

Identification of morphoagronomic traits correlated with the N use efficiency in coffee

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ABSTRACT

The study of nutritional efficiency is an expensive process, as it requires extensive planting areas, several years of evaluation and the destruction of plants. To mitigate these difficulties, a strategy would be to identify easily measurable traits associated with nutritional efficiency in growing a nutritional solution. Thus, the objective of this study was identify morphoagronomic traits correlated with the N-efficiency indices in to assist in selecting coffee genotypes for environments with N restriction. Twenty arabica coffee genotypes were grown in a nutrient solution with a low concentration of nitrogen (1.0 mmol L⁻¹). The experiment was conducted in a randomized block design with three replications. There was variability among the coffee genotypes for all the traits evaluated. Most of the traits evaluated showed greater genetic than environmental influence on phenotypic expression. Heritability (H^2) was greater than 70% for most of the traits evaluated, with an emphasis on plant height and internode length, which also had the highest relative variation indices (RVIs). The associations between morphoagronomic traits and nutritional efficiency indices revealed greater contributions of genotypic correlation than of environmental correlation. Among the traits associated with nutritional efficiency indices, stem diameter has the potential for use in breeding programs for the selection of cultivars that present greater nitrogen efficiency in environments with nitrogen restriction.

Key words: *Coffea arabica*; genetics parameters; indirect selection; mineral nutrition; plant breeding.

1 INTRODUCTION

Brazil is the fourth largest consumer of nitrogen fertilizers in the world and is highly dependent on the import of this agricultural input (Ministério da Agricultura Pecuária e Abastecimento - MAPA, 2022). Nitrogen (N) is a fundamental macronutrient for plant growth and development because it affects the synthesis of amino acids and proteins, photosynthetic events, flower bud formation, and the fruiting and chemical composition of grains (Luo; Zhang; Xu, 2020; Liu; Hu; Chu, 2022). Thus, N is considered an essential factor for crop productivity (Mu; Chen, 2021), and the most required in coffee farming. To achieve high productivity, Brazilian coffee orchards often receive doses of up to 600 kg ha⁻¹ year⁻¹ of N (Martinez et al., 2019). However, is estimated that at least 50% of this nutrient applied to the soil can be lost through volatilization or leaching (Leal; Salamanca-Jimenez; Sadeghian 2010; Cannavo et al., 2013), resulting in a 60% reduction in coffee productivity (Khalajabadi, 2008).

Given such issues and the current fertilizer supply crisis, research focusing on mineral nutrition and the identification of more efficient genetic materials for the use of nutrients has been noted as an alternative to reduce this agricultural input demand, according to the goal established by the National Plan of Fertilizers (NLP) (MAPA, 2022). Several studies have

investigated the nutritional efficiency of zinc (Zn) (Martinez et al., 2011; Pedrosa et al., 2013), potassium (K) (Moura et al. 2015), phosphorus (P) (Neto et al., 2016; Vilela, 2021), and N (Moura et al., 2019; Martinez, et al., 2024) deprivation in coffee. These studies are carried out by estimating nutritional efficiency indices, obtained by the relationship between dry mass production and nutrient content in the different parts of the plant (Bailian; Mckeand; Allen, 1991; Siddiqi; Glass, 1981). From this perspective, the selection of coffee cultivars that are better adapted to soils with low nutrient availability is a promising way to meet this demand (Moura et al., 2016) and contribute to the sustainable production of coffee (Van Der Vossen; Bertrand; Charrier, 2015).

The mechanisms that contribute to plant element uptake, transport, and use of nutrients in plants are under genetic control, and this is a key point for plant breeding programs that seek to select cultivars for more efficient use of nutrients (Gabelman; Gerloff, 1983). Traits involved in plant adaptation to environments with low nitrogen fertility usually present quantitative inheritance thus are strongly influenced by environmental factors (Martinez et al., 2020).

To understand the of more nutritionally efficient plants, it is essential to estimate the genetic parameters underlying traits of cultivars subjected to the absence or restriction of nutrients. Indeed, genetic parameters such as phenotypic

variance, the genotypic variation coefficient, and heritability provide a more accurate evaluation of the degree of genetic variability in a population, supporting the prediction of genetic gains and consequently the chance of success of the plant breeding program (Cruz; Regazzi; Carneiro, 2012).

