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BIOLOGY

Enhancing genetic gains in conilon coffee through intra-population recurrent selection in Espírito Santo, Brazil

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ABSTRACT: Recurrent intrapopulation selection is a key approach for the plant breeding of *Coffea canephora*, enabling the development of progenies superior to their parents while preserving genetic variability. This study was conducted in Espírito Santo, a major Conilon coffee production hub in Brazil, across two environments with contrasting soil and climatic conditions. This study to evaluated the agronomic performance, selection gains, and genetic divergence of 56 hybrid progenies from a late-maturing population, along with six parental plants. Genetic parameter estimates confirmed the presence of genetic variability and selection potential among the genotypes. Using Mulamba and Mock and Additive selection indices, 16 promising progenies were identified for the development of new cultivars. The strategy proved effective in recommending high-yielding genotypes adapted to each environment, highlighting its importance for sustainable cultivation under diverse edaphoclimatic conditions.
Key words: *Coffea canephora*, plant breeding, hybrid progenies, cultivar, selection gains.

Potencialização dos ganhos genéticos no café conilon através da seleção recorrente no Espírito Santo, Brasil

RESUMO: A seleção intrapopulacional recorrente é uma abordagem fundamental para o melhoramento genético de *Coffea canephora*, permitindo o desenvolvimento de progênies superiores aos seus pais, preservando a variabilidade genética. Este estudo foi conduzido no Espírito Santo, um importante polo produtor de café Conilon no Brasil, em dois ambientes com condições edafoclimáticas contrastantes. O objetivo foi avaliar o desempenho agronômico, os ganhos de seleção e a divergência genética de 56 progênies híbridas de uma população de maturação tardia, juntamente com seis plantas parentais. As estimativas dos parâmetros genéticos confirmaram a presença de variabilidade genética e potencial de seleção entre os genótipos. Utilizando os índices de seleção Mulamba e Mock e Additive, 16 progênies promissoras foram identificadas para o desenvolvimento de novas cultivares. A estratégia se mostrou eficaz na recomendação de genótipos de alta produtividade adaptados a cada ambiente, destacando sua importância para o cultivo sustentável sob diversas condições edafoclimáticas.
Palavras chave: *Coffea canephora*, melhoramento genético, progênies híbridas, cultivar, ganhos de seleção.

INTRODUCTION

To tackle the challenges in improving *Coffea canephora*, it is crucial to develop commercial clones with a broad genetic base. The species' self-incompatibility, coupled with widespread clonal plantations, heightens the risk of pollination inefficiency and reduced yields. Breeding strategies should combine asexual and sexual reproduction to ensure genetic recombination, maintain variability, and enhance adaptability while sustaining high yields (FERRÃO et al., 2019).

Self-incompatibility and cross-pollination play a key role in preserving the genetic diversity of *C. canephora*. This diversity is vital for overcoming abiotic and biotic stressors and improving traits like yield, fruit quality, and nutrient absorption. Intra-population recurrent selection is particularly effective for outcrossing species, enabling cumulative genetic gains in both qualitative and quantitative traits by

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continuously selecting and recombining superior progeny over successive cycles (HULL, 1945; BERNARDO, 2020; CAMPUZANO-DUQUE & BLAIR, 2022).

Intrapopulation recurrent selection, paired with the use of clones from distinct genetic compatibility groups, effectively mitigates fertilization challenges and preserves genetic variability. These strategies stabilize production and foster long-term sustainability in commercial plantations (CAMPUZANO-DUQUE & BLAIR, 2022).

By integrating diverse germplasm and systematic breeding, the risks of inbreeding and productivity losses can be minimized, ensuring resilient coffee production across varying conditions. This study evaluated the agronomic performance and genetic variability of 62 *C. canephora* genotypes (56 hybrid progenies and 6 parent clones) from the first cycle of intra-population recurrent selection. These genotypes were assessed over three harvests in two contrasting edaphoclimatic environments in Espírito Santo, Brazil, to estimate genetic parameters and selection gains.

MATERIALS AND METHODS

The experiment was initially implemented in 1998 by planting 11 late-maturing *C. canephora* genotypes in isolated fields at the Marilândia Experimental Farm (MEF), Espírito Santo, Brazil (19°23'56" S, 40°32'07" W). The experiment was conducted in a randomized complete block design with 10 plants per clone and four blocks.

Flowering and recombination occurred in 2000 by open natural pollination in an isolated field. 100 grams of hybrid seeds (seeds from each plant within each parental plot) were harvested in 2001 to compose the half-sib progenies of cycle 01 (HS-P1) in an isolated field.

