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Research article

Initial performance and genetic diversity of coffee trees cultivated under contrasting altitude conditions

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ABSTRACT: This work evaluated the initial performance and genetic diversity of *Coffea canephora* genotypes cultivated in environments at contrasting altitudes. Fourteen morphophysiological traits and seven descriptors of the genus *Coffea* spp. of coffee trees cultivated at altitudes of 140 m and 700 m were evaluated. The design used was Federer's augmented block in a 2 × 112 factorial scheme with six blocks. The first factor was the two environments, and the second was the 112 genotypes, with eight common treatments, being five conilon coffee clones and three arabica coffee cultivars. The data were analyzed by the method of REML/BLUP and genetic correlation method. Genetic diversity was evaluated by estimating the distance matrix, applying the Gower methodology followed by the clustering method by Tocher and UPGMA. The phenotypic means were higher in the environment at an altitude of 700 m, except for plant height, number of leaves, and canopy height (CH). Genotypic effects were significant for most traits except for leaf width, CH, unit leaf area, and total leaf area. A wide genetic diversity was verified, with distances varying from 0.037 to 0.593 for the pairs of genotypes 26 × 93 and T7 × 76, respectively. Most of the traits studied showed high genotypic correlation with the environment and expressive genetic correlation between the evaluated traits thereby demonstrating the possibility of indirect selection. There is an adaptation of conilon coffee genotypes to high altitudes and the possibility of developing a specific cultivar for the southern state of Espírito Santo.

Keywords: *Coffea canephora*, REML/BLUP, ordering, genetic variability, deviance

Introduction

Coffee is one of the top products in the world of agribusiness, with a total production of approximately 170 million bags, whose commercial production depends mainly on the species *Coffea arabica* Lineu and *Coffea canephora* Pierre ex Froehner (ICO, 2021). Brazilian production for 2021 was estimated at 30.73 million bags of *C. arabica* and 16.15 million bags of *C. canephora*, on a planted area extending 1.8 million hectares (CONAB, 2021).

Knowledge of the performance of coffee tree genotypes in contrasting altitude environments is an improvement strategy in identifying and selecting those promising and most adapted under such conditions that is compellingly significant. In higher altitude areas, coffee trees take longer to complete their cycle (Silva et al., 2004). Specifically, conilon coffee has satisfactory growth rates when grown in places with temperatures between 17 and 34 °C (Partelli et al., 2013). When grown at low temperatures, both the net photosynthetic rate and photosystem II efficiency are reduced (Barbosa et al., 2014; Partelli et al., 2009). However, when exposed to low temperatures is gradual, the species can express defense mechanisms and (or) acclimatization, allowing for adjustments to these conditions with different capacities found among the genotypes (Barbosa et al., 2014; Ramalho et al., 2014). Studies involving the evaluation of morphological traits can significantly contribute to defining the best strategy in conilon breeding programs (Alkimim et al., 2021) which maximize the identification of promising genotypes.

Conilon coffee has extensive genetic variability, which is the basic and necessary condition for success in genetic breeding programs (Alkimim et al., 2018; Babova et al., 2016; Ferrão et al., 2019a; Ferrão et al., 2021). With this in mind, discovering new genotypes allied to the evaluation of those still in the initial phase of the study, such as the one carried out in this research, allows for the prior identification of promising ones. This work aimed to study the initial performance and the genetic diversity of genotypes of conilon coffee from field collections in the southern region state of Espírito Santo and the Incaper breeding program, cultivated in regions with contrasting altitudes of 140 and 700 m to select promising genotypes with adaptability and stability.

Materials and Methods

The experiments were implemented and conducted in two contrasting environments in terms of altitude in the municipalities of Cachoeiro de Itapemirim and Alegre, located in the southern region of the state of Espírito Santo. The *C. canephora* genotypes used in this work have three origins: 1 – genotypes from the genetic breeding program of the Instituto Capixaba de Pesquisa, Assistência Técnica e Extensão Rural (Incaper) which are not present in commercial varieties; 2 – elite clones of commercial varieties; 3 – genotypes collected

in commercial plantations in the municipalities located in the southern region of Espírito Santo, above 600 m of altitude, originating from seed seedlings and, or, clonal seedlings from crops with more than thirty years of implantation (Table 1).

In the low altitude environment (A_1) the experiment was carried out at Cachoeiro de Itapemirim, at 20°45′00″ S, 41°17′00″ W, altitude 140 m. In the high altitude environment (A_2) the experiment was installed on a private rural property in the municipality of Alegre, located at 20°52′00″ S, 41°28′00″ W, altitude 700 m. The plantings were carried out in Dec 2020 with a spacing of 2.5 m between rows and 1.0 m between plants. Fertilization for planting and management followed the fertilization and liming manual for the state of Espírito Santo (Ferrão et al., 2019b). The cultural and phytosanitary treatments were carried out according to the requirements of the crop (Ferrão et al., 2019b).

The design used was Federer's augmented block in a 2 × 112 factorial scheme, with six blocks and five plants per plot. The treatments corresponded to the 112 coffee tree genotypes, eight common treatments (controls T1 to T8), cultivated in two contrasting environments for altitude (Table 1).