Assessing nutritional efficiency is a time-consuming, costly, and destructive process. Therefore, indirect selection is viewed as an effective strategy to achieve compensatory genetic gains. This approach not only facilitates the selection of superior genotypes but also enhances genetic progress over time, while saving on labor and resources (Moreira et al., 2022). Therefore, it is important to study the associations between easily measured traits and nutritional efficiency indices to enhance this process (Moura et al., 2016). Understanding the nature of these correlations could lead to greater genetic gains in crops under nutrient-restricted conditions.

Thus, the objective of this study was to identify morphoagronomic characteristics correlated with N efficiency indices to assist in the selection of coffee genotypes for N-restricted environments.

2 MATERIAL AND METHODS

The experiment was carried out in a greenhouse at the Department of Agronomy of Universidade Federal de Viçosa (UFV), Viçosa - MG (648 m, 20° 45' S, and 42° 52' W).

Twenty genotypes of Arabica coffee (*Coffea arabica* L.) were evaluated: four historic genotypes (Caturra Amarelo; São Bernardo; San Ramon and Caturra Vermelho) and sixteen cultivars released by several Research Institutions in Brazil (Catuaí Amarelo IAC 62; Paraíso MG H 419-1; Icatu Vermelho IAC 4045; Obatã IAC 1669/20; Pau Brasil MG1; IPR 102; Catuaí Vermelho IAC 15; Rubi MG 1192; IPR 103; Araponga MG; Topázio MG 1190; Icatu Precoce 3282; Tupi IAC 1669-33; Catucaí 785/15; Acaiaí Cerrado MG 1474 and Oeiras MG 6851).

To obtain coffee seedlings, the seeds of the genotypes were sown in a bed of sand previously disinfected with hydrochloric acid (HCl 0.1 mol dm⁻³). After 120 days, when the plants reached the cotyledonary leaf stage, two seedlings of each cultivar were transplanted to plastic pots with 8.0 L of modified Hoagland and Arnon (1950) nutrient solution to provide a low concentration of N (1.0 mmol. L⁻¹), supplied as potassium nitrate (KNO₃). The nutrient solution was supplemented weekly with deionized water to maintain the initial volume. Whenever necessary, the pH was adjusted between 5.5 and 6.5 using both HCl (0.1 mol dm⁻³) to acidify the solution and sodium hydroxide (NaOH) (0.1 mol dm⁻³) to increase the hydrogen potential (pH). In addition, the nutrient solution was changed when the electrical conductivity (EC) depletion reached 30%.

At 168 days of cultivation, the following morphoagronomic traits were evaluated: stem diameter (SD,

mm), measured at 5 cm from the stem base with a calliper; plant height (PH, cm), measured from the base of the orthotropic branch to the apex of the plant; internode length (IL, cm), calculated by the ratio between the plant height and the number of nodes; the number of leaf pairs (NLP), obtained by counting the whole plant; the number of nodes (NN), obtained by counting in the main branch (orthotropic); and leaf area (LA, dm²), quantified after harvest using the leaf area meter (Delta-T Devices Ltd)

The plants were subsequently sectioned into roots, stems and leaves and dried in an oven with forced air circulation at 70 °C for 72 h to obtain the root dry mass (RDM, g), stem dry mass (SDM, g) and leaf dry mass (LDM, g). The shoot dry mass (SHDM, g) consisted of the sum of the LDM and SDM, whereas the total dry mass (TDM, g) was the sum of the SHDM and RDM. The dried plant material was ground in a “Willey” mill to determine the N content according to the methodology proposed by (Empresa Brasileira de Pesquisa Agropecuária - Embrapa, 2009). N content was calculated as the product of the nutrient content in the different parts of the plant and dry mass production.

The nutritional efficiency indices for N were estimated according to the methodology described by Siddiqi and Glass (1981) and Bailian, Mckeand and Allen (1991): rooting efficiency (RE, g²/mg) = (root dry mass)²/total N in the plant, absorption efficiency (AE, mg/g) = total plant N/root dry mass, translocation efficiency (TE, mg/g) = N in the shoot/total N in the plant, utilization efficiency (UE, g²/mg) = (total dry mass)²/total N in the plant, and biomass production efficiency (BPE, g²/mg) = (dry mass of shoot)²/N in the shoot.

