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BIOLOGY

Genetic foundations of coffee cultivation: diversity of the most cultivated *Coffea canephora* clones in the Western Amazon

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ABSTRACT: The cultivation of *Coffea canephora* in Brazil relies on a limited group of widely adapted clones, including registered cultivars and farmer selections. Despite their central role in coffee production, the diversity of these materials remains insufficiently characterized. In this study, we evaluated 62 *C. canephora* genotypes based on 24 traits categorized into three groups: (I) agronomic, (II) quality-related, and (III) morphological, measured across multiple environments and years. Violin plots revealed broad phenotypic variation, with some traits displaying narrow and homogeneous distributions, while others exhibited wide or bimodal patterns, indicating the coexistence of divergent phenotypic groups. Correlation analyses showed coherent associations within each functional group, reflecting the integrated expression of growth, yield, and quality components. Principal component analyses identified structured gradients of vigor, productivity, and quality, defining reference ideotypes. Distinct genotypes stood out for specific performance attributes: AR106, LB10, and LB80 represented the vigorous growth ideotype; BRS1216 combined high outturn index and large bean size; AS2 exhibited leaf traits associated with stress tolerance; and GJ8 and GJ25 expressed stable yield and uniform canopy structure. This characterization highlighted the structured diversity of key cultivated genotypes that underpin current *C. canephora* production and provides a practical framework for selecting complementary materials in breeding and cultivation.
Key words: Conilon, Robusta, productive traits, quality, morphological traits.

Base genética da cafeicultura: diversidade dos clones de *Coffea canephora* mais cultivados na Amazônia Ocidental

RESUMO: O cultivo de *Coffea canephora* baseia-se em um grupo limitado de clones amplamente cultivados, incluindo cultivares registradas e seleções de agricultores. Apesar da sua importância, esses genótipos ainda são desconhecidos em muitos aspectos. Neste sentido, este estudo teve como objetivo caracterizar a diversidade genética de clones amplamente cultivados. Para isso, foram avaliados 62 genótipos com base em 24 características, organizadas em três grupos: (I) agronômicas, (II) qualidade e (III) morfológicas, mensuradas em múltiplos ambientes e anos. Os gráficos em violino revelam expressiva variabilidade entre os genótipos cultivados, com algumas características apresentando distribuições estreitas e homogêneas, enquanto outras exibiram padrões amplos ou bimodais. Além disso, as análises de correlação mostraram associações coerentes dentro de cada um dos grupos funcionais e as análises de componentes principais identificaram gradientes estruturados de vigor, produtividade e qualidade, definindo genótipos de referência. Ademais, genótipos distintos se destacaram por atributos específicos de desempenho: AR106, LB10 e LB80 representaram o ideótipo de maior crescimento; BRS1216 combinou rendimento e maior tamanho de grãos; AS2 apresentou características associadas à tolerância ao estresse hídrico; e GJ8 e GJ25 apresentaram precocidade de produção e arquitetura uniforme. Portanto, essa caracterização evidencia a diversidade estruturada dos principais genótipos cultivados que sustentam a produção atual de *C. canephora* e fornece uma base prática para o melhoramento e cultivo de materiais complementares.
Palavras-chave: Conilon, Robusta, características produtivas, qualidade, morfológicas.

INTRODUCTION

Brazil is the world's largest producer and exporter of coffee, and its plantations play a decisive role in global supply and market stability. The country cultivates both *Coffea arabica* and *Coffea canephora*, the latter accounting for nearly 40% of total national output (FREITAS et al., 2024). Within this context, *C. canephora* cultivation is concentrated in a few major production zones, mainly the Southeastern states and the Western Amazon. Despite their agronomic success, many farmer-derived clones remain poorly

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characterized. Several of these genotypes were later disseminated to other producing regions, giving rise to widely cultivated clones such as GJ8, GJ25, and AS2 (ESPÍNDULA et al., 2022).

Multi-environment and multi-year evaluations are resource- and time-consuming but provide valuable insights into genotype × year (GY) and genotype × environment (GE) interactions (AKPERTEY et al., 2022; MONTAGNON et al., 2012). In phenotypic evaluations, certain traits are less influenced by environmental variation and are therefore easier to assess, including grain mass, outturn (fruit-to-bean conversion rate), and compatibility (SILVA et al., 2024; PARTELLI et al., 2021; FERRAO et al., 2021). Other traits, such as productivity, bienniality, and beverage quality attributes, are more complex to quantify due to stronger environmental effects and the need for long-term assessments.

The most cultivated genotypes exhibit characteristics derived from two distinct botanical varieties (ROCHA et al., 2025; DAVIS et al., 2006). Conilon is generally associated with early maturation and compact growth, whereas Robusta tends to show greater vigor and larger bean size (OLIVEIRA et al., 2018; MONTAGNON et al., 2008; DAVIS et al., 2011). The coexistence and intercrossing of these gene pools have enhanced the diversity of cultivated populations, shaping the evolution of modern *C. canephora* cultivation (FERRÃO et al., 2024; PARTELLI et al., 2022; ROCHA et al., 2021).

The genetic resources introduced into the Amazon during the 1970s gave rise to clones that were later disseminated to other producing regions and are now among the most cultivated in Brazil. The introduction of *C. canephora* into the Amazon occurred through two distinct routes corresponding to its botanical varieties (FARIA SILVA et al., 2024; SILVA et al., 2025). Conilon coffee was introduced by migrant farmers from Espírito Santo, who brought locally adapted genotypes selected under smallholder conditions. In that same period, Robusta coffee was introduced by Embrapa using seeds of the Instituto Agronomico de Campinas - IAC variety, establishing a genetic base characterized by greater vigor and larger bean size (ESPÍNDULA et al., 2022). The intercrossing of these gene pools in the Western Amazon subsequently enriched the diversity of cultivated populations (ROCHA et al., 2021; OLIVEIRA et al., 2018) (Figure 1).

For commercial cultivation, a clone must combine multiple favorable traits (ADUNOLA et al., 2024; ALKIMIM et al., 2021). Highly productive plants; however, may later express undesirable agronomic characteristics, such as lower outturn index, plant toppling, or reduced vigor. Although some studies have evaluated different traits, these have been conducted separately. Farmer-selected

