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PLANT BREEDING

Selection of differentiated maturity genotypes of *Coffea canephora*

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ABSTRACT. The aim of this study was to select *Coffea canephora* genotypes from the seminal propagation variety 'ES8152' with different harvest times. The experiment was conducted using a Federer augmented block design with three repetitions, evaluating 175 genotypes and four clonal witnesses in two harvests (2022 and 2023), and 20 morphoagronomic characteristics were evaluated. The data were analyzed using the REML/BLUP methodology with the Selegen software, where the variance components and genetic values were estimated. The selection was performed using the Mulamba-Rank index. The bottom sieve (BS) and top sieve (TS) characteristics had high heritability (0.5779 and 0.6694, respectively) and accuracy (0.7602 and 0.8182, respectively). TS also showed high repeatability (0.6827). The genotypic effects were significant at 1% level for days for fruit ripening, fruit size, vegetative vigor, yield per plant, TS, and BS; at 5% level for general scale; and at 10% level for incidence of rust, degree of inclination, and percentage of fruit float. It was possible to distinguish 20 superior genotypes in terms of maturation, among which the selection gains for the genotypic clusters were 46.14, 45.92 and 41.56% for indefinite, early, and late maturation, respectively, by applying a selection intensity of 11.43%. Genotypes 25, 26, 73, 93, and 100 could be used for early maturing varieties, whereas genotypes 155 and 189 could be used for late-maturing varieties. The most promising genotypes for composing a variety, regardless of the maturation period, were 20, 39, 90, 112, and 190, as these were among the five best genotypes ranked in the three selection processes, demonstrating that they added superior desired morphoagronomic characteristics. It is concluded that there is genetic variability among the 175 genotypes evaluated, as well as significant genetic effects to be explored in the pool gene of individuals originating from the 'ES8152' variety.

Keywords: conilon coffee tree; mixed models; mulamba-rank; 'ES8152'.

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Introduction

Coffee tree cultivation is one of the primary activities in global agribusiness and is a commodity for export and import in many countries. Although the genus *Coffea* includes 130 known species (Davis & Rakotonasolo, 2021), the coffee market is centered on two species: *Coffea arabica* (Arabica coffee) and *Coffea canephora* (Conilon/Robusta coffee). Brazil is the world's largest producer of Arabica and Robusta coffee, and in the first eight months of 2023, it had already exported 22.9 million bags (60 kg each) to over 143 countries, with the United States, Germany, Italy, Belgium, and Japan being the main importers (Companhia Nacional de Abastecimento [CONAB], 2023).

The conilon coffee tree is an allogamous and diploid species with gametophytic self-incompatibility (Tran et al., 2017; Moraes et al., 2018). Allogamy and cross-pollination due to incompatibility ensure that seminal varieties arising from the species create new genotypic combinations for each generation. Consequently, each seed-production field has become a crucial selection unit for genetic breeding programs. The main cultivar of seminal propagation is 'ES8152', also known as 'Conquista' developed by the *Instituto Capixaba de Pesquisa Assistência Técnica e Extensão Rural* (Incaper) (Senra et al., 2022). It is a cultivar formed by recombining 56 agronomically genotypes superior for productivity, beverage quality, and tolerance to biotic and abiotic stressors (Senra et al., 2022).

The production of seedlings from the seeds of production fields results in the formation of populations with individuals that differ from others in terms of architecture, shape, and size of grains and leaves, maturation pattern, and susceptibility to biotic and abiotic stresses (Dubberstein et al., 2020). Identifying and exploring the genetic variability of seminal propagation materials is essential for maintaining the sustainability of the genetic breeding of conilon coffee trees (Silva et al., 2022). Evaluation of the potential of seminal materials has been reported by Carvalho et al. (2019), Akpertey et al. (2022), and Moura et al. (2022).

The aim of this study was to select superior genotypes of conilon coffee trees regarding production, tolerance to pests and diseases, vegetative vigor, uniformity of maturation, and post-harvest yield and with different harvest times from a group of genotypes originating from the variety propagated from 'ES8152' seeds.

Material and methods

The experiment was conducted at the Bananal do Norte Experimental Farm (FEBN), belonging to the South Center for Research, Development, and Innovation (CPDI Sul) INCAPER in Pacotuba, district of the municipality of Cachoeiro de Itapemirim, Espírito Santo State, Brazil, at latitude 20º45' S, longitude 41º17' W, and altitude of 140 meters. The soil is classified as dystrophic red-yellow Latosol, Cwa climate with rainy summer and dry winter according to Köpen’s classification, mean annual precipitation of 1,200 mm, mean annual temperature of 23°C, and undulating topography.

