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CROP BREEDING
Article

Evaluation of the genetic potential of coffee trees in agroforestry systems with rubber trees

João Felipe de Brites Senra[1]*, Marcone Comerio[2], Rosana Gomes Oliveira[3], Viviane Alexia Correia Silva[3], Willian Moreira Gomes[2], Maria Amélia Gava Ferrão[4], Abrãao Carlos Verdin Filho[2], Paulo Sérgio Volpi[2], Romário Gava Ferrão[5], Aymbiré Francisco Almeida da Fonseca[4], Marcelo Antonio Tomaz[6]

1. Instituto Capixaba de Pesquisa, Assistência Técnica e Extensão Rural – Centro de Pesquisa Desenvolvimento e Inovação Sul – Cachoeiro de Itapemirim (ES), Brasil.
2. Instituto Capixaba de Pesquisa, Assistência Técnica e Extensão Rural – Centro de Pesquisa Desenvolvimento e Inovação Norte – Marilândia (ES), Brasil.
3. Universidade Federal do Espírito Santo – Programa de Pós-Graduação em Genética e Melhoramento – Alegre (ES), Brasil.
4. Instituto Capixaba de Pesquisa, Assistência Técnica e Extensão Rural – Vitória (ES), Brazil.
5. Instituto Capixaba de Pesquisa, Assistência Técnica e Extensão Rural – Coordenador de Pesquisa Multivix – Vitória (ES), Brazil.
6. Universidade Federal do Espírito Santo – Departamento de Agronomia – Alegre (ES), Brasil.

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***Corresponding author:** joaofelipeagronomo@gmail.com

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ABSTRACT: This study sought to identify superior genotypes of *Coffea arabica* and *Coffea canephora* suitable for agroforestry systems. The experiment took place in two distinct environments: monoculture and an agroforestry system featuring rubber trees (*Hevea brasiliensis*). Employing a randomized complete block design with four replications, the plants were spaced 3 m apart between rows and 1 m between plants in monoculture. In the agroforestry system, the spacing widened to 8 m between rows and 1 m between plants. The evaluation encompassed 11 genotypes, with 10 plants per plot in monoculture and 18 in the agroforestry system. Thirteen morpho-agronomic characteristics, spanning plant shape, uniformity of maturation, fruit size, vigor, pest and disease resistance, and production, were assessed. Employing the restricted maximum likelihood method and the best unbiased linear prediction method in the Selegen software facilitated data analysis, and selection was executed through the Mulamba-Rank index. Comparative analysis revealed that mean values for the evaluated characteristics were consistently higher in the agroforestry system compared to monoculture. Notably, clones A1, 5V, 308 and LB1 (*C. canephora*) emerged as the most promising genotypes in agroforestry system. Consequently, these clones stand out as robust candidates for inclusion in the composition of varieties tailored for agroforestry systems. This research offers valuable insights into optimizing coffee cultivation in the context of sustainable agroforestry practices.

Key words: climate changes; mixed models; *Coffea canephora*; *Coffea arabica*; *Hevea brasiliensis*.

INTRODUCTION

The $200 billion global coffee market, with 75% from exports, primarily revolves around *Coffea arabica* (Arabica coffee), *Coffea canephora* (conilon/robusta coffee), and *Coffea liberica* (liberica coffee), making up approximately 60, 40, and less than 1% of the market, respectively. Brazil leads in conilon coffee production. Climate change, fueled by greenhouse gas emissions, is driving the development of technologies to safeguard coffee farming (Senra et al. 2022a), prompting efforts to create climate-adapted coffee cultivars (Moat et al. 2017, Kath et al. 2022).

Estimates reveal a 0.25°C per decade temperature increase in Brazilian coffee-producing regions since 1974, causing a 20% productivity decline in the southeast (Koh et al. 2020). This has led to a shift in coffee cultivation or the adoption of adaptive technologies like thermal and water stress-tolerant varieties, intercropping, or agroforestry (Baca et al. 2014).

Agroforestry systems (AFS) involve intercropping coffee trees with shade trees, offering benefits such as nutrient cycling, biodiversity, carbon storage, and a milder microclimate (Nair et al. 1998, Duarte et al. 2013). Careful selection of factors, including species, shading level, soil fertility, irrigation, altitude, and climate, is crucial for adopting agroforestry cropping systems (Kuyah et al. 2019).

Research indicates that taller trees reduce air temperature (Zaro et al. 2020), making agroforestry systems viable strategies to mitigate climate change effects (Pham et al. 2019). Despite recognized benefits, no *C. canephora* cultivars specifically designed for agroforestry systems exist (Senra et al. 2022a). Shade effects on Arabica coffee are well-studied, but few studies focus on conilon coffee (Piato et al. 2020). Addressing shade effects separately for conilon and arabica coffee is crucial due to their different ecologies (Tumwebaze and Byakagaba 2016), emphasizing the need for cultivar selection considering economic performance and adaptability to agroforestry systems.