2.1 Experimental Design and Statistical Analysis

A randomized block design with three replications was used. The experimental units consisted of two plants grown in pots with an aerated static nutrient mixture with a low concentration of N (1.0 mmol L⁻¹).

The analysis of variance for each agromorphological trait and nutritional efficiency index was performed according to the statistical model described in Equation (1):

$$Y_{ij} = \mu + G_i + B_j + \varepsilon_{ij} \quad (1)$$

where Y_{ij} is the observation in the j^{th} block, evaluated in the i^{th} cultivar; μ is the overall mean of the experiment; G_i is the effect of the i^{th} genotype considered random, with normal distribution, $G_i \sim N(0, \sigma_g^2)$; B_j is the block effect on the j^{th} block, considered fixed, $B_j \sim N(0, \sigma_b^2)$; and ε_{ij} is the random error associated with the observation Y_{ij} , with normal distribution, $\varepsilon_{ij} \sim N(0, \sigma^2)$.

The phenotypic (σ_f^2), environmental (σ_e^2) and genotypic (σ_g^2) variance components were estimated (Cruz; Regazzi; Carneiro, 2012) as follows in Equation (2):

3 RESULTS

$$\hat{\sigma}_f^2 = \frac{MSG}{b}, \quad \hat{\sigma}_e^2 = MSR, \quad \text{and} \quad \hat{\sigma}_g^2 = \frac{MSG - MSR}{b}.$$

where *MSG* and *MSR* represent the mean squares of the genotypes and residues, respectively, and (*b*) the number of repetitions.

The estimates of the percentage of the genotypic variation coefficient ($\widehat{CV}_g$) and relative variation index (*RVI*) are described below: $\widehat{CV}_g(\%) = \frac{100\sqrt{\sigma_g^2}}{\hat{m}} \times 100$ and $= \frac{\widehat{CV}_g}{\widehat{CV}_e}$,

where $\hat{m}$ is grand mean of a trait.

Broad-sense heritabilities of the traits were calculated from the variance components obtained by the model via the following expression in Equation (3):

$$H^{2(i)} = \frac{\sigma_g^{2(i)}}{(\sigma_g^{2(i)} + \sigma_e^{2(i)})} \quad (3)$$

where $\sigma_g^{2(i)}$ and $\sigma_e^{2(i)}$ are the genetic and residual variations for each trait, respectively.

The correlation coefficients between pairs of traits were obtained as suggested by Falconer (1960) and Piepho et al. (2018) via the expression below for all the models:

$$\rho_{g_{i,j}} = \frac{\sigma_g(i,j)}{\sqrt{\sigma_{gi}^2 \sigma_{gj}^2}} : \text{genotypic correlation between traits } i \text{ and } j;$$

$$\rho_{f_{i,j}} = \frac{\sigma_f(i,j)}{\sqrt{\sigma_{fi}^2 \sigma_{fj}^2}} : \text{phenotypic correlation between traits } i \text{ and } j$$

and

$$\rho_e = \frac{\sigma(i,j)}{\sqrt{\sigma_i^2 \sigma_j^2}} : \text{environmental correlation between traits } i \text{ and } j.$$

Correlation matrices were used to obtain the correlation networks, in which the links between variables were determined by the “adjacency matrix” $A = h(R)$, with the following function: $0.5\{SNG(|r_{ij}| - \rho) + 1\}$, where ρ is the parameter that determines the minimum value that a correlation must present to be represented in the correlation network. In this work, $\rho = 0$ was defined so that all connections between variables could be traced (Silva et al., 2016).

The thickness and colour intensity of the edges were controlled by applying a cut-off value equal to 0.3, which means that only lines with $|r_{ij}| > 0.3$ are highlighted. Finally, positive correlations are coloured in dark green, whereas negative correlations are depicted in red. Analyses were performed using the GENES software (Cruz, 2016).

3.1 Analysis of Variance

Variance analysis of the genotypes revealed significant differences for all the evaluated traits ($p < 0.01$) (Table 1). The lowest CVe was observed for NN (3.88%), and the highest was observed for RE (34.71%) (Table 1). These results are in agreement with those reported in the literature for studies on Arabica coffee in a nutrient solution (Pedrosa et al., 2013; Moura et al., 2016, 2019).