Federer’s augmented block (Federer, 1956) was used with three repetitions, 175 regular treatments (genotypes), and four common treatments (clonal witnesses). The regular treatments constitute the gene pool from the seminal propagation cultivar of ‘ES8152’, popularly known as ‘Conquista’. The witnesses were the commercial clones described in Table 1.

Table 1. Clonal witnesses used in the experiment, their commercial identifications, and the cultivar of origin.

Witnesses	Commercial Identification	Cultivar of origin
Witness 1 (T1)	V8	Clone 8 of ‘ES8142’
Witness 2 (T2)	LB1	Clone 1 of ‘ES8122’
Witness 3 (T3)	A1	Clone 8 of ‘ES8112’
Witness 4 (T4)	V12	Clone 12 of ‘ES8142’

Planting was conducted in 2019 with a spacing of three meters between rows and one meter between plants (3 × 1 m) at a density of 3,333 plants ha^{-1}. Planting, formation, and production fertilization followed the Fertilization and Liming Manual for the State of Espírito Santo (Prezotti et al., 2007). Cultural and phytosanitary management was conducted according to the requirements of the crop, following the recommendations for the conilon coffee tree (Ferrão et al., 2019). During the 2022 and 2023 harvests, 20 morphoagronomic characteristics were evaluated.

Days for fruit ripening (DR): Evaluated the days for harvest of production, using the average coffee tree flowering time as the reference point, with September 15 of the previous year as the starting day.

Fruit size (FS): The phenotypic evaluation of fruit size in the field was estimated using a rating scale ranging from 1 to 5, which were very small, small, medium, large, and very large, respectively, following the descriptors provided by the National Cultivar Protection Service (Guerreiro Filho et al., 2008).

Vegetative vigor (VV): Phenotypic evaluation of vegetative vigor was performed using a rating scale ranging from 1 to 10 regarding the level of acceptance of the genotype required for Conilon coffee tree cultivation according to vegetative vigor, with ratings of 1, very weak; 3, weak; 5, intermediate; 7, vigorous; and 10, excellent vigor.

Incidence of rust (IR): Caused by the fungus *Hemileia vastatrix* Berk. and Br, and evaluated with a rating scale ranging from 1 to 9 with ratings of 1, asymptomatic plants; 3, presence of a few sporulations; 5, sporulation at the beginning of defoliation; 7, severe sporulation and defoliation; and 9, high levels of sporulation and defoliation, leading to plant depletion.

Incidence of cercosporiosis (IC): Caused by the fungus *Cercospora coffeicola* Berk. & Cooke and evaluated using a phenotypic rating scale ranging from 1 to 9 with ratings of 1, asymptomatic plants; 3, presence of few lesions on the leaves; 5, lesions on leaves and fruits; and 9, high levels of lesions on leaves and fruits, leading to plant depletion.

Drying out of plagiotropic branches (DB): Joint phenotypic evaluation of a series of biotic and abiotic factors that result in the loss of leaves at the ends of plagiotropic branches, and evaluated on a rating scale from 1 to 9 with ratings of 1, plants without visible symptoms; 3, plants with few dry branches; 5, moderate level of dry branches; 7, high level of dry branches indicating depletion of the plant; and 9, very severe symptoms indicating possible death of the plant

General scale (GS): Phenotypic evaluation on a rating scale from 1 to 10 regarding the level of acceptance of the genotype required for coffee cultivation with scores of 1, genotypes with a very poor phenotype; 3, poor; 5, intermediate level of acceptance; 7, good phenotypic evaluation; and 10, excellent phenotype.

Incidence of mining insects (IMI): Phenotypic evaluation on a rating scale from 1 to 9 regarding the severity of the attack by the *Leucoptera coffeella* insect with ratings of 1, absence of attacked leaves; 3, leaves with the presence of necrotic mines; 5, many leaves attacked with defoliation on the plant; and 9, defoliates causing depletion of the plant.