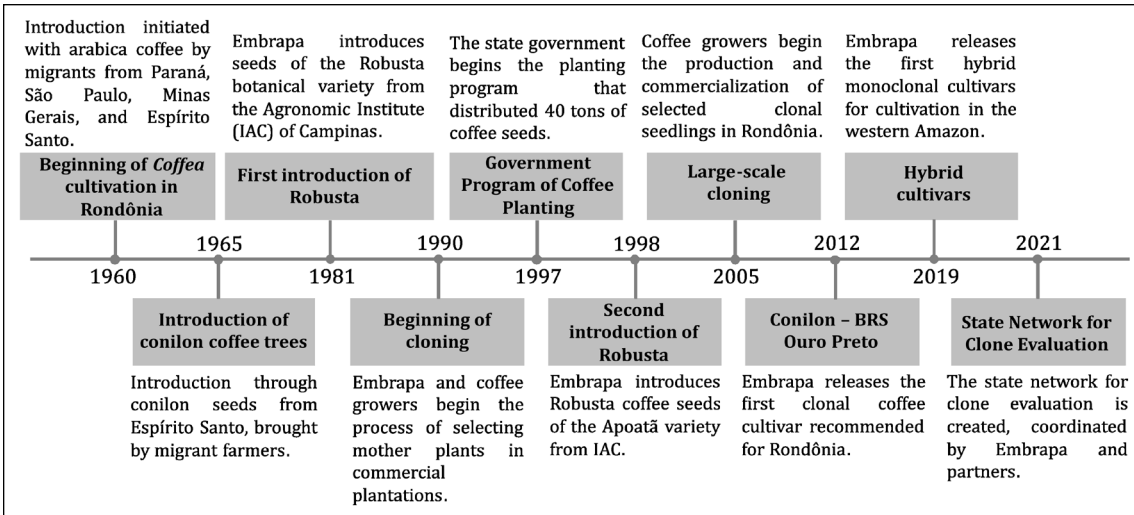

Figure 1 - Timeline of coffee breeding and cultivation in Rondônia, Brazil. Major historical milestones include the introduction of *Coffea arabica* by migrant farmers (1960s), the introduction of *C. canephora* genotypes of the Robusta and Conilon groups (1980s–1990s), the launch of the state "Plante Café Program" (1990), the beginning and scaling up of clonal propagation (1997–2005), and the release of improved cultivars by Embrapa, including the clonal cultivar BRS Ouro Preto (2012) and ten hybrid cultivars for the western Amazon (2019). The creation of the State Network for Clone Evaluation (2021–2025) consolidated regional efforts to coordinate breeding and evaluation trials.

clones and their dissemination history have been documented (ESPÍNDULA et al., 2022), while genetic diversity has been characterized using molecular markers such as SNPs and SSRs (FARIA SILVA et al., 2024; SILVA et al., 2025a). Other studies have focused on specific trait groups, including physicochemical and morphological traits of fruits and beans (LOPES JUNIOR et al., 2024a; LOPES JUNIOR et al., 2024b), outturn index and processing traits (LOURENÇO et al., 2022; PARTELLI et al., 2021; SILVA et al., 2025b), and beverage chemical composition (VIENCZ et al., 2023). In addition, broader assessments of genetic variability in germplasm collections (FERRÃO et al., 2021) and breeding strategies based on Conilon and Robusta gene pools (OLIVEIRA et al., 2018; ROCHA et al., 2025) have contributed to understanding the diversity of the species.

This study integrates previously reported traits with new field evaluations to characterize the genetic diversity of cultivated clones. In the present study, we assessed field growth, first-harvest yield, rainfed yield, plagiotropic branch traits, days to maturation, final beverage quality score, leaf area, leaf dry mass, and stomatal density. In this context, an integrated evaluation of the diversity of cultivated *C. canephora* genotypes provides a more comprehensive basis for breeding and recommendation strategies.

The objective of this study was to characterize the phenotypic performance and genetic structure of *C. canephora* genotypes cultivated in the Western Amazon. By integrating multi-environment and multi-year evaluations, we sought to identify patterns of genetic diversity, phenotypic stability, and trait associations among clones with contrasting genetic backgrounds. The findings are expected to support clone recommendation and selection strategies improving productivity, quality, and adaptation of *C. canephora* to tropical environments.

MATERIALS AND METHODS

Field trials

Two clonal competition trials were established between December 2022 and January 2023 in distinct environments of the Western Amazon, using a spacing of 3.0 × 0.8 m. The first site, in Porto Velho, Rondônia, was installed in the experimental field of the Brazilian Agricultural Research Corporation (Embrapa) at 8°48′05.5″ S, 63°51′02.7″ W, and 88 m above sea level. The second site, in Ouro Preto do Oeste, Rondônia (10°43′55.3″ S, 62°15′23.2″ W, 245 m altitude), included both rainfed and irrigated conditions. The soils of the experimental areas are characterized by acidic conditions and low to moderate base saturation, with chemical properties detailed in table 1. Crop management, including fertilization and liming, was carried out for high-yield systems (>100 bags ha^{-1}). Climatic conditions were characterized using data from the NASA POWER database (SPARKS, 2018), including monthly precipitation and minimum, mean, and maximum air temperatures for the period 2023–2025 (Figure 2). According to the Köppen classification, Porto Velho presents a tropical monsoon climate (Am), while Ouro Preto do Oeste is classified as tropical savanna (Aw) (ALVARES et al., 2013).

Genetic materials

The study encompassed 62 *C. canephora* genotypes capturing the major spectrum of genetic diversity cultivated in Brazil (Table 2). The evaluated material originated from breeders, research institutions, and pioneering farmers from the states of Rondônia, representing both Conilon and Robusta genetic backgrounds. The collection includes elite clones used in commercial plantations, registered cultivars released by Embrapa (prefix “BRS”), and

Table 1 - Chemical properties at the 0–20 and 20–40 cm depth layers of clonal competition trials conducted in two contrasting environments in the Western Amazon.

Environment	Depth	pH	P	K	Ca	Mg	H+Al	Al	OM	V
	cm		mg dm^{-3}	----------$cmol_c$ dm^{-3}----------					g kg^{-1}	%
Porto Velho - RO	0–20	5.3	5.00	0.12	2.74	1.66	11.19	0.42	48	29.0
	20–40	5.1	2.00	0.08	0.51	0.15	4.00	0.20	40	15.60
Ouro Preto do Oeste - RO	0–20	5.9	2.00	0.36	2.55	1.06	2.74	0.00	16	59.20
	20–40	5.8	1.00	0.16	0.48	0.18	1.50	0.00	14	35.30

pH in water (1:2.5); P and K by Mehlich-1; Ca, Mg and Al are exchangeable; H+Al = potential acidity; OM by wet oxidation; V = base saturation.