As shown in Table 2, for most of the traits evaluated, the estimates of phenotypic variances had greater genetic contributions than did the estimates of environmental variances (Table 2). The traits with the highest estimates of genotypic variance were AE, LA, PH, and SD. In contrast, the lowest values were observed for RE, TE, BPE, and UE (Table 2).

3.2 Broad-sense Heritability

Most of the evaluated traits exhibited heritability in the broad sense (H^2) greater than 70% (Table 2). The PH and IL traits were highly heritable: $H^2 = 94.47\%$ and 94.41% , respectively. On the other hand, the lowest estimates were for the AE and TE indices of N: $H^2 = 69.11\%$ and 64.58% , respectively (Table 2).

3.3 Genetic Variability and Relative Variation Index

The highest relative variation indices (RVIs) were found for the traits PH and IL, which had the highest estimates of H^2 (Table 2). On the other hand, the RE, AE, and TE indices had RVI estimates lower than unity,

3.4 Correlation network

The correlation network revealed a strong association between morphoagronomic traits and nutritional efficiency indices.

With respect to the phenotypic correlation network, structures of groups of correlated traits were observed. The first structure occurred between the NN, NLP, PH, and IL traits, which were positively correlated, but with variations in magnitude (Figure 1A). The second structure occurred between the LA and SD traits with the RE, BPE, and EU indices, which presented positive and high magnitude correlations and negative correlations with AE and TE. Another structure involved the UE, RE, and BPE indices, which were positively correlated with each other and highly influential and negatively correlated with AE and TE (Figure 1A). Similar clusters were found for the genotypic correlation network, but with higher magnitudes (Figure 1B). On the other hand, the environment had little influence on the expression of the observed correlations (Figure 1C).

Table 1: Summary of analysis of variance of agromorphological traits and nutritional efficiency indices of Arabica coffee genotypes grown in an N-restricted solution.

Source of variation	DF	Mean Square					
		PH	SD	NN	IL	NLP	LA
Block	2						
Genotype	19	134.2**	117.1**	1.0**	1.31**	1.02**	7815**
Residual	38	7.42	246.5	0.12	0.07	0.13	100.6
Mean		30.08	46.26	9.18	3.28	8.18	114.46
CVe (%)		9.06	10.73	3.88	8.28	4.41	15.57
			RE	AE	TE	UE	BPE
Block	2						
Genotype	19		3.5e-04**	817.9**	0.004**	0.04**	0.02**
Residual	38		9.00E-06	252.5	0.001	5.4E-04	0.003
Mean			0.03	85.05	0.8	0.45	0.33
CVe (%)			34.71	18.68	4.48	16.33	16.07

Significant at the 1% probability level according to the F test; DF: degree of freedom; CVe (%): percentage of the environmental variation coefficient; PH: plant height; SD: stem diameter; NN: number of nodes; IL: internode length; NLP: number of leaf pairs; LA: leaf area; RE: rooting efficiency; AE: absorption efficiency; TE: translocation efficiency; UE: efficiency of use; BPE: biomass production efficiency.

Table 2: Estimates of variance components for agromorphological traits and nutritional efficiency indices of Arabica coffee genotypes grown in a nutrient solution with N restriction.

Trait	$\hat{\sigma}_f^2$	$\hat{\sigma}_g^2$	$\hat{\sigma}_e^2$	H^2	$\widehat{CV}_g$ (%)	RVI
PH	44.76	42.28	2.48	94.47	21.62	2.39
SD	39.01	30.79	8.22	78.94	11.99	1.12
NN	0.33	0.04	0.29	87.40	5.87	1.52
IL	0.44	0.41	0.02	94.41	19.65	2.37
NLP	0.34	0.3	0.04	87.32	6.69	1.51
LA	260.35	226.81	33.54	87.12	15.41	1.5
RE	0.00012	8.3E-05	3.4E-05	70.73	33.25	0.90
AE	272.53	188.37	84.18	69.11	16.14	0.86
TE	0.0012	0.0008	0.0004	64.58	3.54	0.79
UE	0.013	0.012	0.0018	86.50	23.86	1.46
BPE	0.0068	0.0059	0.0009	86.60	23.72	1.47

$\hat{\sigma}_f^2$: phenotypic variance; $\hat{\sigma}_g^2$: genotypic variance; $\hat{\sigma}_e^2$: environmental variance; H^2 : heritability; $\widehat{CV}_g$ (%) percentage of genotypic variation coefficient; RVI: relative variation index; PH: plant height; SD: stem diameter; NN: number of nodes; IL: internode length; NLP: number of leaf pairs; LA: leaf area; RE: rooting efficiency; AE: absorption efficiency; TE: translocation efficiency; UE: efficiency of use; BPE: biomass production efficiency.