Degree of inclination (DI): Evaluated using a rating scale where: rating 1, genetic materials with an upright growth habit with 1 to 35% inclination of orthotropic branches; 2, genotypes semi-erect growth habit with 36 to 50% inclination of orthotropic branches; and 3, genotypes with a prostrate growth habit with 51 to 100% inclination of orthotropic branches.

Incidence of citrus mealybug (ICR): Phenotypic evaluation of the severity of damage and the presence of citrus mealybug (*Planococcus citri*; *P. minor*) on a rating scale from 1 to 5, where 1, 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 insects associated with fruit fall and the presence of sooty mold; and 5, severe infestation with fruit falling, loss of drink quality, and high levels of sooty mold.

Yield per plant (YP): Coffee fruit production per plant, estimated in kilograms (kg).

Percentage of fruit float (PF): Assessment of the percentage of floating ripe fruits in a sample of 100 ripe fruits (%).

Mass of 100 fruits (MF): Estimate of the mass of 100 ripe fruits at the time of harvest (g).

Uniformity of maturation: Estimate of the uniformity of maturation of harvested fruits classified as mature fruits (M), green fruits (G), and dry fruits (D), estimated as a percentage (%).

Yield of field fruits: The yield of field fruits for coconut fruits (FC) and the ratio of field fruits for pounding grains (FP) were estimated. Coconut coffee and pounded coffee at 12% moisture and yields expressed as a percentages (%).

Top sieve (TS): Percentage of pounding grains with 12% moisture separated on a classification sieve with a mesh equal to or greater than 14, expressed as a percentage (%).

Bottom sieve (BS): Percentage of pounding grains with 12% moisture separated on a classification sieve with mesh less than 14, expressed as a percentage (%).

Data analysis was performed using the restricted maximum likelihood method and best unbiased linear prediction (REML/BLUP) using the Selegen software (Resende, 2007), model 70.

$$y = X_m + Z_g + W_b + T_p + e$$

where: y is the data vector, m is the vector of effects assumed to be fixed (year), *g* is the vector of genotypic effects (assumed to be random), *b* is the vector of the environmental effects of blocks (assumed to be random), *p* is the vector of permanent environmental effects (assumed to be random), and *e* is the vector of residuals (random). Capital letters represent the incidence matrices for these effects.

The variance components genotypic variance (σ_g^2); environmental variance between blocks (σ_b^2); permanent environmental variance (σ_p^2); residual variance (σ_e^2); phenotypic variance (σ_{phen}^2); individual broad-sense heritability (h^2); coefficient of repeatability (ρ); coefficient of environmental determination between blocks (b^2); coefficient of determination of permanent environment (p^2); overall average (μ); and average selective accuracy ($\overline{r_{\hat{g}g}}$) were estimated based on this model.

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

$$LRT = -2(LogL - LogL_R)$$

where: LogL is the logarithm of the maximum (L) restricted likelihood function of the full model, and LogLR is the logarithm of the maximum (LR) restricted likelihood function of the reduced model (without evaluating the effect). The LRT was analyzed using the chi-square test with a degree of freedom at 1, 5 and 10 % of significance.

Selection was performed using the Mulamba-Rank index (Resende, 2007), with selection being carried out based on the earliest genotypes (lowest DR value), late genotypes (highest DR value), and without specifying the time spent for fruit maturation. The selection of genotypes independent of the maturation period was based on the superiority of their morphoagronomic characteristics; therefore, they could be used to compose varieties in the future without specifying the harvest time. Based on the results of this index, gains from selection were estimated by considering the predicted genotypic values of the selected genotypes.

Results and discussion

The estimated genetic parameters showed remarkable values for heritability, selective accuracy, and repeatability coefficients in the selection process (Table 2). Heritability is classified as low if it presents values below 0.15, moderate for values between 0.15 and 0.50, and high if it is above 0.5 (Resende & Alves, 2020). Although these parameters are based on restricted heritability and the present study estimated broad-sense heritability, the comparison can be made without significant loss of information, as the goal, in this case, was to highlight the evaluated characteristics with the highest potential for selection gain. Estimating heritability is essential for defining the best selection strategies for the genetic breeding of conilon coffee trees (Alkimim et al., 2021). BS and TS exhibited high heritability (0.5779 and 0.6694, respectively); MF, DI, YP, PF, VV, GS, DR, FS, and IR had moderate heritability (0.2165-0.3823); and the other characteristics had low heritability (0.0123-0.1424).