At six months of age, the following morphophysiological characteristics were evaluated:

PH: Plant height was measured with a graduated ruler by the length of the largest orthotropic branch (cm);

SBD: Stem base diameter was measured with a precision digital caliper (0.01 mm) in the intermediate position of the soil up to the first plant node perpendicular to the planting line (mm);

CDL: Canopy diameter of the coffee tree in line direction was measured with a graduated ruler, taking the greatest distance from the end of the branches that make up the coffee tree canopy in the longitudinal direction of the planting line (cm);

CDT: Canopy diameter of the coffee tree in the transverse direction was measured with a graduated ruler, taking the greatest distance from the end of the branches that make up the canopy of the coffee tree in the perpendicular direction of the planting line (cm);

CDA: Canopy diameter average of the coffee tree was estimated by the average between CDL and CDT (cm);

NL: Number of leaves, was obtained by counting the number of leaves in the plant (und);

NDVI: Normalized Difference Vegetation Index was measured with a PlantPen NDVI-300 portable sensor (Photon Systems Instruments PSI), using two leaves of the third or fourth pair, from the plagotropic branch, from the middle position of the plant (und);
LL: Leaf length was measured with a graduated ruler, taking the length of the leaf from the base of the leaf blade to the opposite end in the longitudinal direction. Leaves of the third or fourth pair were used, starting from the tip of the branch in the direction towards the center of the coffee tree canopy, in the plagiotropic branches of the middle third of the plant (cm);

LW: Leaf width was measured with a graduated ruler using the leaf evaluated for LL, measuring the largest width of the leaf in the transverse direction (cm);

CH: Canopy height was measured with a graduated ruler taking the distance between the beginning of the coffee tree canopy and its end (cm);

ALU: Unit leaf area (cm^2) estimated by the equation of Schmildt et al. (2015)

$$ALU = 0.6723 + 0.6779 * (LL * LW) \quad (1)$$

ALT: Total leaf area estimated by the product of NL and ALU (cm^2);

Table 1 – Identification and origin of the evaluated coffee trees genotypes.

Genotypes	Number of genotypes	Origin
1, 2, 4, 5, 6, 7, 8 and 9.	8	Alegre – ES
10, 11,12, 13, 14, 15, 16, 17, 18 and 19.	10	Iúna – ES
20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 and 31.	12	Jerônimo Monteiro – ES
32, 33, 34, 35, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56 and 57.	25	Muniz Freire – ES
59, 62, 63, 65, 66, 67, 68, 69, 70, 71, 72, 73, 75,76, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111 and 112.	49	Clones of the Incaper conilon coffee tree breeding program
T1, T2, T3, T4 and T5.	5	Elite clones conilon coffee tree of commercial varieties[1] 102, 105, 108, 201 and 405
T6, T7 and T8.	3	Arabica coffee tree cultivars[2]: 24/137, 785/15 and Arara

[1]102, 105 and 108 – Clones two, five and eight of the cultivar 'ES8112' 'Diamante', popularly known as 23/93, 02/86 and A1 respectively; 201 – Clone one of the cultivar 'ES8122' 'Jequitibá', popularly known as LB1; 405 – Clone five of the cultivar 'ES8143' 'Marilândia'. [2]Witness of *Coffea arabica* L.

CV: Canopy volume (m^3) estimated by the equation of Favarin et al. (2002)

$$CV = \frac{\frac{(\pi * CDA^2 * CH)}{12}}{1000000} \quad (2)$$

LAI: Leaf area index ($m^2\,m^{-2}$) estimated by the equation of Favarin et al. (2002)

$$IAF = 0.0134 + 2.7791CV \quad (3)$$

It should be noted that the NDVI, LL and LW measurements were performed on the same leaves.

Concomitantly with the evaluation of the morphophysiological parameters, the genotypes were characterized in relation to seven descriptors of the genus *Coffea* spp. as recommended by the Ministério da Agricultura, Pecuária e Abastecimento – MAPA (Secretaria de Apoio Rural e Cooperativismo, 2000) (Table 2).

Data analysis was obtained by using the restricted maximum likelihood method and best unbiased linear prediction (REML/BLUP), and the Selegen software (Resende, 2007), model 75 Eq. (4).

$$y = X_f + Z_g + W_b + T_i + e \quad (4)$$

where y is the phenotypic data vector, f the vector of effects assumed to be fixed (means of controls and population average of main treatments at each site), g the vector of the genotypic effects (assumed to be random), b the vector of environmental effects of blocks (assumed to be random), i the vector of the effects of the genotype × environment interaction (random) and e the vector of errors or residues (random). The capital letters represent the incidence matrices for these effects.

Table 2 – Phenotypic descriptors of the genus *Coffea* spp. recommended by the Ministério da Agricultura, Pecuária e Abastecimento (MAPA).

Descriptor/Trait	Category	Code	Reference Cultivar
Leaf: form	Elliptical	1	
	Oval	2	
	Lanceolate	3	
Leaf: color in young phase	Green	1	Catuaí
	Bronze	2	
	Green and bronze	3	
	Purple	4	
Leaf: color in adult phase	Light green	1	Obatã
	Dark green	2	
	Purple	3	
Leaf: intensity of edges undulation	Weak	3	New World
	Medium	5	
	Strong	7	
Leaf: secondary rib depth	Low	3	New World
	Medium	5	
	High	7	
Leaf: length	Short	3	
	Medium	5	
	Long	7	
Leaf: width	Narrow	3	
	Medium	5	
	Wide	7	

The significance of the random effects of the statistical model was tested by deviance analysis using the likelihood ratio test (LRT) according to the following expression:

$$LTR = -2(LogL - LogL_R) \quad (5)$$

where LogL is the logarithm of the maximum (L) of the constrained likelihood function of the complete model, and $LogL_R$ the logarithm of the maximum (LR) of the restricted likelihood function of the reduced model (without the effect being tested). The LRT was analyzed considering the chi-square test with a degree of freedom at 1, 5 and 10 % of significance.