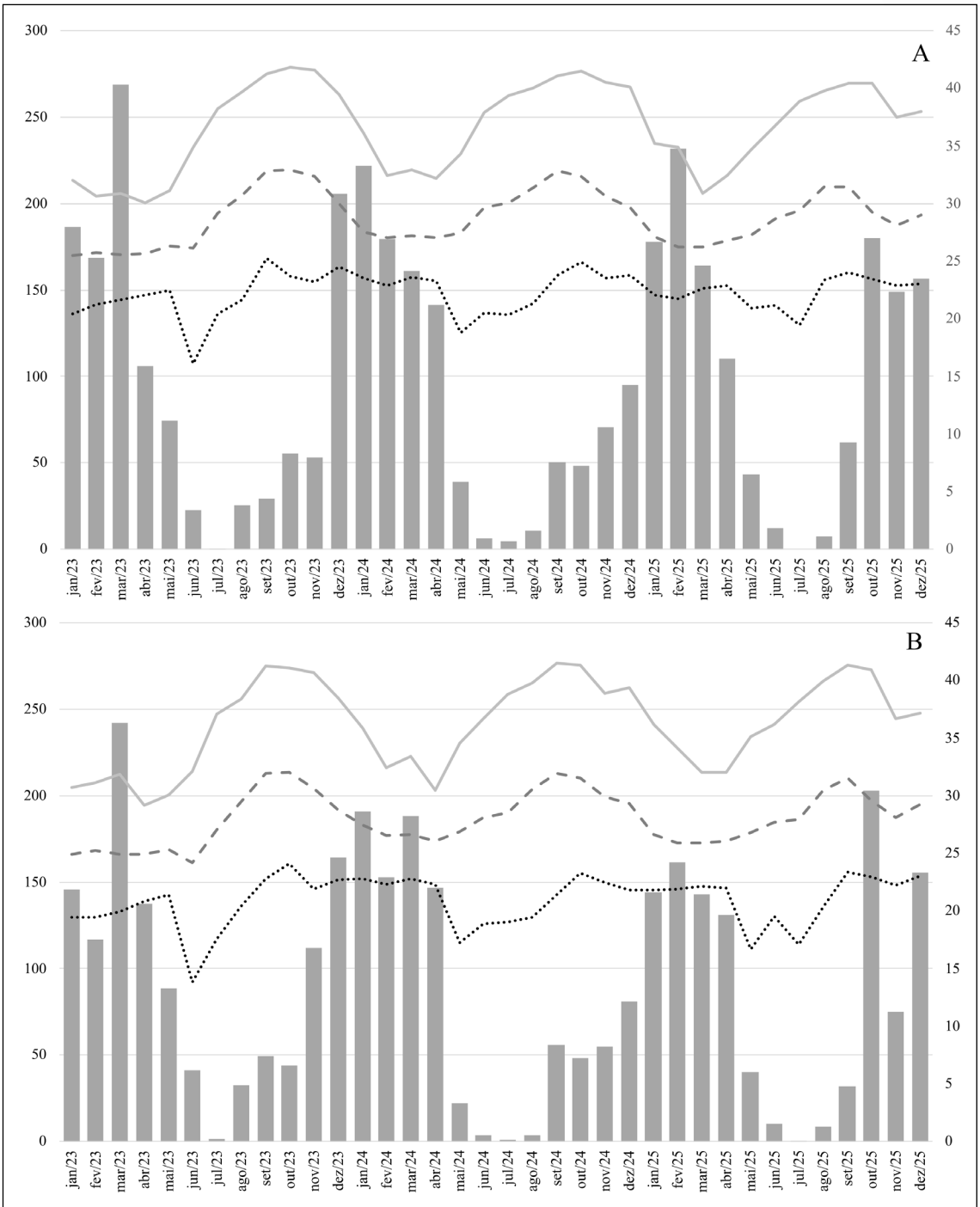

Figure 2 - Monthly climate series for the experimental sites located in Porto Velho (A) and OuroPreto do Oeste (B), Rondônia, Brazil. Bars represent monthly precipitation (mm), and lines indicate minimum, mean, and maximum air temperatures (°C). Period: 2023–2025. Climate data were obtained based on the geographic coordinates of each experimental site. Source: NASA POWER (SPARKS, 2018).

Table 2 - Identification of *Coffea canephora* genotypes, their origins, and membership probabilities to the Conilon (ProbC) and Robusta (ProbR) genetic clusters, estimated by DAPC using SNP markers.

n	Gen	Origin	ProbC	ProbR	n	Gen	Origin	ProbC	ProbR
1	AR106	Aldinei Raasch[1]	28%	72%	32	N14	Nivaldo Ferreira[6]	33%	67%
2	R152	Ronaldo G Oliveira[2]	50%	50%	33	N16	Nivaldo Ferreira[6]	26%	74%
3	BG180	Adilson Berger[3]	42%	58%	34	N6	Nivaldo Ferreira[6]	31%	69%
4	P42	Wanderly Bernabé[7] (Alto Alegre dos Parecis)	29%	71%	35	N8[G8]	Nivaldo Ferreira[6]	68%	32%
5	CA1	Carlos Alves Silva[4]	70%	30%	36	GJ3	Geraldo Jacomin[5]	45%	55%
6	RMD	Fredson Nunes[1]	64%	36%	37	GJ5	Geraldo Jacomin[5]	35%	65%
7	GB7	Gilberto Boone[2]	33%	67%	38	GJ8	Geraldo Jacomin[5]	60%	40%
8	R22	Ronaldo Vitoriano[2]	21%	79%	39	GJ25	Geraldo Jacomin[5]	40%	60%
9	S05	Sirley de Riz[6]	53%	47%	40	GJ2	Geraldo Jacomin[5]	44%	56%
10	WP6	Wanderley Peter[6]	33%	67%	41	GJ20	Geraldo Jacomin[5]	45%	55%
11	L130	Alcides Rosa[3]	38%	62%	42	GJ30	Geraldo Jacomin[5]	54%	46%
12	L1	Alcides Rosa[3]	63%	37%	43	LB10	Laerte Braun[5]	31%	69%
13	GB1	Gilberto Boone[2]	17%	83%	44	LB15	Laerte Braun[5]	31%	69%
14	GB4	Gilberto Boone[2]	19%	81%	45	LB30	Laerte Braun[5]	33%	67%
15	AGL1	Romário Lopes[4]	31%	69%	46	LB33	Laerte Braun[5]	41%	59%
16	SK04	Sérgio Kalk[6]	32%	68%	47	LB68	Laerte Braun[5]	54%	46%
17	SK41	Sérgio Kalk[6]	19%	81%	48	LB80	Laerte Braun[5]	21%	79%
18	SK80	Sérgio Kalk[6]	26%	74%	49	LB88	Laerte Braun[5]	30%	70%
19	SK88	Sérgio Kalk[6]	26%	74%	50	LB101	Laerte Braun[5]	22%	78%
20	SK244	Sérgio Kalk[6]	49%	51%	51	BAG15	Embrapa	29%	71%
21	VP156	Sérgio Kalk[6]	33%	67%	52	BAG21	Embrapa	53%	47%
22	VP148	Sérgio Kalk[6]	22%	78%	53	BAG22	Embrapa	33%	67%
23	P50	Valdecir Piske[2]	67%	33%	54	BAG24	Embrapa	30%	70%
24	Repiado65	Valdecir Piske[2]	52%	48%	55	BAG27	Embrapa	62%	38%
25	AS1	Ademar Schmidt[2]	66%	34%	56	BAG38	Embrapa	34%	66%
26	AS2	Ademar Schmidt[2]	48%	52%	57	BRS1216	Embrapa	42%	58%
27	AS5	Ademar Schmidt[2]	65%	35%	58	BRS2299	Embrapa	55%	45%
28	AS7	Ademar Schmidt[2]	54%	46%	59	BRS2336	Embrapa	58%	42%
29	AS10	Ademar Schmidt[2]	63%	37%	60	BRS2357	Embrapa	100%	0%
30	AS12	Ademar Schmidt[2]	59%	41%	61	BRS2314	Embrapa	40%	60%
31	N13	Nivaldo Ferreira[6]	44%	56%	62	BRS3213	Embrapa	40%	60%

[1]Ouro Preto do Oeste – RO; [2]Alta Floresta do Oeste – RO; [3]Rolim de Moura – RO; [4]Novo Horizonte do Oeste – RO; [5]Nova Brasilândia do Oeste – RO; [6]Cacoal – RO; [7]Alto Alegre dos Parecis – RO; [8]São Miguel do Guaporé – RO. DAPC results adapted from SILVA et al., 2025. Source: research data.

pre-breeding accessions maintained in germplasm collections of Embrapa.

The genetic structure of the population was previously characterized using single nucleotide polymorphism (SNP) markers, and the resulting cluster assignments were integrated into the present study to interpret the origin and genealogical background of the cultivated genotypes (FARIA SILVA et al., 2024) (Table 2). The dataset includes genotypes of diverse origins, encompassing farmer selections (e.g., Geraldo Jacomin, Laerte Braun, and Sergio Kalk) and cultivars developed by Embrapa (e.g., BRS 1216, BRS 2314, BRS 2357, and BRS 3213). This collection represents a broad genetic base derived from the Amazonian Robusta group, characterized by hybrid combinations of Conilon and Robusta botanical varieties.