Table 2. Estimates of variance components genetic and environmental parameters for the following traits: days for fruit ripening (DR), fruit size (FS), 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), yield per plant (YP), percentage of fruit float (PF), mass of 100 fruits (MF), percentage of mature fruits (M), percentage of green fruits (G), percentage of dry fruits (D), ratio field fruits for coconut (FC), ratio fruits for pounding (FP), top sieve (TS), and bottom sieve (BS).

Component	DR	FS	VV	IR	IC	DB	GS	IMI	DI	ICR
σ_g^2	152.9559	0.1402	0.3198	1.0022	0.0237	0.2364	0.2193	0.0188	0.1225	0.0096
σ_b^2	0.6171	0.0038	0.0203	0.0001	0.0000	0.0000	0.0061	0.0007	0.0384	0.0295
σ_p^2	4.1515	0.0035	0.0078	0.0324	0.0112	0.0270	0.0175	0.0184	0.0063	0.0104
σ_e^2	277.4794	0.2226	0.6285	1.5871	0.8951	1.3963	0.4056	0.5909	0.3345	0.5432
σ_{phen}^2	435.2039	0.3701	0.9764	2.6217	0.9300	1.6596	0.6485	0.6289	0.5017	0.5927
h^2	0.3515	0.3787	0.3276	0.3823	0.0255	0.1424	0.3381	0.0300	0.2442	0.0162
ρ	0.3624	0.3985	0.3563	0.3946	0.0375	0.1587	0.3745	0.0603	0.3333	0.0836
b^2	0.0014	0.0103	0.0207	0.0000	0.0000	0.0000	0.0093	0.0011	0.0766	0.0498
p^2	0.0095	0.0095	0.0080	0.0123	0.0120	0.0162	0.0270	0.0293	0.0126	0.0176
μ	271.4264	3.0013	5.6122	3.2852	3.6842	3.4749	5.3251	3.6759	1.6893	2.3580
$\overline{r_{\hat{g}g}}$	0.5928	0.6154	0.5723	0.6183	0.1596	0.3774	0.5815	0.1731	0.4941	0.1273

Component	YP	PF	MF	M	G	D	FC	FP	TS	BS
σ_g^2	2.4355	20.2001	79.5241	46.2035	16.1409	5.4777	0.0001	0.0003	392.6614	412.5857
σ_b^2	0.2115	0.0029	5.2120	4.9116	4.7912	0.0392	0.0000	0.0000	2.8891	6.8583
σ_p^2	0.3187	0.8315	5.5687	7.6648	5.7577	2.8272	0.0000	0.0000	4.9436	6.2715
σ_e^2	5.4229	46.8546	276.9955	408.1276	343.7699	273.3651	0.0047	0.0028	186.1004	288.1778
σ_{phen}^2	8.3886	67.8890	367.3004	466.9074	370.4597	281.7092	0.0048	0.0032	586.5945	713.8933
h^2	0.2903	0.2975	0.2165	0.0990	0.0436	0.0194	0.0123	0.1037	0.6694	0.5779
ρ	0.3535	0.3098	0.2459	0.1259	0.0720	0.0296	0.0193	0.1169	0.6827	0.5963
b^2	0.0252	0.0000	0.0142	0.0105	0.0129	0.0001	0.0000	0.0000	0.0049	0.0096
p^2	0.0380	0.0122	0.0152	0.0164	0.0155	0.0100	0.0069	0.0132	0.0084	0.0088
μ	4.7872	5.9720	98.4091	64.4108	24.7216	12.8952	0.4447	0.2443	54.6165	46.2115
$\overline{r_{\hat{g}g}}$	0.5388	0.5455	0.4653	0.3146	0.2087	0.1394	0.1111	0.3220	0.8182	0.7602

σ_g^2: genotypic variance; σ_b^2: environmental variance between blocks; σ_p^2: permanent environmental variance; σ_e^2: residual variance; σ_{phen}^2: phenotypic variance; h^2: individual broad-sense heritability; ρ: coefficient of repeatability; b^2: coefficient of environmental determination between blocks; p^2: coefficient of determination of permanent environment; μ: overall average; $\overline{r_{\hat{g}g}}$: average selective accuracy.