3.5 Correlations between Morphoagronomic Traits and Nutritional Efficiency Indices

The morphoagronomic traits showed significant phenotypic and genotypic correlations related to at least one of the nutritional efficiencies for N. The PH, NLP, and NN traits showed genotypic correlations ($p < 0.05$) only with TE ($\rho_f > 50\%$). However, the IL trait demonstrated a positive genotypic

correlation with only the BPE index ($\rho_f = 0.44$, $p < 0.05$). The SD had negative genotypic correlations greater than 70% ($p < 0.01$) with the AE and TE indices and positive correlations greater than 80% with the RE, BPE, and UE indices. The highest estimates of genotypic correlations were found for LA with AE and TE; however, they were negative and above 80% and positive above 90% with RE, BPE, and UE indices.

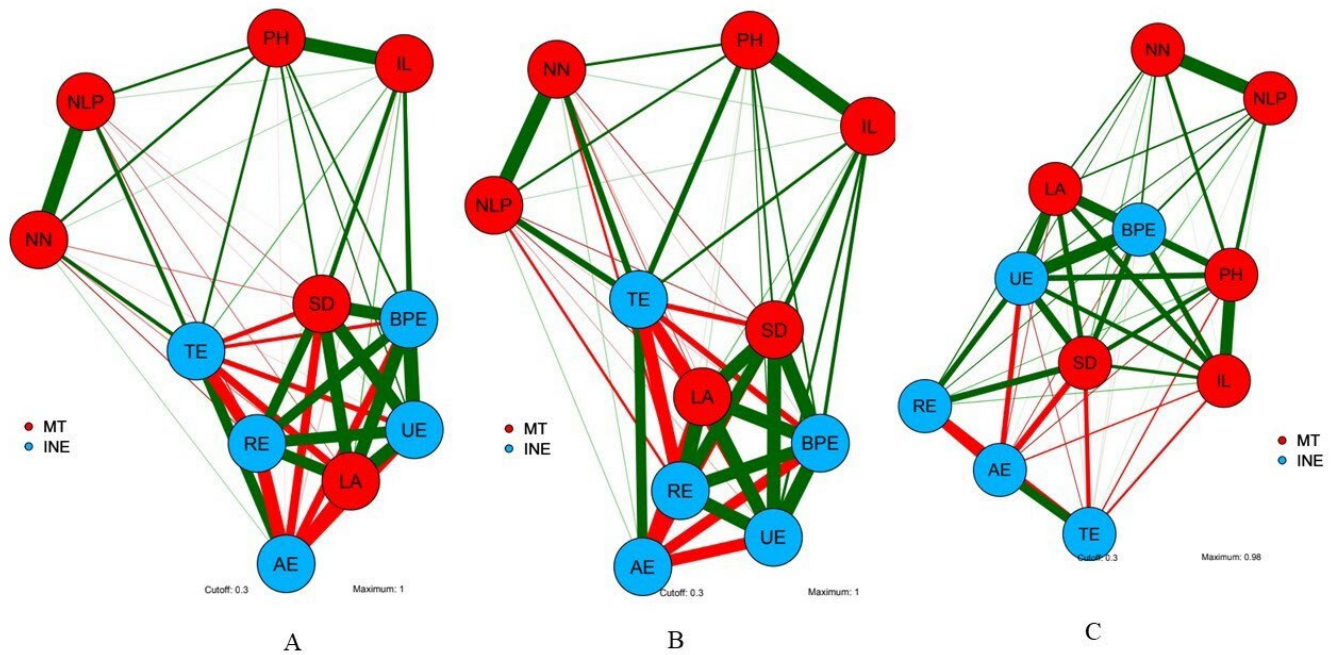


Figure 1: Correlation network of the phenotypic (A), genotypic (B) and environmental (C) traits of Arabica coffee genotypes evaluated in a nutrient solution containing low nitrogen levels. The red and green lines represent negative and positive correlations, respectively. The width of the line is proportional to the strength of the correlation. PH: plant height; SD: stem diameter; NN: number of nodes; IL: internode length; NLP: number of leaf pairs; LA: leaf area; RE: rooting efficiency; AE: absorption efficiency; TE: translocation efficiency; UE: efficiency of use; BPE: biomass production efficiency. MT: morfoagronomics traits; INE: nutritional efficiency indices.