HS-P1 was established in 2002, totaling 1,120 plants. The plants were evaluated over eight growing seasons (2005 to 2013) for productivity, vegetative vigor, disease resistance, drought tolerance, and fruit ripening uniformity. A total of 280 plants with superior traits were selected within each HS-P1 to advance the selection cycle. Selection was made within the HS-P1 so as not to reduce the genetic base. Unselected progenies were eradicated. The 280 selected progenies were conducted with natural open pollination occurring in an isolated field. The result of the fruiting resulting from recombination generated a new population to compose the half-sib progenies of the second intra-population recurrent selection cycle (HS-P2).

Among the progenies of the HS-P1 population (280 progenies) selected for open pollination recombination in an isolated field to generate the new HS-P2 population, the most promising HS-P1 (56 progenies) were selected based on morphoagronomic characteristics for the clonal competition assay.

The 56 progenies were propagated vegetatively through cuttings in MEF. Once the seedlings developed four pairs of leaves, field experiments commenced. In addition to the 56 progenies, six parental genotypes were also propagated, resulting in a total of 62 genotypes. These six parental genotypes were chosen because they are commercial clones commonly used by farmers in the primary coffee Conilon producing regions.

The experiments with 62 genotypes were conducted in two edaphoclimatic environments contrastant: MEF and the Sooretama Experimental Farm (SEF) in Espírito Santo, Brazil. The MEF site is located at 19°23'56" S, 40°32'07" W, with an altitude of 223 meters and wavy relief. The soil type is typical red-yellow latosol dystrophic A moderate (LVAd1; FEITOZA et al., 2018), with average annual precipitation of 1,164 mm and an average annual temperature of 24.2°C. The SEF site is located at 19°07'11" S, 40°04'52" W, with an altitude of 60 meters and flat terrain. The soil type is yellow Argissolo distrocoeso typical A moderate (PAdx5; FEITOZA et al., 2018), with average annual precipitation of 1,249 mm and an average annual temperature of 25.8 °C <https://meteorologia.incaper.es.gov.br/>. The experiments were established in January 2017 (SEF) and September 2017 (MEF).

The progeny from the recurrent intra-population selection was evaluated for three harvests (2019, 2020, and 2021). Fourteen phenotypic traits were assessed in the field during the fruit granulation and maturation stages. These traits included morpho-agronomic characteristics (maturation time (MAT); uniformity of the maturation period (UNIF); bean size (GSIZ); percentage of floating fruits (Bo); plant architecture (PRT); degree of plant inclination (DI); vigor (VIGOR); general scale (GSCE), resistance to diseases and pests (incidence rosette cochineal (COCH); reaction to rust (RUST); Cercospora spot (CER); coffee leaf miner incidence (LMINER); tip/branch dryness (TD), and yield (YIELD) in the field. Measurements were performed as described by ADUNOLA et al. (2023).

The experimental design was randomized blocks with 62 genotypes (treatments), three blocks and five plants per plot. The field experiments were

implemented using a spacing of 3 meters between rows and 1 meter between plants, conducted with supplemental irrigation during periods of high water deficit, and management practices were adopted in accordance with current recommendations for conilon coffee cultivation in Espírito Santo (FERRÃO et al., 2019).

The traits were analyzed using mixed linear models with Restricted Maximum Likelihood (REML) and Best Linear Unbiased Prediction (BLUP) methods. The statistical model used was:

$y = \mu + Xf + Zg + Qgl + Tgm + Wgml + Sp + e$

where y is the vector of phenotypic value, μ is the overall mean, g is the vector of random effects of genotypes, gl is the vector of random effects of genotype × site interactions, gm is the vector of random effects of genotype × measurement interactions, gml is the vector of the triple interaction genotype × measurement × site effects (assumed to be random), p is the vector of the random effects of plot within site, and e is the vector of errors. Capital letters represent the incidence matrices for their respective effects (RESENDE, 2016). The environmental effects of block within site (b), measurement (m), site (l) and the interactions block within site × measurement, and site × measurement were considered as fixed effects in a single fixed effect vector (f) given by the combination block-measurement-site (RESENDE, 2016). Based on this model the genetic values of the clones (BLUP) and the variance components (individual REML) were estimated.

The superior genotypes and the selection gain were determined via a selection analysis using the average rank index adapted from Mulamba and Mock (MULAMBA & MOCK, 1978). In this index, the genotypic values are ranked for each trait, and the average of the rankings of each genotype for all traits is presented as the result. An additive index was provided, in which the selection direction and the relative economic importance or weights assigned to each evaluated trait were established.