Selective accuracy is the correlation between the true genotypic value and the genotypic value estimated from experimental data. Its value is classified as low if it is between 0.1 and 0.4, moderate between 0.4 and 0.7, and high between 0.7 and 0.9 (Resende & Alves, 2020). Classification of characteristics into low, moderate, and high heritability can also be applied to accuracy. Repeatability was classified as low if it had values below 0.3, moderate between 0.3 and 0.6, and high above 0.6 (Resende & Alves, 2020). Among the evaluated characteristics, only TS exhibited high repeatability (0.6827). DI, YP, VV, DR, GS, IR, FS, and BS had moderate repeatability (0.3333–0.5963), whereas the others showed low repeatability, ranging from 0.0193 to 0.3098. In an evaluation of 85 robusta coffee genotypes in the Cerrado, a repeatability coefficient of 0.29 was estimated with three harvests (Santin et al., 2019).

In an evaluation of eight half-sibling families from the recurrent selection program of Incaper, heritability values of 0.4557, 0.4870, 0.2238, and 0.4901 were estimated for FS, YP (in bags ha-1), VV, and DI, respectively (Carias et al., 2016), which were higher than those obtained in this study, except for the VV characteristics. When assessing the genetic parameters of populations of *Coffea canephora,* including conilon, robusta, and hybrids, Alkimim et al. (2021) estimated heritability values for VV, IR, IC, precocity (with a rating scale of 1 to 3 for early, medium and late respectively), FS and YP (liters per plant), lower than those obtained in this study. For IC, the populations evaluated by Alkimim et al. (2021) had higher heritability values, and a higher heritability value for VV was estimated for the hybrid population. The genotypes under evaluation in this study represent a gene pool arising from the variety ‘ES8152’, which has 56 distinct parentals (Senra et al., 2022). Among these, parents are genitors of the conilon, robusta, and hybrid groups, resulting from the identification of superior genotypes in the state of Espírito Santo, the germplasm bank, and Incaper recurrent selection fields. Therefore, the estimated genetic values did not differ from those highlighted by Carias et al. (2016) and Alkimim et al. (2021), who also applied the REML/BLUP methodology.

Although IC showed low heritability, it is possible to obtain selection gains for this trait through indirect selection. Studies have indicated a positive genetic correlation between resistance to rust (*H. vastatrix*) and *Cercospora* (*C. coffeicola*), demonstrating the possibility of simultaneous selection gain (Moreira et al., 2022). Arabica and conilon coffee trees developed cercospora resistance mechanisms that make their evaluation challenging. A small cercospora lesion is sufficient to cause leaf abscission (Waller, 1982), making an accurate assessment challenging. The correlation between rust and cercospora has not always been identified because of the nature of the pathogen, as cercospora is a necrotrophic pathogen, and rust is a biotrophic pathogen (Eastburn et al., 2011). Analyzing the uniformity of coffee tree maturation in terms of the percentages of ripe, green, and dry beans enables a more efficient selection of genotypes with a higher percentage of mature beans. Few studies have quantitatively evaluated these characteristics, particularly when applying the REML/BLUP methodology. Synchronized maturation, with a high percentage of mature grains, is desirable in breeding programs. Efficient coffee cultivation requires varieties with high maturation uniformity to accelerate harvesting, improve bean quality, and improve workforce organization on the properties (Campuzano-Duque & Blair, 2022).

A study on a group of conilon coffee tree genotypes resulting from diallel crosses with 10 parents from Incaper's breeding program estimated high heritability values (above 50%) for traits related to production, post-harvest yield, grain size, pest and disease resistance, general assessment scale, and maturation uniformity (Ferrão et al., 2024). The authors used a complete block design, BLUP/REML methodology, genome-wide association analyses (GWAS), and a greater number of harvests. Comparing these results with those of the present study, it is evident that the gene pool of the ‘ES8152’ variety, from which 20 superior genotypes was selected from the 175 evaluated, is promising for this stage of the breeding program. With these 20 superior genotypes, it will be possible to apply a complete block design and evaluate a greater number of locations, making it possible to establish a variety with higher cultivation and use value than the witnesses used. We selected 20 genotypes for each maturation period, with a moderate intensity appropriate for that phase of the breeding program, which represented a selection intensity of 11.43%. From these 20 clones, it is possible to develop varieties with at least nine superior clones in each future variety.