Phenotypic characterization

The evaluation of *C. canephora* genotypes encompassed a comprehensive set of morphological, agronomic, and quality-related traits (Table 3). Data for each trait were collected across up to three environments and over three consecutive years, depending on the variable and experimental conditions. Field experiments were conducted using

Table 3 - Description of the evaluated traits in Coffea canephora clones, including experimental design, number of environments, years, replicates, plants per plot, measurement units, and references. Traits were assessed under randomized complete block design (RCBD) or completely randomized design (CRD), depending on the experiment.

Trait	Env.	Years	Rep.	Plt.plot^{-1}	Design	Unit	Reference
PH – Plant height	1	3	3	5	RCBD	m	Table 4
1YLD – First yield	1	1	3	5	RCBD	bags.ha^{-1}	Table 4
RFDY – Rainfed yield	1	1	3	5	RCBD	bags.ha^{-1}	Table 4
PL – Plagiotropic branches	1	2	3	5	RCBD	n	Table 4
PL – Plagiotropic length	1	2	3	5	RCBD	m	Table 4
NRS – Number of rosettes	1	2	3	5	RCBD	n	Table 4
DRS – Distance rosettes	1	2	3	5	RCBD	cm	Table 4
FRS – Fruits per rosette	1	2	3	5	RCBD	n	Table 4
BL – Bean length	1	2	10	5	RCBD	mm	[1]
BW – Bean width	1	2	10	5	RCBD	mm	[1]
BT – Bean thickness	1	2	10	5	RCBD	mm	[1]
100BW – 100-bean weight	1	2	3	5	RCBD	g	[1]
DM – Days to maturation	2	2	3	5	CRD	n	Table 4
CC – Caffeine content	3	1	3	5	CRD	%	[2]
OI – Outturn index	1	2	3	5	CRD	%	[3]
FQS – Final quality score	1	3	3	5	CRD	nota	Table 4
FL – Fruit length	1	2	10	5	RCBD	mm	[1]
FW – Fruit width	1	2	10	5	RCBD	mm	[1]
FT – Fruit thickness	1	2	10	5	RCBD	mm	[1]
100FW – 100-fruit weight	1	2	3	5	RCBD	g	[1]
LA – Leaf area	1	1	6	3	RCBD	cm^2	[4]
LDM – Leaf dry mass	1	1	6	3	RCBD	g	[4]
SA – Stomatal area	1	1	6	3	RCBD	um^2	[4]
SD – Stomatal density	1	1	6	3	RCBD	mm^2	[4]

Env., environment; RCBD, randomized complete block design; CRD, completely randomized design; Yr, years; Rep., replicates; Plt.plot^{-1}, plants per plot; Unit, measurement unit. Yield values expressed in 60-kg bags per hectare ("bags.ha^{-1}"); FQS (nota) refers to the final sensory score.[1] LOPES JÚNIOR et al., 2024a, [2] LOPES JÚNIOR et al., 2024b, [3] SILVA et al., 2025, [4] ARAUJO et al., 2021.

either a randomized complete block design (RCBD) or a completely randomized design (CRD), with three to ten replications and five plants per plot (Table 3). Leaf and stomatal traits were exceptions, being measured on six individual plants, following established protocols for anatomical characterization (ARAÚJOet al., 2021).The evaluated traits were grouped as follows: Group I (agronomic traits): PH – plant height; 1YLD – first yield; RFDY – rainfed yield; NPL – number of plagiotropic branches; CPL – plagiotropic branch length; NRS – number of rosettes; DRS – distance between rosettes; FRS – fruits per rosette. Group II (quality-related traits): BL – bean length; BW – bean width; BT – bean thickness; 100BW – 100-bean weight; DM – days to maturation; CC – caffeine content; OI – outturn index; FQS – final quality score. Group III (morphological traits): FL – fruit length; FW – fruit width; FT – fruit thickness; 100FW – 100-fruit weight; LA – leaf area; LDM – leaf dry mass; SA – stomatal area; SD – stomatal density (Table 3).

Statistical analyses

Data analyses were conducted to quantify genetic variability among genotypes, estimate genetic parameters, and evaluate genotype × years (GY) interactions. Phenotypic data were first inspected for outliers and evaluated for normality and homogeneity of variances. According to the experimental structure described in table 3, two analytical approaches were adopted. For traits evaluated in a single year, individual analyses were performed using the model:

$$Y_{ijk} = \mu + G_i + e_{ij}$$

For traits evaluated across consecutive years, a combined analysis was performed using the model:

$$Y_{ijk} = \mu + G_i + Y_j + GY_{ij} + e_{ijk}$$

where μ is the overall mean, G_i is the random effect of the i-th genotype, Y_j is the fixed effect of the j-th measurement (year), GY_{ij} is the genotype × year interaction, and e_{ijk} is the residual error.

The significance of the genotypic effect was initially tested following the procedures described by CRUZ (2013). Genetic parameters were estimated from variance components obtained in the analysis of variance, including the genotypic determination coefficient (H^2), the coefficients of genetic (CVg) and experimental variation (CVe), and the CVg/CVe ratio. The coefficient H^2 was interpreted as the proportion of phenotypic variance associated with genotypic differences among clones. The CVg and CVe were used to assess genetic variability and experimental precision, respectively, while the CVg/CVe ratio was used as an indicator of selection potential.

For traits evaluated across consecutive years, the repeatability coefficient (r) was estimated to quantify the temporal consistency of genotypic expression. Phenotypic distributions were illustrated using violin plots to visualize variability and identify distribution patterns. Principal component analysis (PCA) was applied to explore multivariate relationships among traits and genotypes. All analyses were performed in the R environment (R CORE TEAM, 2024) using the packages agricolae, metan, GGally, ggplot2, and corrplot.

Principal component analysis (PCA) was performed using standardized data to account for differences in measurement scales among traits. The analysis was based on the correlation matrix, and principal components were extracted from the eigenvalues and eigenvectors of this matrix. Eigenvalues were used to quantify the amount of variance explained by each component, while eigenvectors (loadings) represent the contribution of each trait to the formation of the components. The first principal components were retained based on their ability to explain the largest proportion of total variance, allowing the identification of major gradients of variation among genotypes and traits. Biplots were used to visualize the distribution of genotypes and the relative contribution of variables to each component.

RESULTS

The assessment of cultivated *C. canephora* clones revealed extensive genetic diversity underlying plant traits. Violin plots illustrated the distribution of individual values, highlighting both the median and the range of variation for each variable. Some traits exhibited narrow and consistent distributions, while others showed broad dispersion, reflecting heterogeneity within the evaluated germplasm. Plant height, number of plagiotropic branches, and first yield displayed wide variation with extreme values, whereas fruit length and leaf area showed more uniform patterns. Bimodal distributions were detected for bean width and caffeine content, suggesting the presence of distinct performance groups among clones. These contrasting patterns likely reflect underlying genetic differentiation within the cultivated material.

Analysis of variance revealed significant differences ($P < 0.01$) among clones. The genotypic determination coefficient (H^2) ranged from 48.3% (fruits per rosette) to 98.1% (100-bean weight), indicating moderate to high heritable control for most traits (Table 4). Coefficients of variation ranged from 1.77% to 25.72%, confirming high phenotypic diversity and the suitability of the dataset for multivariate analyses (Table 4). The coefficients of genetic (CVg) and experimental variation (CVe) ranged from 2.9% to 38.1%, with CVg/CVe ratios above 1.0 demonstrating experimental precision. Agronomic traits such as first yield and rainfed yield showed high H^2 and broad genetic variability, while quality-related traits—especially 100-bean weight, outturn index, and caffeine content—exhibited the highest heritability and CVg/CVe values. Morphological traits also displayed substantial variability, particularly for leaf area and 100-fruit weight, highlighting the structural diversity among cultivated *C. canephora* clones (Table 4).