The genetic diversity of the clones was analyzed based on genetic values by means of the statistical Mahalanobis distance matrix (MAHALANOBIS, 2008) followed by UPGMA hierarchical clustering and modified Tocher method (SATHURI et al., 2023). All statistical analyses described were performed by the computerized Statistical System for Genetic Selection (Selegen) (RESENDE, 2016). Flowchart with the general schematic description of the methodological strategy is described in figure 1.

RESULTS AND DISCUSSION

Estimation of variance components by REML and genetic values via BLUP

Among the genetic parameters important for plant selection, variance components are particularly noteworthy, especially genotypic variance (ROCHA et al., 2021). Higher magnitudes of genotypic variances (Vg) compared to the variances of genotype × measurement interactions (Vgm), genotype × site interactions (Vgl), and permanent plot effects (Vp) suggested a predominant influence of genotypes on the phenotypic expression of YIELD, GSIZ, and RUST traits. This is due to the distinct genetic expressions among different genetic materials (Table 1).

For the traits MAT, VIGOR, and DI, Vg was higher than Vgl and Vperm but lower than Vgm, indicating that year-to-year variability had a greater influence on the phenotypic expression of these traits. In contrast, the traits PRT, GSCE, and TD showed Vg greater than Vgm and Vperm but lower than Vgl, indicating that site-specific variations had a more significant impact on phenotypic expression. For the traits Bo, UNIF, CERC, LMINER, and COCH, environmental variances exceeded Vg, highlighting a strong influence of environmental factors on phenotypic expression (Table 1).

The selective accuracy parameter (Acgen), which measures the correlation between predicted and true genetic values, is crucial in genetic studies and is linked to trait heritability (AMBRÓSIO et al., 2020). Based on its magnitude, the accuracy values (Acgen) were low for Bo, UNIF, CERC, LMINER, and COCH; moderate for PRT, GSCE, DI, and TD; and high for YIELD, MAT, GSIZ, VIGOR, and RUST. This indicated favorable conditions for selection, given the significance of these traits in the selection process. Accuracy values above 0.7 suggested good selection potential with just three harvests; however, additional harvests are necessary to validate results for other traits (Table 1). Based on the results of the Deviance analysis, the significance of the genotypic, permanent and interaction effects is verified for each characteristic evaluated (Table 2).

CARIAS et al. (2016) evaluated the productivity of eight half-sib progenies from Incaper's breeding program, MEF, using experimental data from three harvests analyzed by the REML/BLUP methodology. They reported Acgen values of 0.6979 and average heritability of genotype (h^2mg) at 0.4870. Later, SENRA et al. (2020), working with 27

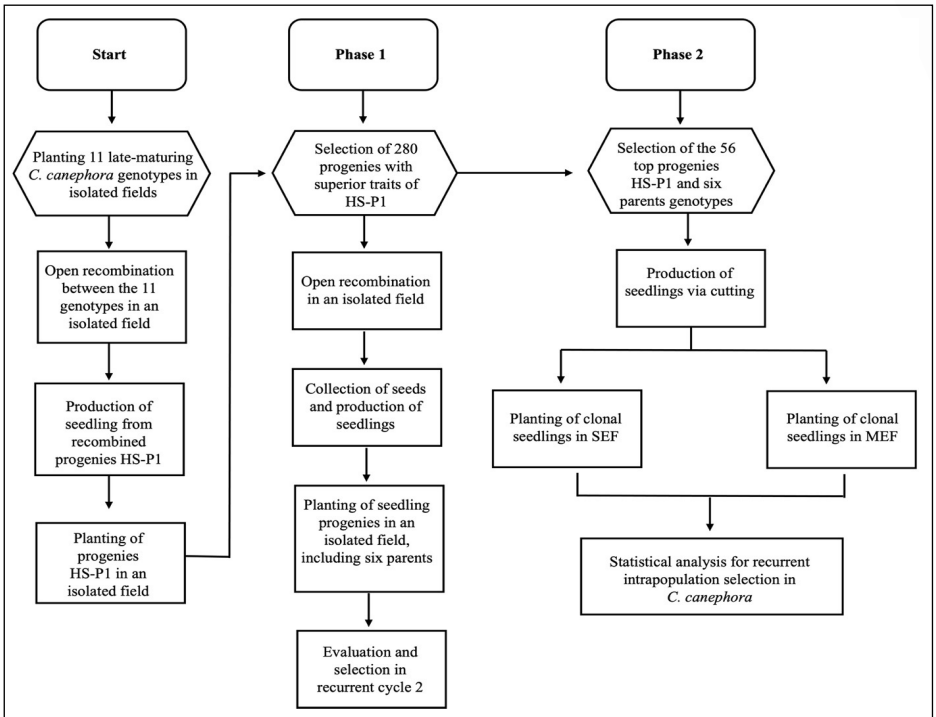

Figure 1 - Flowchart of the methodological approach.