Table 3: Estimates of phenotypic (ρ_f), genotypic (ρ_g) and environmental (ρ_r) correlation coefficients between agronomic traits and nutritional efficiency indices of Arabica coffee genotypes cultivated with N restrictions.

Trait	ρ	RE	AE	TE	UE	BPE
PH	ρ_f	-0.006	-0.030	0.39*	0.33	0.38*
	ρ_g	-0.04	0.011	0.56*	0.31	0.35
	ρ_r	0.22	-0.29*	-0.33*	0.57**	0.65**
NLP	ρ_f	-0.30	0.12	0.46*	-0.053	-0.016
	ρ_g	-0.38	0.14	0.60*	-0.11	-0.073
	ρ_r	0.31	0.38	0.48	0.31*	0.37**
IL	ρ_f	0.11	-0.089	0.26	0.40*	0.45*
	ρ_g	0.098	-0.056	0.41	0.40	0.44*
	ρ_r	0.21	-0.33*	-0.37**	0.50**	0.57**
SD	ρ_f	0.78**	-0.71**	-0.50**	0.91**	0.90**
	ρ_g	0.84**	-0.74*	-0.52	0.96**	0.98**
	ρ_r	0.63**	-0.61**	-0.49**	0.69**	0.56**
LA	ρ_f	0.84**	-0.76**	-0.64**	0.93**	0.92**
	ρ_g	0.99**	-0.91**	-0.84**	0.95**	0.94**
	ρ_r	0.31*	-0.26	-0.051	0.81**	0.83**
NN	ρ_f	-0.29	0.12	0.45*	-0.051	-0.015
	ρ_g	-0.37	0.14	0.58*	-0.10	-0.070
	ρ_r	0.033	0.037	0.055	0.30*	0.36**

**, *: Significant at 1 and 5%, respectively, according to bootstrapping with 5000 simulations. PH: plant height; NLP: number of leaf pairs; IL: internode length; SD: stem diameter; LA: leaf area; NN: number of nodes; RE: rooting efficiency; AE: absorption efficiency; TE: translocation efficiency; UE: efficiency of use; BPE: biomass production efficiency.

4 DISCUSSION

The CVe values observed in this study, as shown in Table 1, are within the low to moderate range, which indicates adequate experimental precision, compatible with the criteria established by Gomes (1985). Therefore, the results obtained indicate that the experimental precision of the study is within an acceptable level.

The demonstration of genetic variability in our study is a basic condition for the development of more efficient genotypes concerning the use of nutrients, which may favour the acclimation of such genotypes in environments with nutritional deficiency to N (Carias et al., 2016; Dubberstein et al., 2020). Similar results have been reported in environments with restrictions on other nutrients (Pedrosa et al., 2013; Moura et al., 2015, 2019; Vilela et al., 2021).

Understanding the nature and intensity of genetic and environmental variations is essential for the success of plant breeding programs that seek to select materials able to grow and develop under conditions of nutritional deficiency. We verified that genetic factors strongly influenced the phenotypic expression of most of the evaluated traits (Table 2). The same behaviour was observed in arabica coffee under K-limiting conditions (Moura et al., 2016).

The high heritability values observed for most of the evaluated traits (Table 2), were similar results reported by Moura et al. (2016) when coffee was cultivated under K restriction in a nutrient solution. This fact confirm that much of the phenotypic variation is related to genetic differences between individuals (Dochtermann et al., 2019), in addition to the reliability with which the phenotypic value represents genetic value (Dubberstein et al., 2020). In this case, there is a chance of selecting superior genotypes with greater precision, as well as with high values of CVg and the CVg/CVe ratio (Dubberstein et al., 2020). Thus, these findings confirm the genetic variability of the evaluated traits and suggest that direct selection for traits with a high estimate of heritability in the broad sense demonstrates favourable conditions in terms of genetic gain.