The rubber tree (*Hevea brasiliensis*) stands out for agroforestry systems, with a well-developed root system exploring soil layers untouched by coffee trees. Positive water relationships between rubber and Arabica coffee trees, with the latter benefiting from increased water absorption, have been observed (Yang et al. 2021). Cultivating coffee in agroforestry systems with rubber trees maintains suitable conditions, reducing average air temperatures by 1 to 2°C (Zaro et al. 2020). This study evaluated the genetic potential of coffee trees (arabic and conilon) in agroforestry systems with rubber trees and monoculture, using the compound symmetry model to identify genotypes suitable for AFS amid climate change.

MATERIAL AND METHODS

The experiment was set up in 2017 at the Marilândia experimental farm (FEM), belonging to the Capixaba Institute for Research, Technical Assistance and Rural Extension (Incaper) Research, Development and Innovation Center North (CPDI North). The FEM is in the municipality of Marilândia, in the northwest of the state of Espírito Santo, at 19º24'26.09"S, 40º32'26.83"W, at altitude of 89 m. The climate is tropical classified as Aw (Köppen and Geiger 1928), typically rainy from November to February and partially dry in March, April and October and dry from May to September, accumulating an average of 1,164 mm of annual precipitation and an average annual temperature of 24.2°C (13.9 to 33.5°C). The experiment was set up in two environments, monoculture and an agroforestry system (AFS) with rubber trees (*H. brasiliensis*), in a randomized block design with four replications. In the monoculture, a spacing of 3 m between rows and 1 m between plants was used, with ten plants per plot. In the AFS, the rubber trees were spaced 8 m between rows and 2.5 m between plants and the coffee trees 8 m between rows and 1 m between plants, with 18 plants per plot. Eleven different genotypes were evaluated (Table 1). The Robusta Tropical genotype, being a cultivar of seminal origin, has the particularity of being a gene pool of the variety, so the evaluation plots represent a sample of the gene combinations.

Table 1. Coffee tree genotypes (*Coffea canephora* and *Coffea arabica*) being evaluated.

Genotype	Cultivar	Species
A1	Clone 8 of the 'ES8112' variety	Coffea canephora
13V	Clone 13 of the 'ES8142' variety	Coffea canephora
8V	Clone 8 of the 'ES8142' variety	Coffea canephora
LB1	Clone 1 of the 'ES8122' variety	Coffea canephora
12V	Clone 12 of the 'ES8142' variety	Coffea canephora
308	Clone 8 of the 'ES8132' variety	Coffea canephora
5V	Clone 5 of the 'ES8142' variety	Coffea canephora
409	Clone 9 of the 'ES8143' variety	Coffea canephora
Arábica 1	'Catuaí 81'	Coffea arabica
Arábica 2	'Catuaí 86'	Coffea arabica
Robusta Tropical (RT)	'Emcapa 8151'	Coffea canephora

Fertilizations were carried out during the planting, formation, and production phases, adjusting them according to the specific requirements of the crop, based on soil analyses. Cultural and phytosanitary management were carried out according to the requirements of the crop, following the recommendations for conilon coffee (Ferrão et al. 2019).

The following characteristics were assessed from 2019 to 2022:

- Fruit ripening time (FT): Phenotypic assessment of the time the fruit is harvested, classified as super early, harvested before May (score 1); early, harvested in May (score 2); medium ripeness, harvested in June (score 3); late ripeness, harvested in July (score 4); and super late ripeness, harvested after July (score 5);
- Uniformity of fruit ripening (UM): Phenotypic evaluation of the uniformity of ripening of the fruit picked during the harvest, with grade 1 given to genotypes with all ripe fruit; grade 2 to genotypes with ripe and green fruit; grade 3 to genotypes with ripe, green and dry fruit;
- Fruit size (FS): Phenotypic evaluation of fruit size in the field, estimated using a scale of scores ranging from 1 to 5, following the list of descriptors of the National Service for the Protection of Cultivars, which presents the classes very small, small, medium, large and very large, respectively (Guerreiro Filho et al. 2008);
- Plant size (PS): Phenotypic assessment of plant size using a scale of scores from 1 to 3, with 1 being low, 2 intermediate and 3 high. For standardization purposes, clone 02/Incaper, which is medium-sized, and clone 04/Incaper, which is tall, were taken as references;
- Vegetative vigor (VV): Phenotypic evaluation on a scale of scores from 1 to 10 on the level of acceptance of the genotype required by coffee growing according to vegetative vigor, in which: score 1 = very weak; score 3 = weak; score 5 = intermediate; score 7 = vigorous; and score 10 = excellent vigor;
- Incidence of rust (IR): Caused by the fungus *Hemileia vastatrix* Berk. & Br. and evaluated with a scale of scores ranging from 1 to 9, in which: score 1 is attributed to asymptomatic plants; score 3 = presence of few sporulations; score 6 = sporulations plus an onset of defoliation; score 7 = sporulations and severe defoliation; and score 9 = sporulations and high-level defoliation causing plant depletion;
- Incidence of cercospora leaf spot (IC): Caused by the fungus *Cercospora coffeicola* Berk. & Cooke and assessed using a phenotypic scale of scores ranging from 1 to 9, in which: score 1 is attributed to asymptomatic plants; score 3 = presence of few lesions on leaves; score 6 = lesions on leaves and fruit; score 9 = high level of lesions on leaves and fruit plus severe plant depletion;
- Drying out of plagiotropic branches (DB): A joint phenotypic evaluation of a series of biotic and abiotic factors that cause the loss of leaves at the end of plagiotropic branches. It is evaluated on a scale of scores from 1 to 9, in which: score 1 is assigned to plants with no visible symptoms; score 3 to plants with few dry branches; score 5 = moderate level of dry branches; score 7 = high level of dry branches indicating plant impoverishment; and score 9 = very severe symptoms indicating possible elimination of the plant;
- General scale (GS): Phenotypic evaluation on a scale of scores from 1 to 10 on the level of acceptance of the genotype for application in coffee growing: score 1 attributed to genotypes with a very poor phenotype; score 3 = poor; score 5 = intermediate level of acceptance; score 7 = good phenotypic evaluation; and score 10 = excellent phenotype;
- Incidence of mining insects (IMI): Phenotypic evaluation on a scale of scores from 1 to 9 on the level of severity of the attack by the insect *Leucoptera coffeella*, in which: score 1 = no leaves attacked; score 3 = few leaves with the presence of necrotic mines; score 6 = many leaves attacked with defoliation of the plant; and score 9 = defoliation causing depletion of the plant;
- Degree of inclination (DI): Assessed using a grading scale in which: grade 1 is assigned to genetic materials with an erect growth habit with 1 to 35% inclination of the orthotropic branches; grade 2 genotypes with a semi-erect growth habit with 36 to 50% inclination of the orthotropic branches; and grade 3 genotypes with a prostrate growth habit with 51 to 100% inclination of the orthotropic branches;
- Incidence of citrus mealybug (ICR): Phenotypic assessment of the level of severity of damage and the presence of rosette mealybug (*Planococcus citri*; *Planococcus minor*) on a scale of scores from 1 to 5, in which: score 1 is attributed to the absence of the pest; 2 = identification of few insects and no economic damage; 3 = beginning of economic damage; 4 = high infestation with easy identification of the insects associated with fruit drop and the presence of fumagina; and 5 = severe infestation with fruit drop, loss of beverage quality and high level of fumagina.

• Yield per plant (YP): Production in bags of roasted coffee per hectare (sc·ha^{-1});

Data analysis was carried out using the restricted maximum likelihood method and the best unbiased linear prediction (REML/BLUP), in the Selegen software (Resende 2007) applying the compound symmetry model shown below (Eq. 1):

$$y = Xf + Zg + Qgl + Tgm + Wgml + Sp + e \quad (1)$$

where: *y*: the vector of data; *f*: the vector of the effects of the repetition, location and measurement combinations (fixed) added to the general average; *g*: the vector of genotypic effects (random); *gl*: the vector of the effects of the interaction of genotypes × locations (random); *gm*: the vector of genotype × measurement interaction effects (random); *glm*: the vector of genotype × location × measurement triple interaction effects (random); *p*: the vector of permanent plot effects within locations (random); *e*: the vector of errors or residue (random).

The environmental effects of blocks within sites, measurements and sites and the interactions were considered fixed effects in the f vector.

Based on this model, the variance components were estimated: genetic variance (σ^2_g); variance of the genotypes × measurements interaction (σ^2_{gm}); variance of the genotypes × locations interaction (σ^2_{gl}); variance of the interaction genotypes × locations × measurements (σ^2_{glm}); permanent environment variance (σ^2_p); residual variance (σ^2_e); phenotypic variance (σ^2_{phen}); heritability of individual plots in the broad sense (h^2); broad-sense heritability of the mean of the genotypes (h^2_{mg}); accuracy of genotype selection ($\overline{r_{gg}}$); coefficient of determination of the effects of the genotypes × locations interaction (c^2_{gl}); coefficient of determination of the effects of the genotypes × measurements interaction (c^2_{gm}); coefficient of determination of the effects of the interaction genotypes × locations × measurements (c^2_{glm}); coefficient of determination of permanent plot effects (c^2_p); individual repeatability (r); genotypic correlation across sites (r_{gl}); genotypic correlation through measurements (r_{gm}); genotypic correlation across locations in a given harvest (r_{gl_m}); genotypic correlation through measurements at a given location (r_{gm_l}); genotypic correlation across sites for the average of all measurements (r_{gl_mm}); genotypic correlation through measurements for the average of all sites (r_{gm_ml}); genotypic correlation across locations and measurements (r_{glocm}); and overall average of the experiment (μ).