Based on the evaluated traits, three main functional dimensions were identified: agronomic, quality-related, and morphological. The agronomic traits (PH, 1YLD, RFDY, PL, CPL, NRS, DRS, FRS) revealed clear differences in growth and productivity among clones. LB10 and AR106 stood out for greater vigor, characterized by faster growth, early production, and longer plagiotropic branches. The N6 and AS2 performed well under non-irrigated conditions, while VP148, GJ8, and BRS1216 showed higher numbers of fruits per rosette. In contrast, BRS2357, R22, and WP6 exhibited shorter internodes and more compact rosettes, reflecting differences in canopy architecture and resource allocation (Figure 3).

Quality-related traits (BL, BW, BT, 100BW, DM, CC, OI, FQS) highlighted SK41 and AGL1 as references for larger bean size, while LB30 and BRS1216 showed higher outturn index values. BRS2314, AS2, and SK80 achieved superior cup quality scores. The longest maturation periods were

Table 4 - Means, genetic parameters, and experimental precision estimates for 24 traits organized into three groups: I. agronomic, II. coffee quality traits, and III. morphological, assessed in 62 widely cultivated *Coffea canephora* genotypes.

Trait	Group	F	Mean	Genetic Param.	CVe	CVg	CVg/ Cve
PH – Plant height	I	3.45**	2.18	71.06[a]	4.26	7.24	1.70
1YLD – First yield	I	8.99**	74.95	88.31[a]	21.04	38.08	1.81
RFDY – Rainfed yield	I	5.41**	31.98	81.51[a]	25.72	38.06	1.48
PL – Plagiotropic branches	I	3.43**	62.8	70.90[b]	11.62	12.55	1.08
PL – Plagiotropic length	I	2.76**	0.88	63.81[b]	9.72	9.14	0.94
NRS – Number of rosettes	I	2.62**	11.49	61.93[b]	15.42	10.49	0.68
DRS – Distance rosettes	I	4.12**	4.88	19.02[b]	9.78	3.81	0.39
FRS – Fruits per rosette	I	1.93**	23.27	48.31[b]	17.29	10.72	0.62
BL – Bean length	II	15.99**	9.08	93.74[b]	5.6	9.79	1.74
BW – Bean width	II	12.06**	6.6	91.71[b]	5.01	8.53	1.7
BT – Bean thickness	II	10.20**	4.2	90.19[b]	8.27	8.03	0.97
100BW – 100-bean weight	II	53.97**	16.34	98.14[b]	1.77	19.06	10.77
DM – Days to maturation	II	13.18**	314.43	92.41[a]	4.93	5.91	1.20
CC – Caffeine content	II	13.32**	2.51	92.49[a]	1.78	13.35	7.5
OI – Outturn index	II	13.94**	22.67	92.83[b]	2.46	8.24	3.35
FQS – Final quality score	II	9.07**	79.93	88.91[b]	1.84	2.94	1.60
FL – Fruit length	III	13.97**	14.82	92.84[b]	5.74	8.19	1.43
FW – Fruit width	III	11.62**	13.24	91.39[b]	4.41	6.04	1.37
FT – Fruit thickness	III	11.21**	10.86	91.08[b]	6.15	7.31	1.19
100FW – 100-fruit weight	III	17.87**	130.5	94.40[b]	4.66	18.79	4.03
LA – Leaf area	III	18.87**	94.32	94.70[a]	19.06	32.9	1.72
LDM – Leaf dry mass	III	7.58**	0.85	86.81[a]	20.46	21.43	1.04
SA – Stomatal area	III	2.48**	351.08	59.79[a]	15.18	7.56	0.49
SD – Stomatal density	III	5.06**	330.63	80.27[a]	17.11	14.09	0.82

a: genotypic determination coefficient (H^2); b: repeatability (r); F: F-test from the analysis of variance for genotype effect; CVe: experimental coefficient of variation; CVg: genotypic coefficient of variation; CVg/CVe: ratio of genotypic to experimental coefficient of variation.

recorded for WP6, AR106, and BRS2336, whereas LB15, AS10, and P50 were characterized by earlier ripening (Figure 3).

Morphological traits (FL, FW, FT, 100FW, LA, LDM, SA, SD) differentiated N6, SK244, and N13 by their larger fruit dimensions, while LB101, AR106, and BRS3213 exhibited higher leaf area and stomatal values, suggesting enhanced photosynthetic capacity and vigor (Figure 3).

Pairwise correlations were analyzed within each trait group to capture diversity across functional dimensions. Strong correlations were detected among traits within the same group, indicating internal consistency in the expression of growth, yield, and quality attributes (Figure 4). In the agronomic group, plant height, canopy length, and number of plagiotropic branches showed the strongest associations, reflecting their joint contribution to vigor and productivity. In the quality-related group, significant correlations were observed among bean length, width, and thickness ($r > 0.70$), and between 100-bean weight and these size traits. Moderate correlations between bean dimensions and dry matter were also found, while cup quality descriptors such as color, odor intensity, and flavor quality score were largely independent of physical traits, suggesting distinct physiological control of beverage quality.

Within the morphological group, fruit length, width, thickness, and 100-fruit weight were strongly correlated ($r > 0.75$), indicating structural coherence in fruit development. By contrast, leaf- and stomata-related traits showed weak or non-significant associations with fruit traits, reflecting independence between photosynthetic and reproductive components.

Multicollinearity diagnostics (VIF) ranged from 1.3 to 8.9, with higher values observed among growth-related variables. Fruit morphology and cup quality descriptors showed low VIF values,