clones from the same breeding program and applying the REML/BLUP mixed linear model methodology, estimated Acgen values of 0.768, 0.385, and 0.577 for productivity traits, defoliation, and percentage of dead plants, respectively, with corresponding h^2mg values of 0.589, 0.148, and 0.333.

CARVALHO et al. (2019) evaluated 20 full-sib progenies derived from crosses between genotypes of the Conilon and Robusta botanical groups across two harvests. They found Acgen values of 0.49 and 0.45, and h^2mg values assuming complete survival, respectively, for the productivity trait.

Genetic selection and estimation of selection gains

In the selection analysis using the average rank index, adapted from Mulamba and Mock, and the Additive index, the direction of selection and the relative economic importance or weights of the traits are established. The weight for each agronomic trait was initially defined based on its importance and the results of accuracy and heritability, as shown in table 3.

The list of genotypes ranked by selection index is provided in table 4. Selection gains ranged from 77.543 to 207.317 for the average rank index, adapted from Mulamba and Mock, and from 16.064 to 30.895 for the Additive index. A selection index threshold of 25% was applied, resulting in the selection of 16 progenies with superior performance and genetic variability.

The high selection gains observed may be attributed to the considerable genetic variability of the evaluated genotypes, which leads to a high selection differential and, consequently, high estimated gains. Although, the average rank index, adapted from Mulamba and Mock, showed higher magnitudes of selection gains, there were no significant differences in the genetic materials selected by either index. Notably, genotypes 39 and 31 were included in the average rank index but not in the Additive index, while genotypes 12 and 26 were included by both indices. Among the top-ranked genotypes, genotype 57 (clone 305 of the Centenary Cultivar ES8132, RNC 31001) ranked ninth according to the average rank index, adapted from Mulamba and Mock, and eleventh according to the Additive index.

The other selected genotypes are hybrid progenies, demonstrating the effectiveness of the intra-population recurrent selection process in generating superior genotypes in this study. Genotypes ranked higher than genotype 57 may be considered for final trials and future cultivar recommendations, as they appear to be superior to the clone already released in the cultivar.

Table 1 - Components of variance estimated by the REML method, obtained from the average evaluation of 62 genotypes of *C. canephora* in two environments and three harvests.

Components of variance	----------Traits----------													
	MAT	UNIF	GSIZ	Bo	PRT	DI	VIGOR	GSCE	RUST	CERC	LMINER	TD	COCH	YIELD
Vg	0.0260	0.0017	0.4715	0.9014	0.0327	0.0118	0.1554	0.1017	0.1489	0.0005	0.0001	0.0356	0.0002	50.5769
Vgm	0.0299	0.0012	0.0453	3.9001	0.0153	0.0301	0.2232	0.0456	0.0925	0.0028	0.0016	0.0063	0.0022	10.8904
Vgl	0.0010	0.0365	0.0719	29.1689	0.0427	0.0074	0.0423	0.1185	0.0067	0.0011	0.0046	0.0682	0.0006	10.7058
Vglm	0.0848	0.0119	0.0994	59.0780	0.0319	0.0148	0.1524	0.1922	0.1781	0.0454	0.0106	0.2875	0.0367	98.6951
Vperm	0.0026	0.0079	0.1882	1.0610	0.0104	0.0073	0.0581	0.0865	0.1575	0.0092	0.0058	0.0145	0.0052	12.5070
Ve	0.1403	0.2226	0.6791	47.9652	0.2015	0.1010	1.1808	0.7396	1.2987	0.3807	0.3402	0.4893	0.2008	126.3160
Vf	0.1997	0.2699	1.4560	82.9966	0.3026	0.1576	1.6598	1.0918	1.7042	0.3942	0.3523	0.6138	0.2090	210.9962
h2g	0.1301	0.0063	0.3238	0.0109	0.1080	0.0749	0.0937	0.0932	0.0874	0.0012	0.0004	0.0579	0.0011	0.2397
h2mg	0.4995	0.0687	0.8482	0.0332	0.4887	0.4018	0.5351	0.4627	0.6376	0.0340	0.0169	0.2845	0.0247	0.6495
Acgen	0.7068	0.2621	0.9210	0.1823	0.6991	0.6339	0.7315	0.6802	0.7985	0.1844	0.1299	0.5333	0.1570	0.8059
General Mean	3.8587	2.0033	5.1465	14.4712	1.8696	1.3459	6.3315	5.9574	3.5972	1.9852	2.8522	2.2751	1.5478	42.0661
Marilândia Mean	4.2443	1.5604	4.5422	6.1955	1.9095	1.2616	6.1192	5.4901	2.9391	1.1864	2.9453	1.2527	2.0956	29.7607
Sooretama Mean	3.4731	2.4462	5.7509	22.7469	1.8297	1.4301	6.5439	6.4247	4.2554	2.7841	2.7590	3.2975	1.0000	54.3716

