicting genotypic values from repeated assessments (Falconer & Mackay, 1996). Similar considerations regarding the importance of accuracy-related parameters for supporting robust genotype evaluation and recommendation have been reported by Ferrão et al. (2024) and Partelli, da Silva et al. (2022).

Based on the results, the analysis of multiple harvests is essential to reduce the influence of environmental factors and ensure greater reliability in the estimates, as reinforced by Resende and Alves (2020). The integration of modern tools, such as GWS, has shown promise by promoting greater genetic gain per unit of time (Alkimim et al., 2020; Paixão et al., 2022), further expanding opportunities for advancement in coffee breeding programs.

The analysis of mean components, performed using the individual BLUP approach, revealed significant genetic variability among the *C. canephora* genotypes evaluated across the six harvests (Table 5). This variability is essential for the success of breeding programs, as it allows the identification of superior genotypes with high production potential (Zaidan et al., 2023). Among the genotypes analyzed, LB1 stood out

due to its highest predicted genotypic value ($u + g = 19.16$) and an adjusted mean of $106.6 \text{ bags ha}^{-1}$, positioning it as one of the most promising materials for recommendation and advancement in selection programs.

The REML/BLUP approach enables accurate prediction of genetic values, allowing the selection of individuals with greater precision because the method allows a more precise partitioning of variance (Resende, 2016). The reliability of these estimates is evidenced by the genetic gains observed in the ten most productive genotypes, whose gains ranged from 11.48 to $19.16 \text{ bags ha}^{-1}$, with adjusted population means above $98.91 \text{ bags ha}^{-1}$. These data demonstrate the method's efficiency in increasing average crop yield and promoting greater phenotypic stability across harvests, agreeing with previous findings (Martins et al., 2019; D. O. Silva et al., 2018).

Genotypes LB1, Bicudo, AD1, Z21, Peneirão, Z39, A1, and 143 exhibited the highest predicted genotypic values (g between 9.5 and 19.2), adjusted means between 97.0 and $106.6 \text{ bags ha}^{-1}$, and genetic gains ranging from 12.5 to $19.2 \text{ bags ha}^{-1}$. With these characteristics, these genotypes can be considered “elite” and of high genetic value, recommended for commercial plantings and inclusion in breeding programs. In contrast, genotypes with lower performance, such as B01 and Alecrim, showed negative predicted genetic values ($g = -25.01$ and -20.61 , respectively), with adjusted means of 62.41 and $66.81 \text{ bags ha}^{-1}$, both below the overall mean of the experiment ($87.43 \text{ bags ha}^{-1}$). While the elimination of chronically underperforming genotypes from productivity-focused programs may be warranted (Akpertey et al., 2022; Falconer; Mackay, 1996), it is important to recognize that genotypes with lower gross yield may still carry valuable alleles for traits not captured by the yield criterion alone—including beverage quality, pest and disease resistance, or tolerance to abiotic stresses. Robust plant selection must therefore consider multiple attributes simultaneously; a genotype discarded solely on the basis of yield may retain strategic genetic value for pre-breeding purposes or as a parent in targeted crosses (Salvador et al., 2024).

The adoption of the REML/BLUP approach for longitudinal analysis in perennial crops such as coffee has proven to be highly effective. Studies such as that by D. O. Silva et al. (2018) demonstrated that selecting the top 10% of genotypes based on BLUP led to yield increases of up to 49.88% in processed coffee, highlighting the method's power in capturing gains across multiple harvests. Similar results were reported by Bergo et al. (2020) in evaluations over five harvests, reinforcing the methodology's ability to account for environmental effects and biennial production, which are common in perennial species.

Group I comprised genotypes LB1, Bicudo, AD1, Z21, Peneirão, Z39, A1, and 143, which exhibited the highest predicted yields, ranging from 98 to 109 bags ha^{-1} . These

genotypes represent the most promising candidates for direct selection and for use as parents in breeding programs aimed at increasing yield potential. Their superior performance over multiple harvests indicates favorable genetic merit and reinforces their value for future cultivar development (Viana et al., 2022).