The significance of the random effects of the model was tested by deviance analysis using the likelihood ratio test (LRT) according to Eq. 2:

$$LRT = -2\ (Log_L - Log_L) \quad (2)$$

where: LogL: the logarithm of the maximum (L) of the restricted likelihood function of the full model; $LogL_R$: the logarithm of the maximum (LR) of the restricted likelihood function of the reduced model (without the effect being tested).

The LRT was analyzed using the chi-square test with a degree of freedom of 1, 5 and 10% significance. Subsequently, the selection was carried out separately for each environment, considering both environments, using the Mulamba-Rank index (Resende 2007) to determine the five best genotypes for each location and for both. For this analysis, a multicollinearity assessment was performed to discard redundant variables, employing the classification table proposed by Montgomery and Peck (1981). The collinearity analysis was conducted using the Genes software (Cruz 2016).

RESULTS

The estimated genetic parameters revealed significant values for heritability, selective accuracy, repeatability coefficient, genotypic correlation between locations, genotypic correlation between crops, and genotypic correlation across locations in a given crop (Table 2). Heritability is considered low when values are below 0.15, moderate for values between 0.15 and 0.50, and high when they exceed 0.5 (Resende and Alves 2020). Among the traits analyzed, FT, FS, PS, VV, GS, DI and YP showed high broad-sense heritability of the mean of the genotypes (0.8371; 0.5598; 0.8862; 0.8950; 0.7444; 0.5400; 0.7592). The IC trait showed moderate heritability (0.2531), while the others showed low heritability, ranging from 0.0111 to 0.0511.

Table 2. Estimates of variance components genetic and environmental parameters for the following traits: Fruit ripening time (FT); uniformity of fruit maturation (UM); fruit size (FS); plant size (PS); vegetative vigor (VV); incidence of rust (IR); incidence of cercosporiosis (IC); drying out of plagiotropic branches (DB); general scale (GS); incidence of mining insects (IMI); degree of inclination (DI); incidence of citrus mealybug (ICR); and yield per plant (YP).