Vg: genotypic variance; Vgm: variance of the interaction genotype × measurement; Vgl: variance of the interaction genotype × site; Vglm: variance of the interaction genotype × site × measurement; Vperm: variance of the permanent effects of the plot; Ve: residual variance; Vf: individual phenotypic variance; h2g = h2: heritability of individual plots in the broad sense. that is. of the total genotypic effects; h2mg: heritability in the broad sense of the average of the genotypes; Acgen: accuracy of genotype selection.

In breeding programs utilizing the intra-population recurrent selection strategy, the sample of progenies drawn from the population under selection should represent its genetic variability. Small samples risk losing favorable alleles or fixing undesirable alleles, while very large samples may be impractical due to high experimental costs (MISTRO et al., 2019).

The high genetic gains achieved using the Mulamba and Mock index are consistent with the findings of (CARIAS et al., 2016), who conducted similar work within Incaper's plant breeding program for Conilon coffee.

Genetic divergence analysis

Genotype grouping was conducted using the modified Tocher method, with the genetic dissimilarity measured by a distance matrix obtained through the Mahalanobis method. This analysis utilized a set of 14 morphoagronomic traits and resulted in the formation of 11 distinct groups (Table 5). The findings indicate that the intra-population recurrent selection strategy effectively increased genetic variability and aided in selecting genotypes with superior agronomic traits.

Group I contained 48 genotypes, Group III had three genotypes, and Groups II and IV each had two genotypes. Groups V to XI consisted of only one genotype each, including two parents (clones 153 and 76/2). The parents were distributed across different groups, with genitors 57, 60, 61, and 62 in Group I, genitor 58 in Group VII, and genitor 59 in Group IX (Table 5). It is worth noting that the 56 progenies originate from 11 parents, but only six parents that are widely commercialized are being evaluated in this study. This method often forms groups with only one genotype when dealing with those that exhibit greater dissimilarity since grouping is influenced by the distance between already-grouped genotypes (SATHURI et al., 2023).

Similar studies by IVOGLO et al. (2008) and CARIAS et al. (2016) on *C. canephora*, Conilon variety, identified 13 and 4 different groups of genetic dissimilarity, respectively. FONSECA et al. (2006) grouped 32 Conilon coffee clones from three

Table 2 - Deviance analysis and coefficients of determination for the index of 14 characteristics evaluated in *C. canephora* genotypes in two environments and three harvests.