The genetic diversity of coffee trees plants was estimated based on the Gower distance (Gower, 1971), from morphophysiological characters (quantitative data), standardized with a mean of zero and standard deviation equal to one, and the descriptors (qualitative data) followed by the clustering method by optimization by Tocher and UPGMA hierarchical. The genetic correlation between the evaluated traits was evaluated using the correlation matrix. All statistical analyses were performed with the help of Selegen (Resende, 2016) and R version 4.0.5 and GENES (Cruz, 2016) software programs. The dendrogram image was development in the 'PerformanceAnalytics' package (Peterson and Carl, 2020) and the genetic correlation in the 'factoextra' package (Kassambara and Mundt, 2020).

Results and Discussion

The phenotypic means were higher in the A2 environment, except for the PH, NL and CH traits (Table 3). The estimates of variance components and prediction of genetic parameters were efficient in detecting genetic variability and differentiated performance between genotypes, since the genotypic effects were significant for most traits, except for LW, CH, ALU, ALT (Table 3). Only the NL, LW, ALU and ALT traits were not significant for the bocks. As for the effect of the genotype and environment interaction, significance was observed exclusively for NL and CH (Table 3). Expressive effects indicate the presence of genotypic variability, differences between environments and the possibility of selecting genotypes for the two environments or specific locations (Resende and Duarte, 2007). Studies with *C. canephora* clones have shown wide genetic variability detected by estimating the variance components (Alkimim et al., 2021). Furthermore, when the effects are significant, as for most traits in this study, future selection of promising genotypes becomes increasingly efficient.

The LL, LW, CH, ALU and ALT traits showed low magnitude heritability estimates, and the other traits moderate heritability, with the highest heritability found at 37.60 % for PH. According to Resende and Alves (2020)

Table 3 – Components of variance, genetic parameters and phenotypic means of morphophysiological traits of 112 coffee trees genotypes cultivated in two environments, Cachoeiro do Itapemirim, Espírito Santo, Brazil at an altitude of 140 m and in the municipality of Alegre, Espírito Santo, Brazil at an altitude of 700 m

	PH	SBD	CDL	CDT	CDA	NL	NDVI
Components of variance							
V_g	29.1524**	0.6716**	24.3197*	25.6807**	26.6059**	232.8829**	1.9E-04**
V_b	3.6423**	0.0802*	11.4254**	6.9030**	9.8275**	23.1830^{ns}	9.2E-05**
V_i	6.9543^{ns}	0.0698^{ns}	12.3960^{ns}	14.7792^{ns}	8.3398^{ns}	71.4964^{o}	2.2E-05^{ns}
V_e	37.7812	1.3236	84.1093	66.1412	54.1513	507.5686	4.2E-04
V_f	77.5303	2.1453	132.2504	113.5040	98.9245	835.1309	7.3E-04
Genetic parameters							
h^2	0.3760	0.3131	0.1839	0.2263	0.2690	0.2789	0.2615
c_b^2	0.0470	0.0374	0.0864	0.0608	0.0993	0.0278	0.1269
c_i^2	0.0897	0.0325	0.0937	0.1302	0.0843	0.0856	0.0301
r_{gl}	0.8074	0.9058	0.6624	0.6347	0.7613	0.7651	0.8969
Phenotypic means							
General	43.7794	6.6610	42.2694	40.3682	41.3284	59.4823	0.6274
A1	46.0147	6.4513	40.2029	36.9307	38.5968	68.7781	0.6151
A2	41.5441	6.8707	44.3358	43.8056	44.0601	50.1864	0.6396
	LL	LW	CH	ALU	ALT	CV	LAI
Components of variance							
V_g	0.7315*	0.0547^{ns}	3.9529^{ns}	5.4577^{ns}	403722.314^{ns}	1.8E-05**	1.4E-04**
V_b	0.2214*	0.0056^{ns}	3.0101*	0.9954^{ns}	1598.6263^{ns}	5.0E-06**	4.0E-05**
V_i	0.0729^{ns}	0.0918^{ns}	23.0638^{o}	10.1473^{ns}	50491.6590^{ns}	6.0E-06^{ns}	4.8E-05^{ns}
V_e	4.0724	14.1880	39.8362	1724.5989	5562514.0464	3.9E-05	3.0E-04
V_f	5.0982	14.3400	69.8630	1741.1993	6018326.6456	6.8E-05	5.2E-04
Genetic parameters							
h^2	0.1435	0.0038	0.0566	0.0031	0.0671	0.2607	0.2607
c_b^2	0.0434	0.0004	0.0431	0.0006	0.0003	0.0765	0.0765
c_i^2	0.0143	0.0064	0.3301	0.0058	0.0084	0.0919	0.0919
r_{gl}	0.9093	0.3732	0.1463	0.3497	0.8888	0.7394	0.7394
Phenotypic means							
General	14.7566	6.0884	20.3564	63.1039	3614.8519	0.0103	0.0419
A1	13.8203	5.3319	22.9854	51.6467	3526.4270	0.0102	0.0418
A2	15.6928	6.8449	17.7274	74.5611	3703.2769	0.0103	0.0420

^{ns}, ^{o},*, ** Not significant and significance levels of 10 %, 5 % and 1 % for the tabulated Chi-square test: 2.71, 3.84 and 6.63, respectively with 1 degree of freedom. Plant height (PH, cm), Stem base diameter (SBD, mm), Canopy diameter of the coffee tree in line direction (CDL, mm), Canopy diameter of the coffee tree in the transverse direction (CDT, cm), Canopy diameter average of the coffee tree (CDA, cm), Number of leaves (NL), Normalized Difference Vegetation Index (NDVI), Leaf length (LL, cm), Leaf width (LW, cm), Canopy height (CH, cm), Unit leaf area (ALU, cm^2), Total leaf area (ALT, cm^2), Canopy volume (CV, cm^3), Leaf area index (LAI, und). V_g = Genotypic variance; V_b = environmental variance between blocks; V_i = Variance of genotype × environment interaction; V_e = Residual variance; and V_f = Individual phenotypic variance; h^2 = Heritability of individual plots in the broad sense; c_b^2 = Coefficient of determination of block effects; c_i^2 = Coefficient of determination of the effects of genotype × environment interaction; r_{gl} = Genotypic correlation between performance in different environments; A1 = Environment at 140 m altitude and; A2 = Environment at 700 m altitude.