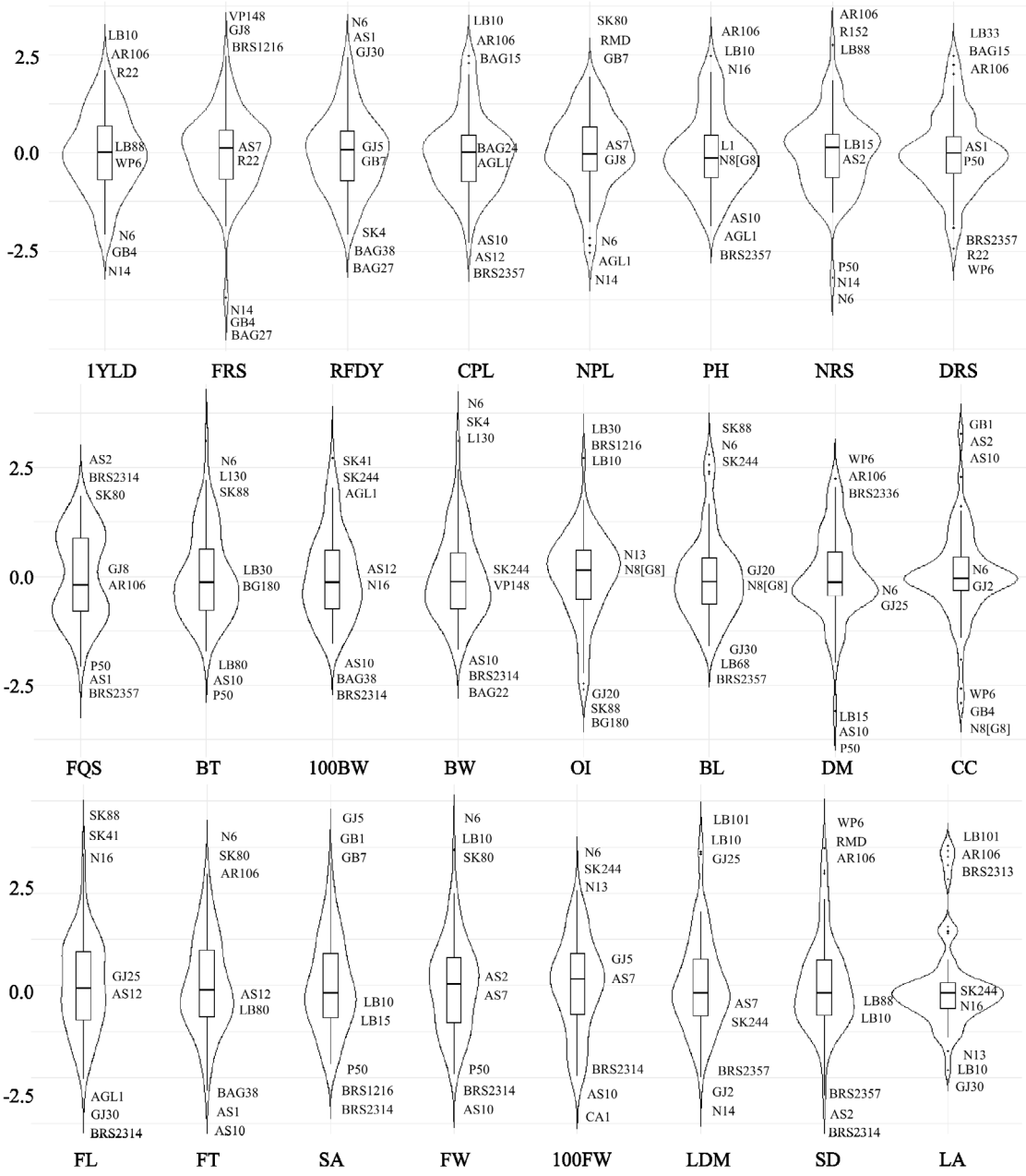

Figure 3 - Violin plots showing the distribution of 62 *Coffea canephora* genotypes for 24 agronomic, morphological, and physiological traits (PH, 1YLD, RFDY, NPL, CPL, NRS, DRS, FRS, GL, GW, GT, 100BW, DM, CC, OI, FQS, FL, FWi, FT, 100FW, LA, LDM, SA, SD). Central boxplots indicate medians, interquartile ranges, and outliers, while violin shapes represent kernel density estimation of the data distribution. Highlighted genotype codes correspond to representative clones selected for each trait.

confirming the absence of redundancy and supporting the inclusion of all variables in multivariate analyses. Principal component analysis (PCA) based on agronomic traits revealed clear patterns of association among descriptors related to plant vigor and productivity (Figure 5). The first two components explained 52.2% of the total variance, capturing most of the agronomic variation. Plant height (PH) and number of plagiotropic branches (NPL) were the main contributors to PC1, representing vegetative

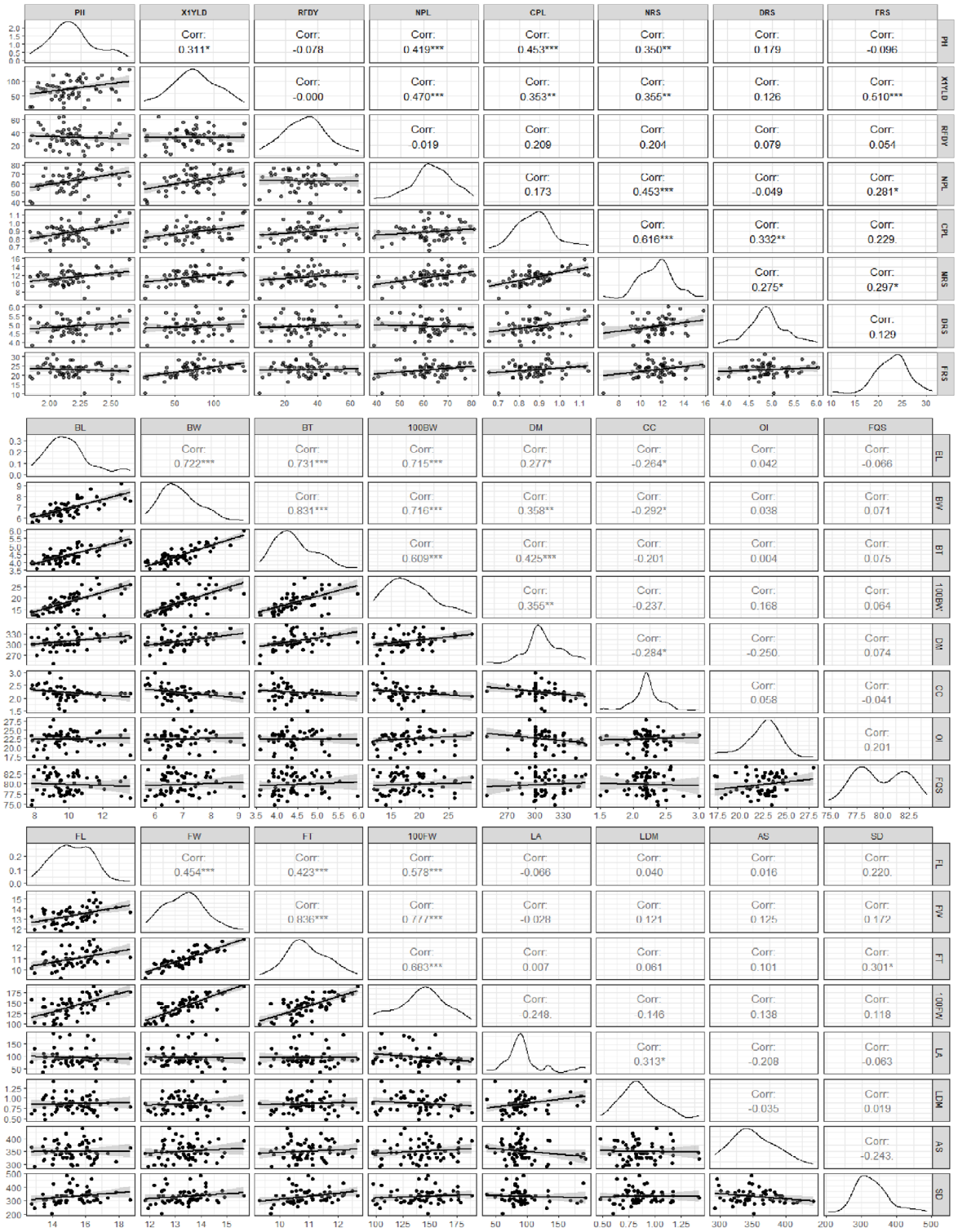

Figure 4 - Pairwise scatterplots, histograms, and Pearson correlation coefficients among 24 traits in 62 *Coffea canephora* genotypes. The diagonal panels show trait distributions, the lower panels display pairwise scatterplots and the upper panels present correlation coefficients, with significance levels indicated as $P < 0.05(^{*})$, $P < 0.01(^{**})$ and $P < 0.001(^{***})$. Traits are shown in the following order: PH, 1YLD, RFDY, NPL, CPL, NRS, DRS, FRS, GL, GW, GT, 100BW, DM, CC, OI, FQS, FL, FWi, FT, 100FW, LA, LDM, SA, SD (Materials and Methods for traits abbreviations).