The likelihood ratio test (LRT) analysis did not identify significant effects of the permanent environment, and the blocks were only significant for the characteristics DI and ICR at 1% (Table 3). Genotypic effects were significant at 1% for the characteristics DR, FS, VV, YP, TS, and B; 5% for GS; and 10% for IR, DI, and PF, demonstrating the genetic variability among the 175 genotypes evaluated. Significant genetic effects were identified by LRT analysis of production parameters and resistance to pests and diseases in clones of the Conilon, Robusta, and hybrid groups (Alkimim et al., 2021). Significant genetic effects and variability have been identified in other studies (Ramalho et al., 2016; Mistro et al., 2019).

It was possible to distinguish 20 superior genotypes of early, late, and indefinite maturation by applying a selection intensity of 11.43% (Table 4). In an analysis comparing additive, multiplicative, and Mulamba-Rank selection indices for conilon coffee tree genotypes, greater efficiency of Mulamba-Rank index was observed (Carias et al., 2016). Criteria for increased production, grain size, vegetative vigor, general scale, percentage of ripe fruits, lower scores in the evaluation of pests and diseases, percentage of floating grains, and degree of plant inclination were adopted. The selection of genotypes with a lower degree of inclination makes it possible to establish cultivars with a growth habit that is better suited to produce specialty coffees and adapt to mechanical harvesting. None of the witnesses was selected for different maturation times. Thus, considering all characteristics simultaneously, the 20 selected genotypes within the 'ES8152' variety were superior.

Table 3. Deviance and likelihood ratio test (LRT) for the following traits: days for fruit ripening (DR), fruit size (FS), 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), yield per plant (YP), percentage of fruit float (PF), mass of 100 fruits (MF), percentage of mature fruits (M), percentage of green fruits (G), percentage of dry fruits (D), ratio field fruits for coconut (FC), ratio fruits for pounding (FP), top sieve (TS), and bottom sieve (BS).

	Deviance				LRT		
Trait	CM	GE	BE	PEE	GE	BE	PEE
DR	2599.26	2608.24	2599.27	2599.25	8.98^{**}	0.01^{ns}	-0.01^{ns}
FS	-23.64	-14.62	-23.03	-23.63	9.02^{**}	0.61^{ns}	0.01^{ns}
VV	340.12	351.83	342.13	340.12	11.71^{**}	2.01^{ns}	0^{ns}
IR	702.33	705.99	702.33	702.33	3.66^{*}	0^{ns}	0^{ns}
IC	353.11	353.32	353.11	353.09	0.21^{ns}	0^{ns}	-0.02^{ns}
DB	562.42	563.55	562.42	562.41	1.13^{ns}	0^{ns}	-0.01^{ns}
GS	188.29	194.48	188.86	188.34	6.19^{*}	0.57^{ns}	0.05^{ns}
IMI	207.88	208.02	207.9	207.94	0.14	0.02^{ns}	0.06^{ns}
DI	83.11	85.84	94.52	83.11	2.73^{*}	11.41^{**}	0^{ns}
ICR	168.9	169	176.99	169.01	0.1^{ns}	8.09^{**}	0.11^{ns}
YP	1130.08	1141.07	1132.46	1130.24	10.99^{**}	2.38^{ns}	0.16^{ns}
PF	1689.51	1692.41	1689.51	1689.51	2.9^{*}	0^{ns}	0^{ns}
MF	2303.94	2306.21	2304.95	2303.95	2.27^{ns}	1.01^{ns}	0.01^{ns}
M	2385.36	2386.28	2386.03	2385.36	0.92^{ns}	0.67^{ns}	0^{ns}
G	2240.46	2240.83	2241.46	2240.39	0.37^{ns}	1^{ns}	-0.07^{ns}
D	2041.74	2041.85	2041.74	2041.77	0.11^{ns}	0^{ns}	0.03^{ns}
FC	-1433.11	-1433.06	-1433.11	-1433.09	0.05^{ns}	0^{ns}	0.02^{ns}
FP	-1565.83	-1564.61	-1565.83	-1565.83	1.22^{ns}	0^{ns}	0^{ns}
TS	2336.99	2348.87	2337.1	2336.98	11.88^{**}	0.11^{ns}	-0.01^{ns}
BS	2451.44	2461.78	2451.85	2451.44	10.34^{**}	0.41^{ns}	0^{ns}

CM, complete model; GE, genotypic effect; BE, block effect; PEE, permanent environmental effect. ^{ns}, * and **: not significant, significant at 5%, and significant at 1%, respectively, based on the chi-square test with one degree of freedom.