heritability values greater than 50 % are considered high, between 15 and 50 % moderate, and if less than 15 %, low. It is worth mentioning that heritability plays a significant predictive role as it expresses the confidence with which the phenotypic value represents the genetic value. Estimates of parameters, such as heritability, are essential to defining the best selection strategies for conilon coffee tree breeding (Alkimim et al., 2021). In general, the coefficients of determination for blocks (c_b^2) and of the genotype × environment interaction (c_i^2) presented values of low magnitude. For blocks, the highest value found was 0.1269 for the NDVI characteristic. For the interaction, the highest magnitude found was 0.3301 for CH.

The genotypic correlation between the performance in the two environments (r_{gl}) presented values from 0.1463 to 0.9093 for the CH and LL traits, respectively. According to Resende and Alves (2020) the values, in module, of r_{gl} can be classified as low (0 to 0.33), medium (0.34 to 0.66) and high (0.67 to 1.0) and these classes can be interpreted as high, mean, and low variance of the genotype × environment interaction, respectively. Thus, the results revealed a high interaction for CH (low r_{gl} value), medium interaction for CDL, CDT, LW and ALU (mean r_{gl} value) and low interaction for the other characteristics. It should be

noted that low correlation implies a high interaction of the complex type, in addition to a difficulty in indirect selection, since the selection of a superior individual in one environment may not express gains for the other environment, which consequently reduces the gains with the indirect selection. Most of the characteristics under study showed a low variance of the genotype × environment interaction, which according to Andrade et al. (2013), could be interpreted as a positive as it facilitates selection gains.

Table 4 presents the general rankings for each specific environment of the ten genotypes that presented the best and worst performances for each morphophysiological trait based on their predicted genetic values. For PH, genotype 10 was superior in the general analysis and both environments, followed by genotypes 76, 25, 21 and 28 in the general analysis and by genotypes 76, 21, 25 and 57 in A1, 20, 76, 37, and 25 in A2. Among the genotypes that occupied the last positions are 48, 79, 80, 95 and 102, in addition to the controls T2, T7 and T8. For SBD, the best performance was presented by genotype 63 in the general analysis and both environments, followed by genotypes 76, 28 and 91. Among the genotypes that presented a lower performance for SBD are 81, 11, 29, 35, 108, 39, 79 and 53.

The T3 genotype generally showed better performance for canopy diameter assessments (CDL, CDT and CDA), except for CDT in A2 in which genotype 63 occupied the first position in the ranking. For CDL, in the general ordering and each specific environment, in addition to T3, genotypes 4, 25, 69 and 76 occupied the first positions. For CDT in the general ordering, genotype T3 is followed by genotypes 69, 63, 101 and 105, in A1 by 69, 76, 63 and 4. Genotype 63 showed better performance for CDT in A2, followed by genotypes 91, T3 105 and 69. For CDA, in the general order and each specific environment, in addition to T3, genotypes 4, 69, 76 and 91 occupied the first positions. Among the genotypes that showed lower performance for canopy diameter are T7, T8, 53 and 90.

Genotypes 76 and 63 had higher NL, and in the general ordering, the first positions were occupied by genotypes 76, 63, 91, 69 and 92. In A1 the first positions were occupied by genotypes 76, 63, 69, T3 and 91 and in A2 the first ones were 76, 63, 91, 62 and 25. The genotypes that presented lower performance are T8, 13, 29, 39, 56 and 80. The T7 genotype presented better performance for NDVI and the general ordering of the first positions were occupied by genotypes T7, T3, 55, 31 and 1. In A1, the first positions were occupied by genotypes T7, T3, 1, 104 and 31 and in A2, the first positions in the order were 55, 31, 1, 104. Among the genotypes that showed lower performance for NDVI are 35, 14, 53, 47, 67, 39 and 90.

Genotypes 69 and 57 had the highest LL values. In the general ordering, the first positions were occupied by genotypes 69, 57, 2, 112 and 18. In A1, the first positions were occupied by genotypes 69, 57, 18, 2 and 112 and in A2, genotypes 57, 69, 2, 112 and 110. The genotypes with the lowest values were 1, T2, T8, 14, 67, 73, 88 and 92. For the LW trait, the first positions were occupied by genotypes T7, 12, T8, T1 and 57 in the general ordering and genotypes T7, 12, T1, T8 and 14 for A1 and T7, T8, 12, 110 and 46 for A2. Among the genotypes that occupied the last positions for LW are T2, T5, T6, 14 and 16.

For the characteristic CH in the general ordering, the first positions were occupied by genotypes 69, T3, 55, 28 and 6. In A1 the highest values were for genotypes 69, 28, 68, 70 and T3 and in A2, accessions 55, 23, T1, 42 and 69. Among the genotypes that occupied the last positions are 24, 53, 54 and 102. For the ALU characteristic, the highest values were observed in genotypes T7, 12, 110, 57 and T8, in the general ordering, genotypes T7, 12, T1, 57 and T4 on A1 and T7, 110, T8, 54 and 76 on A2. Among the genotypes with the lowest values are T2, T5 and T6. For the ALT trait, in the general ordering, the first positions were occupied by genotypes 76, 69, T3, 91 and 25. In A1, genotypes 76, 69, T3, 57 and 63 occupied the first positions. In A2, the first positions were occupied by genotypes 76, 69, 91, T3 and 25. Among the genotypes that occupied the last positions are 1, T6, T8, 13, 29, 39, 53 and 56. Genotypes 69 and T3 performed better for CV and LAI. For both traits, in the general ordering, the first positions were occupied by genotypes 69, T3, 76, 91 and 28. In A1, genotypes 69, T3, 76, 28 and 91 occupied the first positions. In A2, the first positions were occupied by genotypes 69, T3, 91, 76 and 55. Among the genotypes that presented lower performance for CV and LAI were T8, 15, 39, 53, 54 and 90.