Group II included genotypes with predicted yields between 88 and 97 bags ha^{-1} , all above the overall population mean. Although less productive than those in Group I, these materials also constitute valuable genetic resources for breeding programs and may be considered for recurrent selection or direct evaluation under different production environments. Previous studies have similarly highlighted the importance of exploiting superior-performing *C. canephora* genotypes to maximize genetic gain while accounting for environmental influences on productivity (Rocha et al., 2021).

In contrast, Groups III and IV comprised genotypes with below-average predicted yields, ranging from 78 to 87 and 60 to 72 bags ha^{-1} , respectively. Although these materials are less suitable for direct selection based on productivity, they should not be disregarded, as they may harbor favorable alleles for other agronomic traits and therefore represent valuable sources of genetic diversity for strategic crossing schemes. In *C. canephora*, the conservation and exploitation of genetically diverse germplasm have been recognized as essential strategies to sustain long-term breeding progress and prevent genetic narrowing of breeding populations (Salvador et al., 2024; Zaidan et al., 2023).

5 | CONCLUSIONS

Wide genetic variability was observed among the evaluated materials, and variance component estimates revealed the predominance of permanent environmental effects and genotype $\times$ harvest interactions. Nevertheless, the significant genotypic variance and heritability of the genotype mean indicate high potential for selection response based on multi-year means. Repeatability and average genotypic correlation between harvests support the relative stability of genotypes over time, validating the feasibility of early selection from the third harvest onward.

The BLUP approach proved efficient in predicting true genetic values, allowing for the accurate identification of superior genotypes. Genotypes LB1, Bicudo, AD1, Z21, Peneirão, Z39, A1 and 143 exhibited the highest genetic values, with adjusted means between 97.0 and $106.6 \text{ bags ha}^{-1}$, and significant genetic gains, making them suitable for commercial planting and strategic crosses. In contrast, Beira Rio 8, 18, Alecrim, and B01, with performance below the overall mean, should be considered for elimination or use in pre-breeding programs aimed at recovering specific agronomic traits.

Stratifying genotypes by yield enabled the classification of materials into four distinct groups, reinforcing the applicability of the REML/BLUP approach in coffee breeding and highlighting the value of longitudinal data for enhancing accuracy and selection efficiency.

The results demonstrate that genotype selection based on predicted genetic values can be performed reliably from the third year of evaluation, as selection accuracy surpassed 0.70 from the third measurement onward. This enables the attainment of earlier genetic gains and the shortening of experimental cycles, thereby facilitating the selection of more productive genotypes that exhibit enhanced stability and resilience in the face of contemporary environmental challenges.

AUTHOR CONTRIBUTIONS

Leandro Mendel da Cruz: Data curation; formal analysis; investigation; methodology; validation; visualization; writing—original draft; writing—review and editing. **Gleison Oliosi:** Formal analysis; investigation; methodology; visualization; writing—original draft; writing—review and editing. **Flavia Alves da Silva:** Conceptualization; data curation; formal analysis; investigation; methodology; validation; visualization; writing—original draft; writing—review and editing. **Henrique Duarte Vieira:** Data curation; formal analysis; investigation; methodology; validation; writing—review and editing. **Alexandre Pio Viana:** Conceptualization; data curation; investigation; methodology; supervision; writing—review and editing. **Marcelo Antonio Tomaz:** Investigation; methodology; validation; writing—review and editing. **Raphael Ricon de Oliveira:** Conceptualization; formal analysis; investigation; methodology; supervision; validation; writing—review and editing. **José Cochicho Ramalho:** Conceptualization; formal analysis; investigation; methodology; validation; writing—original draft; writing—review and editing. **Fábio Luiz Partelli:** Conceptualization; data curation; investigation; methodology; resources; supervision; validation; writing—original draft; writing—review and editing.

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CONFLICT OF INTEREST STATEMENT

The authors declare no conflicts of interest.

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