Traits	--------Deviance--------			----------LTR---------			-----Variance----- component			---Coefficient of--- determination			----------P-value----------			Model
	GE	PEE	IE	GE	PEE	IE	GE	PEE	IE	GE	PEE	IE	GE	PEE	IE	
MAT	-787.030	-789.420	-767.810	2.390	0.000	21.610	0.009	0.000	0.020	0.069	0.004	0.155	1.2E-01	1.0E+00	3.3E-06	-789.42
UNIF	-268.280	-264.400	-263.350	4.350	8.230	9.280	0.026	0.034	0.032	0.097	0.129	0.121	3.7E-02	4.1E-03	2.3E-03	-272.63
GSIZ	760.500	816.960	737.650	29.730	86.190	6.880	0.589	0.428	0.143	0.367	0.267	0.089	5.0E-08	0.0E+00	8.7E-03	730.77
Bo	4372.710	4371.310	4421.880	1.400	0.000	50.570	10.159	0.583	39.167	0.064	0.004	0.248	2.4E-01	1.0E+00	1.1E-12	4371.31
PRT	-153.180	-154.200	-108.540	1.040	0.020	45.680	0.018	0.002	0.080	0.055	0.007	0.249	3.1E-01	8.9E-01	1.4E-11	-154.22
VIGOR	1006.040	1001.440	1003.620	5.240	0.640	2.820	0.118	0.058	0.081	0.083	0.041	0.057	2.2E-02	4.2E-01	9.3E-02	1000.8
GSCE	534.730	532.800	573.500	2.050	0.120	40.820	0.068	0.012	0.207	0.080	0.014	0.245	1.5E-01	7.3E-01	1.7E-10	532.68
RUST	970.580	970.130	968.800	1.910	1.460	0.130	0.047	0.084	0.019	0.036	0.064	0.015	1.7E-01	2.3E-01	7.2E-01	968.67
CERC	276.940	276.960	278.410	0.000	0.020	1.470	0.001	0.004	0.015	0.002	0.009	0.029	1.0E+00	8.9E-01	2.3E-01	276.94
LMINER	182.770	182.830	184.420	0.000	0.060	1.650	0.001	0.006	0.015	0.002	0.014	0.034	1.0E+00	8.1E-01	2.0E-01	182.77
TD	630.120	629.530	654.850	0.580	-0.010	25.310	0.029	0.004	0.154	0.033	0.004	0.175	4.5E-01	1.0E+00	4.9E-07	629.54
COCH	-302.750	-319.150	-319.170	16.420	0.020	0.000	0.022	0.002	0.000	0.094	0.008	0.001	5.1E-05	8.9E-01	1.0E+00	-319.17
YIELD	4716.970	4698.270	4702.660	18.680	-0.020	4.370	46.224	0.924	13.514	0.192	0.004	0.056	1.5E-05	1.0E+00	3.7E-02	4698.29

GE: Genotypic Effect; PEE: Permanent Effect; IE: Interaction Effect.

improved clonal varieties into three distinct groups, with the first group subdivided into 10 subgroups, using the same method. More recently, (FERRÃO et al., 2021) analyzed the genetic diversity of 600 *C. canephora* accessions from Incaper's active germplasm bank using 38 traits. Their grouping with the modified Tocher method revealed the formation of 30 groups, with the highly dissimilar clone 76/2 among them. SENRA et al. (2020) and FERRÃO et al. (2021) also observed significant genetic variability among accessions in the Active Germplasm Bank of *C. canephora* at Incaper, based on traits related to plant architecture, fruit production, and ripeness.

Table 3 - Economic weight and direction of selection for selection analysis via average rank index, adapted from Mulamba and Mock and Additive index.

Traits	Rank	Economic weight
YIELD	Higher	35
GSCE	Higher	15
GSIZ	Higher	10
VIGOR	Higher	10
DI	Minor	10
RUST	Minor	10
PRT	Minor	5
TD	Minor	5
Bo	Null	0
CERC	Null	0
COCH	Null	0
LMINER	Null	0
MAT	Null	0
UNIF	Null	0

Among the selected materials (Table 4), 14 progenies were selected in Group I using both indexes, with one selected progeny in Group III and one in Group VII. Group I is particularly noteworthy because it includes progenies from seven different parents. Specifically, genotypes 6 and 27 are progeny of clone 139; genotypes 17 and 52 are progeny of clone 153; genotype 12 is progeny of clone 25+8; genotype 31 is progeny of clone 76/1; genotypes 38, 42, 48, and 26 are progeny of clone 76/2; genotype 49 is progeny of clone 79; and genotypes 13, 7, 8, and 40 are progeny of clone 80.

Some selected progenies share the same female parent. Given the genetic self-incompatibility of the species, this should be carefully considered. When determining which progenies to group for

Table 4 - Ranking of the 25% best genotypes using selection indexes via average rank, adapted from Mulamba and Mock and Additive index, with estimates of genetic gains in percentage (GS) through the joint evaluation of variables via REML/BLUP and genealogy of the genotypes.

----------Mulamba e Mock----------				----------Additive----------			
Order	Genotypes	Genealogy	GS	Order	Genotypes	Genealogy	GS
1	7	Progeny of clone 80	207.317	1	7	Progeny of clone 80	30.895
2	52	Progeny of clone 153	205.455	2	52	Progeny of clone 153	27.756
3	6	Progeny of clone 139	191.892	3	6	Progeny of clone 139	26.033
4	48	Progeny of clone 76/2	179.224	4	48	Progeny of clone 76/2	25.028
5	40	Progeny of clone 80	171.552	5	13	Progeny of clone 80	23.723
6	42	Progeny of clone 76/2	153.266	6	40	Progeny of clone 80	22.823
7	13	Progeny of clone 80	136.461	7	42	Progeny of clone 76/2	21.985
8	17	Progeny of clone 153	124.000	8	27	Progeny of clone 139	21.248
9	57	Clone 76/1	115.180	9	8	Progeny of clone 80	20.466
10	27	Progeny of clone 139	107.921	10	37	Progeny of clone 106	19.723
11	38	Progeny of clone 76/2	102.336	11	57	Clone 76/1	19.104
12	37	Progeny of clone 106	97.776	12	38	Progeny of clone 76/2	18.514
13	8	Progeny of clone 80	93.732	13	17	Progeny of clone 153	17.949
14	39	Progeny of clone 79	88.562	14	12	Progeny of clone 25+8	17.315
15	31	Progeny of clone 76/1	82.697	15	26	Progeny of clone 76/2	16.662
16	49	Progeny of clone 79	77.543	16	49	Progeny of clone 79	16.064