Component	FT	UM	FS	PS	VV	IR	IC	DB	GS	IMI	DI	ICR	YP
σ^2_g	0.3600	0.0012	0.1283	0.0800	0.4227	0.0060	0.0044	0.0090	0.3220	0.0003	0.0220	0.0002	76.8345
σ^2_{gm}	0.2647	0.0576	0.2048	0.0014	0.0137	0.3138	0.0137	0.0215	0.3246	0.0354	0.0542	0.0009	2.6172
σ^2_{gl}	0.0008	0.0003	0.0663	0.0022	0.0025	0.0645	0.0010	0.0083	0.0051	0.0244	0.0007	0.0103	32.9654
σ^2_{glm}	0.0219	0.0574	0.1173	0.0542	0.2855	0.3967	0.0515	0.2027	0.1732	0.0043	0.0345	0.0679	52.6752
σ^2_p	0.0036	0.0012	0.0156	0.0237	0.1636	0.0107	0.0125	0.0089	0.0601	0.0042	0.0067	0.0010	9.5215
σ^2_e	0.1699	0.1714	0.3667	0.3311	1.0507	0.4793	0.5895	0.3987	0.8459	0.4377	0.0889	0.1956	88.6744
σ^2_{phen}	0.7990	0.2316	0.7816	0.4385	1.6532	0.8744	0.6211	0.4464	1.5578	0.5020	0.1725	0.2080	210.6130
h^2	0.4506	0.0052	0.1642	0.1824	0.2557	0.0069	0.0071	0.0201	0.2067	0.0005	0.1276	0.0011	0.3648
h^2_{mg}	0.8371	0.0511	0.5598	0.8862	0.8950	0.0359	0.2531	0.1962	0.7444	0.0111	0.5400	0.0149	0.7592
$\overline{r_{\hat{g}g}}$	0.9149	0.2261	0.7482	0.9414	0.9461	0.1894	0.5031	0.4429	0.8628	0.1053	0.7349	0.1220	0.8713
c^2_{gl}	0.0009	0.0012	0.0848	0.0050	0.0015	0.0737	0.0016	0.0186	0.0033	0.0486	0.0039	0.0494	0.1565
c^2_{gm}	0.3313	0.2485	0.2620	0.0033	0.0083	0.3589	0.0220	0.0482	0.2084	0.0706	0.3140	0.0045	0.0124
c^2_{glm}	0.0275	0.2478	0.1500	0.1236	0.1727	0.4537	0.0829	0.4541	0.1112	0.0086	0.2000	0.3264	0.2501
c^2_p	0.0045	0.0050	0.0199	0.0541	0.0990	0.0123	0.0201	0.0200	0.0386	0.0084	0.0389	0.0046	0.0452
r	0.4560	0.0114	0.2689	0.2415	0.3561	0.0929	0.0289	0.0586	0.2486	0.0576	0.1705	0.0551	0.5665
r_{gl}	0.9979	0.8132	0.6594	0.9731	0.9942	0.0857	0.8126	0.5192	0.9843	0.0107	0.9703	0.0211	0.6998
r_{gm}	0.5763	0.0205	0.3852	0.9823	0.9685	0.0189	0.2444	0.2940	0.4980	0.0074	0.2889	0.1914	0.9671
r_{gl_m}	0.9988	0.9953	0.8341	0.9736	0.9944	0.8323	0.9466	0.7860	0.9921	0.5939	0.9912	0.1011	0.7068
r_{gm_l}	0.5768	0.0251	0.4872	0.9828	0.9687	0.1835	0.2847	0.4451	0.5019	0.4104	0.2952	0.9183	0.9767
r_{gl_mm}	0.9983	0.9908	0.7591	0.9770	0.9951	0.7402	0.9530	0.8869	0.9886	0.2949	0.9850	0.6291	0.7333
r_{gm_ml}	0.5838	0.3429	0.5180	0.9869	0.9763	0.4299	0.6916	0.8419	0.5588	0.2923	0.4223	0.9768	0.9786
r_{glocm}	0.5561	0.0104	0.2484	0.5803	0.5835	0.0077	0.0627	0.0371	0.3903	0.0041	0.1977	0.0028	0.4654
μ	3.2679	1.5383	4.8410	1.8807	5.6903	2.3722	1.6705	1.6818	5.5647	2.6023	1.2784	1.7684	19.0485

σ^2_g: genetic variance; σ^2_{gm}: variance of the genotypes x measurements interaction; σ^2_{gl}: variance of the genotypes × locations interaction; σ^2_{glm} variance of the genotypes × locations × measurements interaction; σ^2_p: permanent environment variance; σ^2_e: residual variance; σ^2_{phen}: phenotypic variance; h^2: heritability of individual plots in the broad sense; h^2_{mg}: broad-sense heritability of the mean of the genotypes; $r_{\hat{g}g}$: accuracy of genotype selection; c^2_{gl}: coefficient of determination of the effects of the genotypes × locations interaction; c^2_{gm}: coefficient of determination of the effects of the genotypes × measurements interaction; c^2_{glm}: coefficient of determination of the effects of the interaction genotypes × locations × measurements; c^2_p: coefficient of determination of permanent plot effects; r: individual repeatability; r_{gl}: genotypic correlation across sites; r_{gm}: genotypic correlation through measurements; r_{gl_m}: genotypic correlation across locations in a given harvest or measurement; r_{gm_l}: genotypic correlation through measurements at a given location; r_{gl_mm}: genotypic correlation across sites for the average of all measurements; r_{gm_ml}: genotypic correlation through measurements for the average of all sites; r_{glocm}: genotypic correlation across locations and measurements; μ: overall average of the experiment.

Selective accuracy is defined by the correlation between the true genotypic value and the genotypic value estimated from experimental data. Its classification is considered low if it is between 0.1 and 0.4, moderate if it ranges from 0.4 to 0.7, and high if it is between 0.7 and 0.9 (Resende and Alves 2020). The accuracy of trait evaluation ranged from 0.1053 (IMI) to 0.9149 (FT), values which have a direct impact on the reliability of identifying the most promising genotypes. Repeatability is classified as low if it is below 0.3, moderate if it is between 0.3 and 0.6, and high if it is above 0.6 (Resende and Alves 2020). Among the characteristics evaluated, only FT showed moderate repeatability (0.4560), while the others showed low repeatability, ranging from 0.114 to 0.2689. The correlations for the traits IR, IMI and ICR between locations (0.0857, 0.0107 and 0.0211) and UM, IR, IMI and ICR across harvests (0.0205, 0.0189, 0.0074, 0.01914) were low.