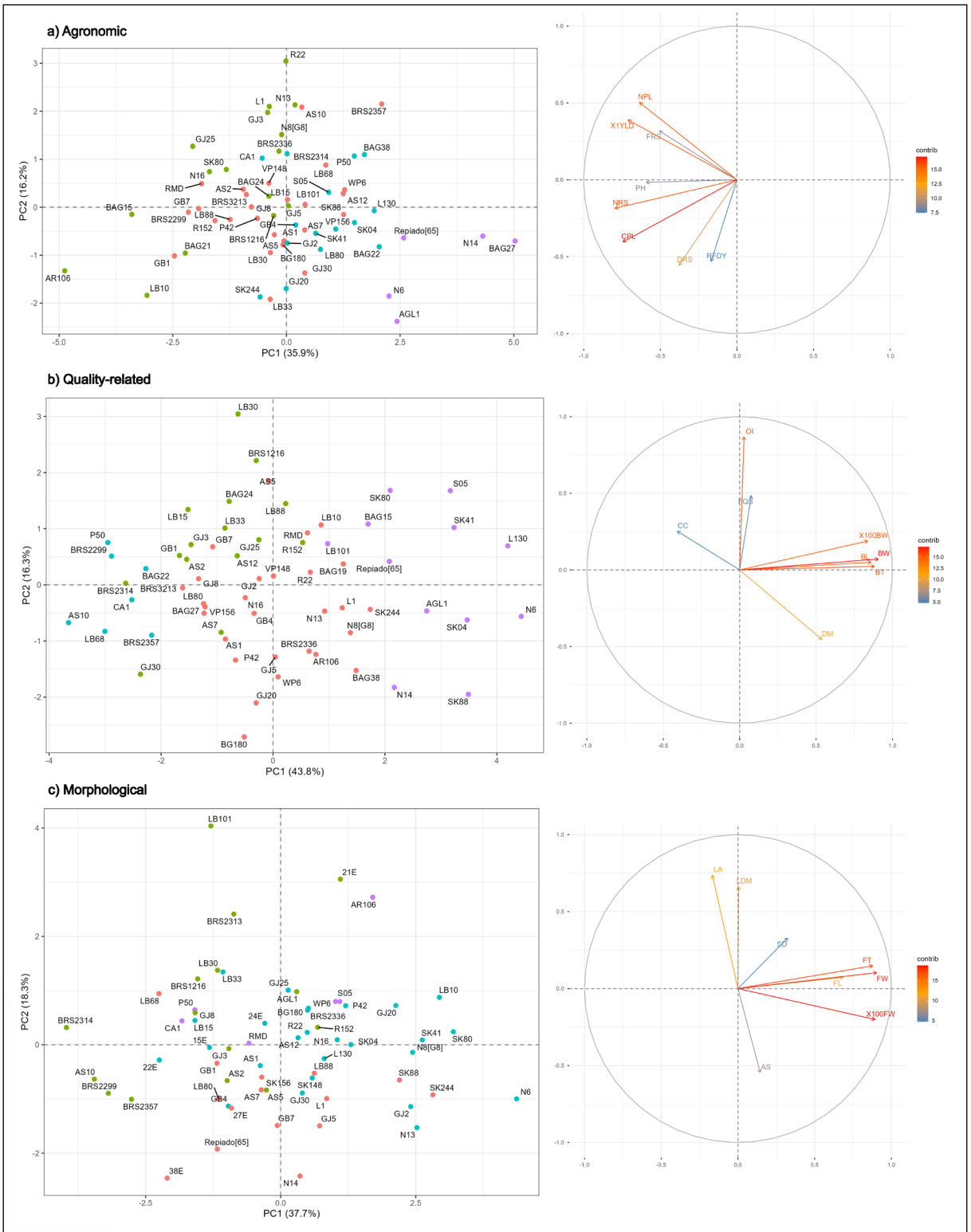

Figure 5 - Principal component analysis (PCA) of 62 *Coffea canephora* genotypes based on 24 agronomic, quality-related and morphological traits. Panels A–C show the ordination of genotypes on the first two principal components (left) and the corresponding variable correlation circles (right), with colors indicating the relative contribution of each trait to the principal components. Trait abbreviations: PH, 1YLD, RFDY, NPL, CPL, NRS, DRS, FRS, GL, GW, GT, 100BW, DM, CC, OI, FQS, FL, FWi, FT, 100FW, LA, LDM, SA, SD.

vigor, while yield components (1YLD, RFDY, FRS) were aligned in the same direction, reinforcing the coherence of growth-related traits. The number (NRS) and distance (DRS) between rosettes showed partially opposite orientations, indicating compensatory effects between branch density and fruit distribution. The ordination plot displayed a continuous dispersion of genotypes, with LB10, AR106, and GJ8 positioned at the positive extremes of PC1, characterized by vigorous growth and high productivity, while BRS2357, R22, and WP6 occupied the opposite side, representing more compact growth architectures.

The PCA of quality-related traits explained 60.1% of the total variance across the first two components. PC1 was mainly associated with bean physical dimensions—length (BL), width (BW), thickness (BT), and 100-bean weight (100BW)—which defined a gradient of seed size and density. Days to maturation (DM) contributed moderately in the same direction, partially associated with bean size. PC2 captured variation in cup quality descriptors, particularly the flavor quality score (FQS), which was oriented nearly orthogonal to the physical traits, confirming their independence from seed size. The ordination plot revealed a continuous distribution of clones, with SK41, AGL1, and SK80 positioned at the positive extreme of PC1 (larger beans), while LB30, LB15, and BRS1216 were located in the opposite quadrant (smaller seeds and earlier maturation). BRS2314 and AS2 stood out along PC2, reflecting superior beverage quality independent of bean morphology (Figure 5).

The PCA of morphological traits explained 56.0% of the total variance in the first two components. PC1 was strongly associated with fruit dimensions—length (FL), width (FW), thickness (FT), and 100-fruit weight (100FW)—defining a clear gradient of fruit size and mass. PC2 was influenced mainly by leaf and stomatal variables, including leaf area (LA), leaf dry mass (LDM), stomatal area (SA), and stomatal density (SD), which were oriented nearly perpendicular to the fruit traits, indicating weak associations between vegetative and reproductive structures. The ordination plot revealed partial separation among clones: N6, SK244, and N13 occupied the positive extremes of PC1 (larger fruits), while LB101, AR106, and BRS3213 showed higher values along PC2, associated with greater leaf area and stomatal density (Figure 5). These patterns indicated distinct morphological strategies among clones, reflecting variation in both reproductive and photosynthetic components within the germplasm.

DISCUSSION

Coffee canephora clones cultivated in the Western Amazon showed high diversity, reflecting the coexistence of Conilon and Robusta botanical varieties. The integration of phenotypic distributions, correlation patterns, and multivariate analyses revealed structured variation across agronomic, quality, and morphological dimensions. These results confirmed that this diversity is not random but derives from hybrid ancestry and targeted selection for adaptation and productivity.

This study consolidated the main phenotypic and genetic assessments on these cultivated genotypes. Some of these evaluations were originally focused on specific traits, including fruit and bean morphology (LOPES JUNIOR et al., 2024b), outturn index (SILVA et al., 2025b), caffeine content and molecular diversity (VIENCZ et al., 2023; SILVA et al., 2025a). The present research integrates these datasets with additional field and laboratory measurements, enabling a comprehensive characterization of the cultivated germplasm.