developing a new clonal hybrid cultivar, it is essential to select genetically diverse and compatible materials to ensure effective pollination, fruit set, and adequate production (FERRÃO et al., 2019).

Furthermore, to enhance genetic compatibility, improve pollination efficiency, and broaden the genetic base, it is recommended to include new genotypes with genetic divergence in the ongoing improvement process through a intra-population recurrent selection strategy.

Table 5 - Groupings among 62 genotypes of *C. canephora*, obtained by the modified Tocher method, based on the matrix of Genetic Mahalanobis Distances, considering 14 morphoagronomic traits[1].

Group	Genotypes
I	1, 2, 4, 5, 6, 7, 8, 9, 12, 13, 14, 17, 18, 19, 20, 21, 22, 23, 25, 26, 27, 28, 30, 31, 32, 33, 34, 35, 36, 38, 40, 42, 43, 44, 46, 47, 48, 49, 50, 51, 52, 53, 55, 56, 57, 60, 61, 62
II	16, 24
III	10, 39, 45
IV	15, 41
V	11
VI	3
VII	37
VIII	58
IX	59
X	29
XI	54

[1]MAT, UNIF, GSIZ, Bo, PRT, DI, VIGOR, GSCE, RUST, CERC, LMINER, TD, COCH and YIELD.

CONCLUSION

The study confirmed that there is significant genetic variability among Conilon coffee genotypes (*C. canephora*), which makes them suitable for selection using a intra-population recurrent selection strategy. This genetic diversity is crucial for developing improved coffee cultivars in the future.

The research identified 15 hybrid progenies and one parent with outstanding agronomic traits. These selected genotypes provide valuable opportunities for developing heterotic hybrids and enhanced populations. These can be used in coffee breeding programs to boost yield, enhance disease resistance, and improve other important traits.

The intra-population recurrent selection strategy was effective in choosing superior genotypes while preserving genetic diversity. This approach resulted in high selection gains due to the significant genetic variability found among the evaluated genotypes, reinforcing its value for ongoing breeding efforts in *C. canephora*.

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DECLARATION OF CONFLICT OF INTEREST

The authors declare no conflict of interest.

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.

REFERENCES

ADUNOLA, P. et al. Genomic selection for genotype performance and environmental stability in *Coffea canephora*. **G3: Genes, Genomes, Genetics**, v.13, 2023. Available from: <https://doi:10.1093/g3journal/jkad062>. Accessed: Aug. 21, 2024. doi: 10.1093/g3journal/jkad062.

AMBRÓSIO, M. et al. Genotypic superiority of Psidium Guajava S1 families using mixed modeling for truncated and simultaneous selection. **Scientia Agricola**, v.78, 2020. Available from: <https://doi:10.1590/1678-992x-2019-0179>. Accessed: Mar. 17, 2024. doi: 10.1590/1678-992x-2019-0179.

BERNARDO, R. **Reinventing quantitative genetics for plant breeding: something old, something new, something borrowed, something BLUEHeredity** Springer Nature, 2020. Available from: <https://doi.org/10.1038/s41437-020-0312-1>. Accessed: Jun. 10, 2022. doi: 10.1038/s41437-020-0312-1.

CAMPUZANO-DUQUE, L. F.; BLAIR, M. W. **Strategies for Robusta Coffee (*Coffea canephora*) Improvement as a New Crop in Colombia Agriculture (Switzerland) MDPI**, 2022. Available from: <https://doi.org/10.3390/agriculture12101576>. Accessed: Aug. 18, 2024. doi: 10.3390/agriculture12101576.

CARIAS, C. M. et al. Predição de ganhos genéticos via modelos mistos em progênies de café conilon. **Coffee Science**, v.11, p.39-45, 2016. Available from: <http://www.sbicafe.ufv.br:80/handle/123456789/8171>. Accessed: Feb. 02, 2024.