Analysis of the LRT showed no significance for the effect of permanent environments (experimental plot). However, significant genetic effects were estimated at 1% for the FT, VV and YP characteristics, and at 5% for PS and GS (Table 3). In addition, significant genetic effects were identified at 5% when analyzing the parameters of the interaction between genotype and environment, particularly yield per plant (YP). When exploring the interaction between genotype and crop, significance was found at 1% for the FT, FS, GS, DI traits, and at 5% for the UM and IR traits, indicating specific relationships between the genotypes and the measurements taken.

Table 3. Deviance and likelihood ratio test (LRT) for the following traits: fruit ripening time (FT); uniformity of fruit maturation (UM); fruit size (FS); plant size (PS); vegetative vigor (VV); incidence of rust (IR); incidence of cercosporiosis (IC); drying out of plagiotropic branches (DB); general scale (GS); incidence of mining insects (IMI); degree of inclination (DI); incidence of citrus mealybug (ICR); and yield per plant (YP).

Trait	Deviance					
	CM	G	G×L	G×M	G×L×M	Parc
FT	-24.12	-10.02	-24.11	14.37	-21.08	-23.95
UM	-63.66	-63.65	-63.66	-58.50	-49.51	-63.65
FS	208.37	210.32	210.77	215.69	217.77	208.92
PS	118.85	125.08	118.85	118.85	125.16	120.45
VV	524.76	534.02	524.76	524.78	535.45	530.76
IR	321.80	321.78	322.58	326.74	361.04	321.96
IC	264.39	264.50	264.38	264.51	266.00	264.55
DB	205.80	205.89	205.83	205.90	227.17	205.97
GS	458.98	465.37	458.95	467.03	465.03	460.56
IMI	167.77	167.76	170.44	170.38	167.77	167.79
DI	-235.06	-232.94	-235.10	-225.56	-219.66	-233.35
ICR	-47.75	-47.75	-47.01	-47.75	-29.28	-47.74
YP	1897.92	1902.06	1901.06	1897.92	1920.92	1900.84
Trait	**LRT**					**Average**
	G	**G×L**	**G×M**	**G×L×M**	**Parc**	**AFS** **Mon**
FT	14.10**	0.0100^{ns}	38.49**	3.04^{o}	0.17^{ns}	3.3295 3.2063
UM	0.01^{ns}	0.0000^{ns}	5.16*	14.15**	0.01^{ns}	1.6591 1.4175
FS	1.95^{ns}	2.4000^{ns}	7.32**	9.40**	0.55^{ns}	4.9679 4.7142
PS	6.23*	0.0000^{ns}	0.00^{ns}	6.31*	1.60^{ns}	2.1477 1.6136
VV	9.26**	0.0000^{ns}	0.02^{ns}	10.69**	6.00^{ns}	5.9886 5.3920
IR	-0.02^{ns}	0.7800^{ns}	4.94*	39.24**	0.16^{ns}	2.7727 1.9716
IC	0.11^{ns}	-0.0100^{ns}	0.12^{ns}	1.61^{ns}	0.16^{ns}	1.6250 1.7159
DB	0.09^{ns}	0.0300^{ns}	0.10^{ns}	21.37**	0.17^{ns}	1.5114 1.8523
GS	6.39*	-0.0300^{ns}	8.05**	6.05*	1.58^{ns}	5.6692 5.4602
IMI	-0.01^{ns}	2.6700^{ns}	2.61^{ns}	0.00^{ns}	0.02^{ns}	2.6477 2.5568
DI	2.12^{ns}	-0.0400^{ns}	9.50**	15.40**	1.71^{ns}	1.3580 1.1989
ICR	0.00^{ns}	0.7400^{ns}	0.00^{ns}	18.47**	0.01^{ns}	1.7130 1.8239
YP	4.14**	3.1400*	0.00^{ns}	23.00**	2.92^{o}	13.2480 24.8490

CM: complete model; GE: genotypic effect; G×L: effect of genotype × location interaction; G×M: effect of genotype × measurement interaction; G×L×M: effect of the triple interaction genotype × locations × measurement; Parc: experimental plot effect; ns: not significant based on the chi-square test with 1 degree of freedom; *significant at 5% based on the chi-square test with 1 degree of freedom; **significant at 1% based on the chi-square test with 1 degree of freedom; average of the agroforestry system with rubber trees (AFS) and monoculture (Mon) environments.