The wide phenotypic variation among clones indicates that significant variability remains within cultivated *C. canephora*. Narrow distributions reflected more uniform traits, whereas wide or bimodal patterns indicated internal heterogeneity typical of an allogamous, self-incompatible species. This variability, reinforced by farmer selection and natural hybridization, mirrors patterns reported for Brazilian and African germplasm (ESPÍNDULA et al., 2022; AKPERTEY et al., 2022) and remains essential for maintaining genetic progress and resilience.

Grouping traits by function improved the interpretation of phenotypic structure. In the agronomic group, plant height (PH), number (NPL), and length (CPL) of plagiotropic branches were strongly aligned, indicating a coordinated vegetative architecture closely associated with yield components such as first yield (1YLD) and fruits per rosette (FRS). In contrast, the partial opposition between number (NRS) and distance (DRS) between rosettes indicates a structural trade-off between branch density and the spatial distribution of fruiting sites. Within this framework, genotypes exhibited distinct functional profiles: GJ8 was positioned at the positive extreme of the vigor–productivity axis; R22 was primarily associated with the secondary axis, indicating a distinct rosette organization; and AS2 and BRS1216 occupied an intermediate position, reflecting a balance between growth and yield traits.

In the quality group, bean physical attributes—length (BL), width (BW), thickness (BT), and 100-bean weight (100BW)—defined a primary axis associated with grain size and mass. The final quality score (FQS), however, was oriented nearly orthogonally to these variables, indicating that beverage quality is largely independent of bean size. Days to maturation (DM) showed a distinct direction, suggesting partial independence from both physical and sensory traits. Within this structure, genotypes expressed contrasting profiles: SK41 and VP156 were positioned at the positive extreme of the bean size axis, reflecting larger grains; BRS2314 was more closely aligned with the quality axis, indicating superior beverage performance; while BRS1216 and LB30 combined high outturn index and physical attributes.

In the morphological group, fruit traits—length (FL), width (FW), thickness (FT), and 100-fruit weight (100FW)—formed a primary axis related to fruit size and mass, whereas leaf and stomatal traits—leaf area (LA), leaf dry mass (LDM), stomatal area (SA), and stomatal density (SD)—defined a secondary and largely independent axis. The near-orthogonal relationship between these groups indicates weak association between reproductive structures and leaf physiological traits. Genotypes were distributed accordingly: N6, SK244, and N13 were positioned at the positive extreme of the fruit axis, reflecting larger fruits; while AS2, AR106, and BRS3213 were more strongly associated with the leaf–stomatal axis, indicating greater leaf development and potential physiological capacity.

Principal component analyses supported these relationships and highlighted some traits. In the agronomic group, the separation between vigorous and compact genotypes has consequences for management and planting density. In the quality group, the independence between bean size and beverage traits indicates that selection for larger grains does not necessarily result in improved cup quality, reinforcing the need for simultaneous evaluations. In the morphological group, the decoupling between fruit and leaf–stomatal traits suggested that reproductive and physiological functions are partially independent. Together, these patterns reveal that the diversity within cultivated germplasm is organized into functional dimensions with direct implications for selection and cultivar development.

Several clones emerged as reference genotypes with consistent functional roles across trait groups. GJ8 consistently represented the extreme of vigor and productivity, while AR106 and LB10 also showed high vegetative growth and early yield potential. R22 was distinguished by its architectural organization of rosettes, reflecting a specific structural arrangement of fruiting sites. SK41 and VP156 were associated with larger beans and favorable quality attributes, whereas BRS2314 was more closely linked to beverage quality, reinforcing the independence between physical and sensory traits. AS2 was consistently associated with leaf and stomatal traits, indicating enhanced physiological capacity and potential adaptation. The BRS1216 occupied an intermediate position, combining balanced performance across agronomic, quality, and morphological dimensions. The BAG19 and BAG24 further contributed to this diversity by representing contrasting maturation patterns and intermediate profiles. Together, these genotypes define a coherent set of complementary ideotypes that can support targeted breeding strategies and germplasm management.

Associating our findings with previous genomic analyses, the high variability observed among clones is consistent with the hybrid nature of the plants. The relative contribution of each gene pool varied widely, ranging from 30% to 70%. Genotypes with approximately balanced ancestry—around 50% Conilon and 50% Robusta, such as R152, SK244, AS2—likely represent simple hybrids resulting from early intervarietal crosses. Others showed asymmetric compositions, including AR106, SK41, and LB101, which retained a predominantly Robusta background, and CA1, AS1, and P50, which are mainly Conilon-derived. This mosaic genetic structure reflects spontaneous hybridizations subsequently refined by farmer and institutional selection. The predominance of hybrid genotypes explains the broad phenotypic variation observed across agronomic, morphological, and quality-related traits.

From a breeding perspective, these clones provide complementary parental types for hybridization. Crosses between high-yielding (AR106, LB10) and quality-oriented (AS2, BRS2314) genotypes can generate balanced progenies combining productivity and sensory potential. Multipurpose clones such as BAG24 and BAG19 expand opportunities for heterosis and broad adaptation. The complementary gene pools of Conilon and Robusta remain central to strategies aiming at hybrid vigor and resilience (ROCHA et al., 2025).

The Western Amazon germplasm preserves remarkable genetic richness shaped by hybridization, farmer selection, and formal breeding. Integrating multivariate analyses into germplasm management

enables objective identification of divergent and complementary genotypes, guiding conservation and cross design. These results position the regional germplasm as a strategic reservoir for developing next-generation *C. canephora* cultivars that unite vigor, quality, and stability under tropical conditions.

The findings also have practical implications for cultivar registration and genetic resource management. Due to the lack of standardized descriptors specific to *C. canephora*, the Brazilian Ministry of Agriculture still relies on *C. arabica* parameters to guide the registration of *C. canephora* cultivars. This limitation reflects the insufficient characterization of reference genotypes capable of defining contrasting growth habits, yield potential, and quality profiles. By interpreting the phenotypic and genetic attributes of the most widely cultivated clones, this study contributed to establishing a reliable reference framework for *C. canephora* descriptors. Such information enables producers to select genetic materials with specific agronomic and morphological profiles suited to their production systems. In practical terms, this knowledge reduced the risk associated with large-scale cultivation of poorly characterized materials and enhanced the long-term security and sustainability of coffee production in the Western Amazon.

CONCLUSION

This study provided an integrated assessment of the phenotypic diversity of 62 *Coffea canephora* genotypes cultivated in the Western Amazon, revealing structured patterns of variation across agronomic, morphological, and quality-related traits. The results showed that this diversity is organized into functional dimensions associated with the genetic background of Conilon and Robusta lineages. Reference clones representing complementary ideotypes were identified, including vigorous and high-yielding, compact, quality-oriented, and physiologically adapted types, supporting their use in breeding strategies and germplasm management. Overall, these findings provided relevant information to support breeding programs, germplasm conservation, and future genomic-assisted selection strategies for the development of cultivars combining productivity, quality, and adaptation to tropical conditions.

DATA AVAILABILITY STATEMENT

The data supporting the findings of this study are available from the corresponding author upon reasonable request.

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DECLARATION OF CONFLICT OF INTEREST

The authors declare no conflict of interest. The funding sponsors had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript, and in the decision to publish the results.

AUTHORS' CONTRIBUTIONS

All authors contributed equally to the conception and writing of the manuscript. All authors critically reviewed the manuscript and approved the final version.

DECLARATION OF USE OF ARTIFICIAL INTELLIGENCE

Artificial intelligence tools were used only to support language revision. All AI-assisted edits were reviewed by the authors, who take full responsibility for the final content.

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