A study on the initial performance of coffee genotypes identified early those with better adaptation and superior growth (Silva et al., 2021b). The study emphasizes that the average height of plants at 180 days after planting may indicate greater adaptation to environmental conditions. This information points to the potential of genotype ten and the possibility of its recommendation in a future variety of conilon coffee. Specifically in *C. canephora*, growth and initial development of genotypes have been studied, recommending those with superior development and better performance (Contarato et al., 2010; Covre et al., 2013; Covre et al., 2016).

The genotypes under study showed wide genetic diversity. The Gower distance, estimated from the morphophysiological characters and descriptors, presented values ranging from 0.037841 to 0.593763, for the respective pairs of genotypes 26 × 93 and T7 × 76 (Table 5). In addition, genotype 69, clone two of the variety 'ES8143' 'Centenária', is involved in the longest distances. The shortest distance found was among a genotype from the locality of Jerônimo Monteiro and a clone from the Incaper breeding program, supporting its possible inclusion in the breeding program. The

Table 4 – Orderings of coffee tree genotypes cultivated in Cachoeiro do Itapemirim, Espírito Santo, Brazil at an altitude of 140 m (A1) and in the municipality of Alegre, Espírito Santo, Brazil at an altitude of 700m (A2) based on the predicted genetic values for the traits Plant height (PH), Stem base diameter (SBD), Canopy diameter of the coffee tree in line direction (CDL), Canopy diameter of the coffee tree in the transverse direction (CDT), Canopy diameter average of the coffee tree (CDA), Number of leaves (NL), Normalized Difference Vegetation Index (NDVI), Leaf length (LL), Leaf width (LW), Canopy height (CH), Unit leaf area (ALU), Total leaf area (ALT), Canopy volume (CV), Leaf area index (LAI).

Order	PH			SBD			CDL			CDT			CDA			NL			NDVI		
	General	A1	A2	General	A1	A2	General	A1	A2	General	A1	A2	Geral	A1	A2	General	A1	A2	General	A1	A2
1	10	10	10	63	63	63	T3	T3	T3	T3	T3	63	T3	T3	T3	76	76	76	T7	T7	T7
2	76	76	20	76	76	76	76	76	4	69	69	91	69	69	69	63	63	63	T3	T3	55
3	25	21	76	28	28	28	4	69	76	63	76	T3	76	76	91	91	69	91	55	1	31
4	21	25	37	91	91	91	69	4	25	91	63	105	4	4	4	69	T3	62	31	104	1
5	28	57	25	T3	T3	69	25	25	69	105	4	69	91	91	76	62	91	25	1	31	104
6	37	28	28	69	69	T3	103	10	103	4	91	4	25	25	25	T3	62	105	104	55	62
7	20	63	21	89	89	89	89	103	91	76	105	71	105	28	105	5	101	5	62	69	T3
8	45	37	45	25	25	25	28	59	89	28	28	19	28	10	71	25	5	69	10	65	10
9	57	45	24	21	57	21	91	28	28	71	10	28	71	105	28	59	8	T3	65	62	65
10	24	24	62	59	21	62	10	98	105	10	T5	78	10	103	103	105	25	59	69	10	85
103	1	81	95	T2	80	18	80	34	30	108	14	T7	99	29	83	54	29	90	112	71	35
104	78	95	80	81	81	81	79	75	79	T7	54	35	54	14	99	1	54	1	40	23	112
105	95	T7	1	11	90	11	108	54	99	13	T7	108	108	108	39	52	52	T7	35	33	40
106	80	T6	78	29	11	29	40	80	53	90	13	83	29	54	108	29	56	T8	41	35	14
107	48	48	48	90	29	35	53	108	63	70	29	70	39	39	T6	56	T6	29	14	53	41
108	T7	80	T2	35	35	90	99	99	40	T6	70	39	T7	53	29	13	13	56	53	47	53
109	79	79	T7	108	108	108	T7	90	T8	29	53	29	53	T7	T7	39	39	13	47	14	47
110	T2	102	79	39	39	39	90	T7	T6	39	39	53	T6	90	53	80	80	80	67	67	67
111	102	T8	T8	79	79	53	T8	T8	T7	53	T8	90	90	T8	T8	T8	53	39	39	39	39
112	T8	T2	102	53	53	79	T6	T6	90	T8	T6	T8	T8	T6	90	53	T8	53	90	90	90
Order	LL			LW			CH			ALU			ALT			CV			LAI		
	General	A1	A2	General	A1	A2	General	A1	A2	General	A1	A2	General	A1	A2	General	A1	A2	General	A1	A2
1	69	69	57	T7	T7	T7	69	69	55	T7	T7	T7	76	76	76	69	69	69	69	69	69
2	57	57	69	12	12	T8	T3	28	23	12	12	110	69	69	69	T3	T3	T3	T3	T3	T3
3	2	18	2	T8	T1	12	55	68	T1	110	T1	T8	T3	T3	91	76	76	91	76	76	91
4	112	2	112	T1	T8	110	28	70	42	57	57	54	91	57	T3	91	28	76	91	28	76
5	18	112	110	57	T4	46	6	T3	69	T8	T4	76	25	63	25	28	91	55	28	91	55
6	62	62	62	110	57	54	T1	40	5	T1	69	46	63	91	62	55	25	25	55	25	25
7	110	110	18	41	70	84	76	34	91	112	18	78	57	25	63	25	4	72	25	4	72
8	78	39	78	46	41	41	105	38	T3	78	39	84	62	62	57	105	55	28	105	55	28
9	39	78	76	T4	112	72	107	99	30	69	112	57	12	12	12	4	105	105	4	105	105
10	76	76	91	70	78	T1	70	104	76	46	T8	72	21	21	21	103	63	T1	103	63	T1
103	40	106	106	56	86	19	29	14	83	86	82	56	52	83	83	102	24	41	102	24	41
104	13	T8	14	40	14	98	39	37	100	56	83	59	29	52	29	29	102	99	29	102	99
105	14	13	40	86	T3	14	65	22	102	40	13	1	T5	29	39	T7	90	29	T7	90	29
106	92	92	92	19	82	100	96	96	93	14	10	100	39	39	1	T6	15	15	T6	15	15
107	T8	14	88	14	10	90	24	95	40	13	14	90	1	1	T5	15	T7	108	15	T7	108
108	88	1	1	73	16	40	15	53	53	16	16	92	56	56	T6	39	39	39	39	39	39
109	1	88	T8	16	73	16	90	15	90	73	73	40	13	13	56	90	53	90	90	53	90
110	T2	T2	T2	T6	T6	T6	102	102	1	T5	T5	T5	T6	53	13	53	54	53	53	54	53
111	67	67	67	T5	T2	T5	53	54	29	T6	T6	T6	53	T6	53	54	T6	T8	54	T6	T8
112	73	73	73	T2	T5	T2	54	24	54	T2	T2	T2	T8	T8	T8	T8	T8	54	T8	T8	54