The presence of genetic variability is confirmed and quantified through the coefficient of genetic variation $\widehat{CV}_g$ (%), which expresses the intensity of the genetic variation in the average of the trait. The estimates of $\widehat{CV}_g$ above 7% are considered high (Sebbenn et al., 1998), which is in agreement with what was observed for most of the evaluated traits (Table 2), with emphasis on the indices of RE, BPE, and UE. This implies that the variability observed in these traits has a genetic predominance.

Most of the characteristics evaluated presented a relative variation index (RVI) above unity (Table 2), within the range reported by Moura et al. (2016), reinforcing that the observed variations were more influenced by the cultivation environment and consequently had higher H^2 estimates.

This means that the CVe values were lower than the CVg values (Tables 1 and 2), suggesting that the observed

variations had greater contributions of a genetic nature rather than an environmental nature (Cruz; Regazzi; Carneiro, 2012; Rodrigues et al., 2016; Dubberstein et al., 2020), which is in close agreement with the genetic gain observations.

The associations between evaluated traits via correlation networks increase the effectiveness of genotype selection since both correlated and groups of traits can be identified (Silva-Junior et al., 2021). The formation of correlated groups involving morphoagronomic traits and specific nutritional efficiency indices was observed, as were associations between them (Figure 1A, 1B and 1C). This reveals that there are possibilities for selection both for suitability for agronomic purposes and for the potential adaptation of coffee trees to develop in environments with low N levels.

The phenotypic correlation network is a result of interactions between genotypic and environmental correlation networks. Therefore, it is essential to assess their contribution to the phenotypic associations between evaluated traits. In this study, we observed that the genotypic correlation networks had greater contributions to the phenotypic associations between the evaluated traits (Figure 1B). This fact may be related to the high heritability values for most of the traits (Table 2), which means that the phenotypic variability is mainly determined by genotypic variability. Therefore, the correlation networks demonstrate the possibility of using morphoagronomic traits in the indirect selection of more efficient genotypes in an environment with N restriction.

The estimates of the phenotypic correlation coefficients (ρ_p), genotypic correlation coefficients (ρ_g) and environmental correlation coefficients (ρ_e) can be interpreted in three ways: magnitude, direction, and significance (Table 3). The positive magnitude of correlation coefficients indicates the tendency of one variable to increase when the other increases, whereas negative correlations indicate a tendency for one variable to increase while the other decreases (Cruz; Regazzi; Carneiro, 2012). The genotypic correlation for most pairs of traits was greater than the phenotypic correlation (Table 3), indicating greater contributions of genetic factors compared to environmental factors to the associations between traits. This result favours the selection process since the genetic effects overlap with the environmental effects in the manifestation of the phenotype.

The identification of morphoagronomic traits that correlated with the nutritional efficiency indices revealed that by selecting genotypes with relatively high values of PH, NLP and NN, genotypes with relatively high N translocation efficiency in the plant can be indirectly selected. Similarly, the selection of genotypes with longer internode lengths contributes to increases in biomass production efficiency.

Although it had negative correlations with the AE and TE traits, the SD trait had a highly significant, positive correlation with the RE, BPE and UE indices. Similar results were observed under potassium-restricted conditions (Moura et al., 2016).

This trait is highly important because it is correlated with the production of coffee and its components (Martinez et al., 2007; Carvalho et al., 2010). LA is also related to plant yield, as both the photosynthetic process and biochemical compound production occur in the leaves, and they are subsequently translocated to produce coffee beans (Bote et al., 2018). In general, this trait displayed the highest values of genotypic correlations with the index of biomass production (Table 3).

Among the evaluated traits, SD and LA were highlighted as potential indicators to indirectly select efficient genotypes in an N-restricted culture environment. In addition, they were clustered into groups presenting N-use efficiency indices on the basis of networks of phenotypic and genotypic correlations (Figure 1A and 1B), in addition to showing high heritability in the broad sense and relative variation indices greater than one unit (Table 2). However, since SD is easy to measure and is a nondestructive assessment, this trait can be used more effectively during the indirect selection of N-efficient plants to obtain genetic gains. As this research was conducted in a controlled environment, it is suggested that future work be replicated in the field under different soil and climate conditions.

5 CONCLUSIONS

The estimates of genetic parameters demonstrate variability in the evaluated morphoagronomic traits and nutritional efficiency indices. The SD trait can support the selection of N-efficient genotypes when cultivated in environments with restrictions on this nutrient.

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7 AUTHORS' CONTRIBUTIONS

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