CARVALHO, H. F. et al. Selection and genetic parameters for interpopulation hybrids between kouilou and robusta coffee. **Bragantia**, v.78, p.52-59, 2019. Available from: <https://doi.org/10.1590/1678-4499.2018124>. Accessed: Feb. 07, 2024. doi: 10.1590/1678-4499.2018124.

FEITOZA, L. et al. **Atualização da legenda do mapa de reconhecimento de solos do Estado do Espírito Santo e implementação de interface no Geobases para uso de dados em SIG**. Artigo em periódico indexado, 2018. Available from: <http://biblioteca.incaper.es.gov.br/digital/handle/123456789/4257>. Accessed: Jun. 15, 2022.

FERRÃO, L. F. V. et al. Accurate genomic prediction of *Coffea canephora* in multiple environments using whole-genome statistical models. **Heredity**, v.122, p.261-275, 2019. Available from: <https://doi.org/10.1038/s41437-018-0105-y>. Accessed: Aug. 15, 2024. doi: 10.1038/s41437-018-0105-y.

FERRÃO, M. A. G. et al. Characterization and genetic diversity of *Coffea canephora* accessions in a germplasm bank in Espírito Santo, Brazil. **Crop Breeding and Applied Biotechnology**, v.21, p.36132123, 2021. Available from:<https://doi.org/10.1590/1984-70332021v21n2a32>. Accessed: Sept. 18, 2024. doi: 10.1590/1984.

HULL, F. H. Recurrent selection for specific combining ability in corn. **Agronomy Journal**, v.37, p.134-145, 1945. Available from: <https://doi.org/10.2134/agronj1945.00021962003700020006x>. Accessed: Jun. 10, 2022. doi: 10.2134/agronj1945.00021962003700020006x.

IVOGLO, M. G. et al. Divergência genética em café robusta. **Bragantia**, v.67, p.823-831, 2008. Available from: <https://doi.org/10.1590/S0006-87052008000400003>. Accessed: Jun. 05, 2024. doi: 10.1590/S0006-87052008000400003.

MAHALANOBIS, P. C. On The Generalized Distance in Statistics. **The Indian Journal of Statistics, Series A**, v.80, p.1-7, 2008. Available from: <https://www.jstor.org/stable/48723335>. Accessed: Jun. 12, 2023.

MISTRO, JC et al. Effective population size and genetic gain expected in a population of *Coffea canephora*. **Crop Breeding and Applied Biotechnology**, v.19, p.1-7, 2019. Available from: <https://doi.org/10.1590/1984-70332019v19n1a01>. Accessed: Jul. 17, 2024. doi: 10.1590/1984.

MULAMBA, N. N.; MOCK. J. J. Improvement of yield potential of the ETO blanco maize (*Zea mays* L.) population by breeding for plant traits [Mexico]. **Egyptian Journal of genetics and Cytology**, 1978. Available from: <https://www.cabidigitallibrary.org/doi/full/10.5555/19791677302>. Accessed: Jun. 12, 2022.

RESENDE, M. D. V. Software Selegen-REML/BLUP: a useful tool for plant breeding. **Crop Breeding and Applied Biotechnology**, v.16, p.330-339, 2016. doi: 10.1590/1984. Available from:<https://doi.org/10.1590/1984-70332016v16n4a49>. Accessed: Jun. 10, 2022. doi: 10.1590/1984-70332016v16n4a49.

ROCHA, R. B. et al. *Coffea canephora* breeding: Estimated and achieved gains from selection in the western amazon, Brazil. **Ciencia Rural**, v.51, 2021. Available from: <https://doi.org/10.1590/0103-8478cr20200713>. Accessed: Sept. 18, 2024. doi: 10.1590/0103-8478cr20200713.

SATHURI, P. et al. Genetic grouping of selected RILs for yield and attributing traits in determinate type of Indian bean. **Electronic Journal of Plant Breeding**, v.14, p.1206-1214, 2023. Available from: <https://doi.org/10.37992/2023.1403.146>. Accessed: Sept. 19, 2024. doi: 10.37992/2023.1403.146.

SENRA, J. F. B. et al. Genetic Variability of Access of the Active Germplasm Bank of *Coffea canephora* of Incaper in Southern Espírito Santo. **J Genet**, v.6, p.172-184, 2020. Available from: <http://biblioteca.incaper.es.gov.br/digital/handle/123456789/4231>. Accessed: Oct. 19, 2024.