greatest distance found in this study, between a genotype of *C. arabica* and another of *C. canephora*, was 25 % greater in magnitude than the maximum estimated by Ferrão et al. (2021), who analyzed 600 accessions from the active germplasm bank of *C. canephora* from Incaper, thereby confirming the high genetic variability present.

Tocher's clustering allowed for the formation of 11 groups (Table 6). Groups G9, G10 and G11 comprised a single genotype, 110, 55 and 10, respectively. The G1 group gathered the most genotypes, 78 of the 112 studied, including those with the smallest genetic distance and the controls T2, T4, T5 and T6. In addition, the G8 group gathered only controls, the

T7 and T8 genotypes, which are *C. arabica*. Recent works have used Tocher's clustering methodology, highlighting its efficiency in discriminating the most divergent coffee trees (Dubberstein et al., 2020; Ferrão et al., 2021; Senra et al., 2020). Thus, genotypes identified as divergent by Gower's genetic distance and grouped by Tocher's method can be monitored for their agronomically important traits. The UPGMA clustering method (Figure 1) showed a high level of agreement with Tocher, reinforcing confidence in the formed groups. The estimated cophenetic correlation coefficient was 0.6969, demonstrating no expressive distortions between the matrix of graphical distances and the Gower distance.

In *C. canephora* genetic diversity work has been very important for breeding the species with valuable information on morphoagronomic characteristics (Akpertey et al., 2019; Giles et al., 2018; Senra et al., 2022), germplasm banks (Ferrão et al., 2021; Huded et al., 2020; Senra et al., 2020), nutritional concentration in the coffee tree (Schmidt et al., 2022; Silva et al., 2021a) and leaf morphoanatomical characteristics (Dubberstein et al., 2021). In summary, the broad genetic base among the genotypes in this work, an essential factor for the success of the breeding, guarantees gains with the future selection of those agronomically superior and more adapted to environmental conditions, thereby effectively contributing to the sustainability of coffee production in the face of the dynamics of climate change.

The values of genetic correlation between the evaluated traits (Figure 2) ranged from –0.13 to 1.00 between CDT and LW and CV and LAI, respectively, with significance ranging from 0.1 to 10 %. Correlation was not significant between NDVI and PH and LL. The LW characteristic was only significant with NDVI, ALU and ALT. The CH trait was not significant with only LW and ALU and the CV and LAI characteristics did not correlate with LW and ALU. The genetic correlation associated with the predominance of traits with low genotype-environment interaction (Table 3) suggests the possibility of selection gains for both environments through the multiple possibilities of indirect selection.

In the process of developing new cultivars, it is essential to know the genetic variability of the species and the relationships between the characteristics under study (Oliveira et al., 2010), as this information optimizes the indirect selection process (Reuben et al., 2003) in addition to determining redundant features (Yan and Fregeau-Reid, 2008) that should be discarded. It was concluded that evaluating 56 genotypes of *Coffea canephora* in Ghana through genetic correlation made it possible to bring forward the selection process, since the morphological characteristics evaluated showed high genetic correlation with productivity (Akpertey et al., 2022).

Table 5 – Description of the ten longest and shortest distances, estimated by the Gower method using morphophysiological data and descriptors of the genus Coffea recommended by MAPA, among coffee tree genotypes evaluated in Cachoeiro do Itapemirim, Espírito Santo, Brazil at an altitude of 140 m and in the municipality of Alegre, Espírito Santo, Brazil at an altitude of 700 m.

Greater Distances	Genotypes	Shorter Distances	Genotypes
0.593763	T7 and 76	0.053041	81 and 84
0.592207	T8 and 69	0.052897	46 and 97
0.590409	T7 and 69	0.052664	44 and 66
0.587429	T3 and T7	0.052318	23 and 42
0.585569	69 and 90	0.048171	103 and 105
0.578425	53 and 69	0.047270	97 and 111
0.578126	14 and 69	0.046733	95 and 100
0.556115	69 and 102	0.044915	11 and 93
0.548608	69 and 83	0.042407	11 and 26
0.546465	T3 and T8	0.037841	26 and 93

Table 6 – Grouping by Tocher of 112 genotypes of coffee trees cultivated in two environments, Cachoeiro do Itapemirim, Espírito Santo, Brazil at an altitude of 140 m and in the municipality of Alegre, Espírito Santo, Brazil at an altitude of 700m.