The multicollinearity analysis reduced the number of traits for constructing the selection indices from 13 to seven. The traits FS, PS, IC, DB, DI, GS, and YP were the ones that allowed the estimation of selection indices with weak collinearity, with a value of 6.2219 according to the classification of Montgomery and Peck (1981). By applying a selection intensity of 45.45% (selection of the top five genotypes), the ranking of the selection gain of the genotypic aggregate was determined for AFS, monoculture, and both environments simultaneously (Table 4). Genotypes A1, Catuaí 86, 5V, 308 and Catuaí 81 stood out in the joint analysis of the sites, while in the AFS environment the top five were A1, 308, 5V, Catuaí 81, and LB1. In the monoculture environment, the five best genotypes were A1, 5V, Catuaí 86, 8V, and 12V. Selection gains for genotypic aggregates were estimated at 25.75, 25, and 22.81% for joint analysis, AFS and monoculture, respectively (Table 4).

Table 4. Selection by the Mulamba-Rank index of the coffee trees selected for agroforestry systems (AFS), monoculture and both environments (general selection) based on characteristics: fruit ripening time (FT); uniformity of fruit maturation (UM); fruit size (FS); plant size (PS); vegetative vigor (VV); incidence of rust (IR); incidence of cercosporiosis (IC); drying out of plagiotropic branches (DB); general scale (GS); incidence of mining insects (IMI); degree of inclination (DI); incidence of citrus mealybug (ICR); and yield per plant (YP).

Order	General Selection			
	Genotype	Rank-Medium	Gain	Gain%
1	A1	3.5714	3.5714	68.0000
2	Catuai86	4.2857	3.9286	52.7273
3	5V	4.4286	4.0952	46.5116
4	308	5.5714	4.4643	34.4000
5	Catuai81	6.0000	4.7714	25.7485
6	LB1	6.1429	5.0000	20.0000
7	8V	6.2857	5.1837	15.7480
8	409	7.1429	5.4286	10.5263
9	13V	7.2857	5.6349	6.4789
10	RT	7.2857	5.8000	3.4483
11	12V	8	6.0000	0.0000
Order	**AFS selection**			
	Genotype	**Rank-Medium**	**Gain**	**Gain%**
1	A1	3.8571	3.8571	55.5556
2	308	4.7143	4.2857	40.0000
3	5V	4.8571	4.4762	34.0426
4	Catuai81	4.8571	4.5714	31.2500
5	LB1	5.7143	4.8000	25.0000
6	Catuai86	6.0000	5.0000	20.0000
7	409	6.2857	5.1837	15.748
8	13V	6.5714	5.3571	12.0000
9	8V	7.1429	5.5556	8.0000
10	RT	7.8571	5.7857	3.7037
11	12V	8.1429	6.0000	0.0000
Order	**Monoculture selection**			
	Genotype	**Rank-Medium**	**Gain**	**Gain%**
1	A1	4.0000	4.0000	50.0000
2	5V	4.2857	4.1429	44.8276
3	Catuai86	4.7143	4.3333	38.4615
4	8V	5.4286	4.6071	30.2326
5	LB1	6.0000	4.8857	22.8070
6	308	6.2857	5.1190	17.2093
7	RT	6.4286	5.3061	13.0769
8	12V	6.8571	5.5000	9.0909
9	13V	7.0000	5.6667	5.8824
10	409	7.4286	5.8429	2.6895
11	Catuai81	7.5714	6.0000	0.0000

DISCUSSION

Evaluating heritability plays a crucial role in identifying the characteristics evaluated with the greatest potential for gain in selection. This estimate is essential for defining the most appropriate selection strategies for the genetic improvement of

Conilon coffee trees (Alkimim et al. 2021). This same classification of low, moderate and high heritability can be applied to accuracy. The closer the accuracy value is to 1, the greater the reliability in estimating the genetic values of the genotypes under study, resulting in a reduction in the number of harvests needed to develop cultivars. The significant genetic effects detected by deviance analysis show that the process of selecting the best genotypes is viable. Significant genotypic effects have been reported for *C. canephora* in different studies, considering different populations of conilon coffee, as in the study by Ramalho et al. (2016), analyzing clones of conilon coffee of the botanical variety Conilon; by Alkimim et al. (2021), working with the varieties Conilon, Robusta and families from hybridization between them; and by Senra et al. (2022b), evaluating a seed population of the cultivar 'ES8152-Conquista', demonstrating the genetic variability of the population.

Although the IC trait has moderate heritability, it is feasible to achieve selection gains through indirect strategies. Research indicates a positive genetic correlation between resistance to rust (*H. vastatrix*) and cercospora (*C. coffeicola*), suggesting the possibility of obtaining simultaneous selection gains (Moreira et al. 2022). Coffee trees, both arabica and conilon, have mechanisms of resistance to cercospora that complicate their evaluation. Even a small lesion caused by cercospora can lead to leaf abscission (Waller 1982), making accurate assessment a challenging task. Identifying the correlation between rust and cercospora is not always obvious due to the nature of the pathogens, cercospora being a necrotrophic pathogen and rust a biotrophic pathogen (Eastburn et al. 2011).