Table 4. Classification of the 20 genotypes (Gen) selected based on the Mulamba-Rank index (MR) considering indefinite maturation period, early maturation and late maturation considering the characteristics: days for fruit ripening (DR), fruit size (FS), 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), yield per plant (YP), percentage of fruit float (PF), mass of 100 fruits (MF), percentage of mature fruits (M), percentage of green fruits (G), percentage of dry fruits (D), ratio field fruits for coconut (FC), ratio fruits for pounding (FP), top sieve (TS), and bottom sieve (BS).

Order	Maturation period								
	Indefinite			Early			Late		
	Gen	MR	Gain (%)	Gen	MR	Gain (%)	Gen	MR	Gain (%)
1	39	49.00	83.67	39	47.00	91.49	112	48.75	84.62
2	112	49.58	82.59	20	49.30	86.92	39	55.10	73.33
3	20	51.68	79.68	90	50.75	83.61	190	56.60	68.28
4	90	52.47	77.57	190	52.50	80.41	90	57.30	65.33
5	190	52.68	76.18	112	54.50	77.13	20	57.40	63.55
6	89	58.53	72.00	89	57.75	73.19	16	57.95	62.11
7	16	59.95	68.50	85	61.15	68.92	198	62.20	59.37
8	85	63.47	64.62	62	61.25	65.82	89	62.35	57.33
9	62	63.74	61.64	157	63.80	62.65	206	62.45	55.74
10	198	64.05	59.25	16	64.90	59.89	131	62.90	54.37
11	206	64.26	57.29	156	65.05	57.66	189	66.25	52.48
12	157	65.42	55.43	4	65.25	55.80	85	67.70	50.64
13	4	65.89	53.80	240	65.90	54.13	93	68.40	48.98
14	131	65.89	52.43	25	67.05	52.51	155	68.80	47.52
15	156	66.11	51.22	26	67.20	51.12	4	68.90	46.25
16	240	66.63	50.10	93	67.65	49.84	209	69.15	45.13
17	93	66.95	49.08	100	67.65	48.74	62	69.35	44.13
18	209	67.79	48.07	194	67.90	47.74	156	69.65	43.21
19	194	68.37	47.10	73	68.50	46.77	240	70.00	42.36
20	98	69.26	46.14	198	68.50	45.92	157	70.35	41.56

The selection gains for the genotypic clusters were 46.14, 45.92, and 41.56% for indefinite, early, and late maturation, respectively (Table 4). A selection gain of 43.8% was obtained for coffee trees from the Robusta group during the first harvest in the state of Rondônia (Ramalho et al., 2016). In the Distrito Federal, selection gains of 40% were obtained in the evaluation of three harvests, assessing coffee trees with different ripening and under irrigation (Santin et al., 2019). Alkimim et al. (2021) obtained selection gains of approximately 55, 32, and 17% for conilon, robusta, and hybrid group genotypes, respectively.

Applying the selection index for sorting the early and late genotypes did not differentiate between the three groups. This can be attributed to the small difference in amplitude between the earliest and latest accesses. Genotype 98 was the only one selected for individuals with an indefinite maturation period, genotypes 25, 26, 73, 93, and 100 for early maturation, and genotypes 155 and 189 for late maturation. However, the most promising genotypes for composing a variety, regardless of the maturation period, were 20, 39, 90, 112, and 190, as these were the five best genotypes ranked in the three selection processes, demonstrating that they were superior in terms of the morphoagronomic characteristics under evaluation.

Conclusion

The gene pool of individuals originating from the 'ES8152' variety contains notable genetic variability, which needs to be explored. From this group of individuals, it will be possible to obtain gains in production selection, uniformity of maturation, postharvest yield, tolerance to pests and diseases, and improved plant architecture for cultural treatments. Genotypes 25, 26, 73, 93, and 100 could be used in the formation of early maturing varieties, whereas genotypes 155 and 189 could be used in late-maturing varieties. Genotypes 20, 39, 90, 112, and 190 can be used to create varieties with indefinite maturation and controlled crossing. These have great prominence, as they were the five best genotypes ranked in the three selection processes, demonstrating that they add superior desired morphoagronomic characteristics. Based on genetic parameters, it will be possible to design experimental units in multiple environments using orthogonal designs to improve precision and define a minimum of 10 genotypes with early, intermediate, and late maturation to compose new varieties for the state of Espírito Santo.

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