Group	Genotypes
G1	1, 2, 5, 6, 7, 8, 9, 11,13, 15, 16, 17, 19, 20, 23, 26, 27, 29, 30, 31, 32, 34, 35, 37, 38, 40, 41, 42, 43, 44, 45, 46, 47, 48, 50, 51, 52, 54, 56, 59, 65, 66, 67, 68, 70, 71, 75, 79, 80, 81, 82, 84, 85, 86,87, 88, 92, 93, 94, 95, 96, 97, 98, 99,100, 101, 102, 103, 104, 106, 107, 108, 109, 111, T2, T4, T5 and T6
G2	4, 21, 25, 28, 62, 63, 78, 89, 91 and 105
G3	22, 24, 33, 49, 73, 53, 83 and 90
G4	18 and 39
G5	12, 57, 112 and T1
G6	14 and 72
G7	69, 76 and T3
G8	T7 and T8
G9	110
G10	55
G11	10

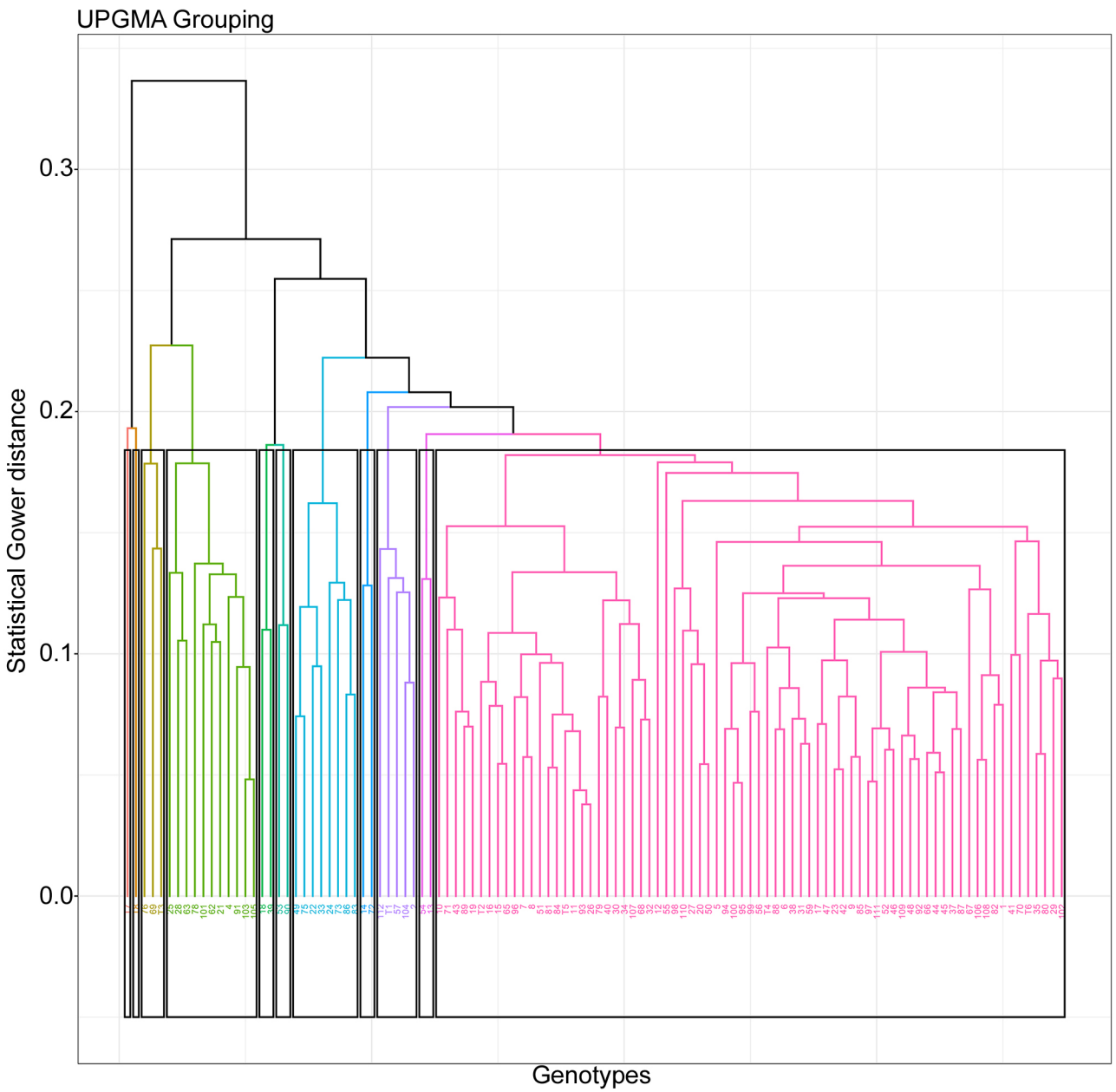

Figure 1 – Grouping by UPGMA of 112 genotypes of coffee trees cultivated in two environments, Cachoeiro do Itapemirim, Espírito Santo, Brazil at an altitude of 140 m and in the municipality of Alegre, Espírito Santo, Brazil at an altitude of 700 m. Cophenetic correlation coefficient of 0.6969.

Conclusions

The high altitude environment provided the highest averages for most of the traits under study, stimulating the initial development of conilon coffee. The significant genetic variances and the result of the Gower distance and the Tocher and UPGMA clusters evidence genetic diversity among the 112 genotypes under study.