Evaluating genotypic correlations between locations and crops is fundamental to understanding the development of genotypes in different experimental environments. These analyses provide information on genotype-environment interactions, adaptability and stability. The presence of interaction limits the development of high-yielding coffee cultivars with greater adaptability (Belete et al. 2014, Beksisa et al. 2018). Knowledge of interaction patterns can help to efficiently design appropriate breeding strategies, optimize selection for target production environments, and define suitable areas of recommendation domain in which a given cultivar may be best adapted (Yan and Kang 2003). Additionally, knowledge of interaction patterns helps breeders to reduce the costs of genotype evaluation by eliminating unnecessary spatial and temporal yield trials (Basford and Cooper 1998). In breeding programs, genotypes are commonly evaluated in different environments, according to the purpose of this study. When considering two or more environments, in addition to the genetic and environmental effects, the effect resulting from the interaction between them can be quantified.

The inherent complexities of agroforestry systems make the process of quantifying genotype-environment interactions more challenging. It is worth noting that, for most of the characteristics under study, the overall average in the AFS was higher than in the monoculture, except for IC, DB and ICR. The performance of conilon coffee in agroforestry systems and intercropping depends on a set of factors such as coffee genotypes, shade level, and tree density per hectare (Senra et al. 2024). A study carried out in the southwestern region of the Amazon demonstrated that reforestation of coffee plantations with Bandarra (*Schizolobium parahyba* var. amazonicum) reduced the productivity of conilon coffee, while reforestation with Brazil nut (*Bertholletia excelsa*) and teak (*Tectona grandis*) at a density of 222 trees per hectare did not affect coffee productivity (Bezerra et al. 2024).

Shading is a point of discussion in the literature and is considered by many to be one of the main aspects in the development of coffee plants in AFS (Senra et al. 2024). Research indicates that shading levels between 30 and 50% can increase coffee production (Venancio et al. 2019). Other studies have reported that a shading level of up to 10% was the maximum tolerated to achieve maximum fruit productivity per plant (Assis et al. 2019). The impact of shading on coffee productivity depends on the genotype under study (Assis et al. 2019), the location where the AFS is being evaluated, and the type of pollination (Prado et al. 2018). In Costa Rica, it was observed that shading positively affected the production and grain size of *C. arabica* (Vaast and Raghuramulu 2012).

The process of selecting the best genotypes for multiple locations is a routine but complex activity for breeders. It is essential to consider the environments for which the genotypes will be recommended, as well as the complexity of the traits being evaluated. The high correlation between the traits can generate collinearity problems, leading to overparameterization of the models and the possibility of overestimating or underestimating the selection gains. Therefore, the reduction from 13 to seven traits was a conservative and efficient strategy in the selection process, since the application of the Mulamba methodology was based on non-redundant traits with high-selective accuracy. It is worth noting that the Mulamba selection index is more efficient for the species *C. canephora* than the additive and multiplicative indices (Carias et al. 2016).

CONCLUSION

The correlation between the performance of the genotypes across environments and harvests shows the possibility of indirect selection gains for the traits under study. Although the deviance analysis did not reveal significance for the effects of permanent environments, genotypic effects and their interactions with environment and harvest were identified. Genotypes A1 and 5V showed stability by remaining in the ranking in both environments, revealing a remarkable ability to adapt regardless of the environment. On the other hand, the Catuaí 86, 308 and 8V genotypes showed significant gains in at least one of the environments evaluated, indicating the presence of a more complex interaction. Notably, the 'Catuaí 86' genotype ranked 2nd overall in both environments, but showed no significant gains in the AFS compared to the monoculture. Genotypes A1, 5V, 308 and LB1 stood out as potential and promising for cultivation in AFS.

CONFLICT OF INTEREST

Nothing to declare.

AUTHORS' CONTRIBUTION

Conceptualization: Senra, J. F. B., Comerio, M., Ferrão, M. A. G., Fonseca, A. F. A. and Tomaz, M. A.; **Methodology:** Comerio, M., Gomes, W. M., Ferrão, M. A. G., Verdin Filho, A. C., Volpi, P. S., Ferrão, R. G., Fonseca, A. F. A. and Tomaz, M. A.; **Investigation:** Comerio, M., Gomes, W. M., Ferrão, M. A. G., Verdin Filho, A. C. and Volpi, P. S.; **Writing – Original Draft:** Senra, J. F. B., Oliveira, R. G. and Silva, V. A. C.; **Writing – Review and Editing:** Senra, J. F. B., Oliveira, R. G. and Silva, V. A. C.; **Statistical Analysis:** Senra, J. F. B.; **Supervision** Senra, J. F. B.; **Final approval:** Senra, J. F. B.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available on request from the corresponding author.

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