For most of the characteristics under evaluation, low values for the variance of the genotype and environment interaction were observed. Consequently, a high genotypic correlation between the performance of the genotypes and the environments points to a possible indirect selection that will maximize the breeding program.

The genotypic correlation between the evaluated characteristics will allow for discarding variables with high correlation in future studies. It will be possible to optimize the breeding program with indirect selection gains due to the high values of genotypic correlation between traits and the correlation of genotypic

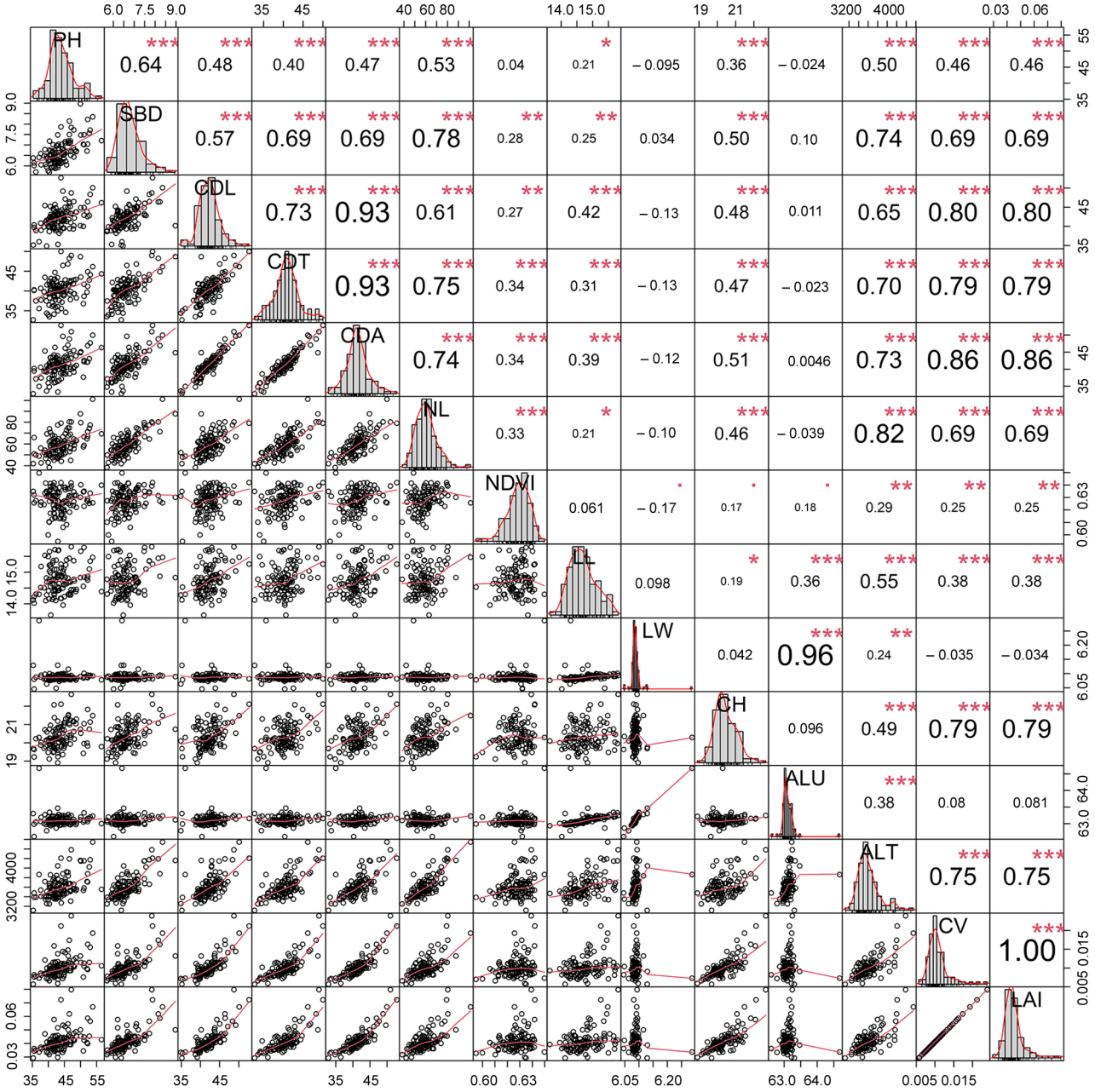

Figure 2 – Genetic correlation matrix among the evaluated morphoagronomic traits: Plant height (PH), Stem base diameter (SBD), Canopy diameter of the coffee tree in line direction (CDL), Canopy diameter of the coffee tree in the transverse direction (CDT), Canopy diameter average of the coffee tree (CDA), Number of leaves (NL), Normalized Difference Vegetation Index (NDVI), Leaf length (LL), Leaf width (LW), Canopy height (CH), Unit leaf area (ALU), Total leaf area (ALT), Canopy volume (CV), Leaf area index (LAI). Correlations evaluated by Pearson's test at 0.01 (***), 1 (**), 5 (*) and 10 % (°) significance.

performance of genotypes across environments. It will be possible to develop a specific cultivar for the south of Espírito Santo.

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Conceptualization: Senra JFB, Silva JA, Ferreira A, Esposti MDD, Ferrão MAG. **Data curation:** Senra JFB, Silva JA, Fassarella KM, Silva RU, Milheiros IS, Silva FG. **Formal analysis:** Senra JFB, Silva JA. **Funding acquisition:** Senra JFB. **Investigation:** Senra JFB, Silva JA, Ferreira A. **Methodology:** Senra JFB, Silva JA, Fassarella KM. **Project administration:** Senra JFB, Silva JA. **Writing – original draft:** Senra JFB, Silva JA, Ferrão MAG. **Writing – review & editing:** Senra JFB, Silva JA.

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