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ARTICLE

Clonal selection in S_0 and S_1 peach trees evaluated in a subtropical environment

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Abstract: *The aims of this study were to estimate genetic parameters, predict genotypic values, and analyze the genotypic divergence in S_0 and S_1 peach trees evaluated in a subtropical environment by the mixed model methodology. For this, twenty-two clones were evaluated for plant and fruit traits. Genotypic variance among clones was significant. The individual broad-sense heritabilities ranged from 0.11 to 0.84, and the individual repeatability coefficients ranged from 0.15 to 0.89. The genotypic coefficients of variation were higher than 10% for most of the traits. Clustering based on plant and fruit traits led to the formation of two and five mutually exclusive groups, respectively. Multivariate analysis of principal components indicated that some traits could be excluded from genetic evaluation. Considering the yield trait and the selection of five clones, predicted gain from selection was 70%, which shows the possibility of considerable genetic progress from clonal selection in peach trees.*

Keywords: *Prunus persica, fruit tree breeding, mixed model methodology, multivariate analysis, genetic selection.*

INTRODUCTION

The peach tree is an autogamous plant, originally adapted to temperate and subtropical zones, which needs a determined accumulation of winter cold to break the period of dormancy and have normal flowering and budding (Silva et al. 2020a). The main peach producing regions are situated between latitudes 30º and 45º, north and south. Low temperatures in the winter and late freezes in the spring are the main limiting factors for peach production in temperate zones. In contrast, the cold necessary for vegetative and flower buds, when insufficient, limits production in subtropical zones (Scorza and Sherman 1996).

The viability of peach growing in regions with mild winters is a result of the use of cultivars with low chill requirements (Santana et al. 2020). Therefore, the breeding of peach for those regions is aimed mainly at the development of cultivars with a chill requirement compatible with the climate of those locations (Corrêa et al. 2019, Silva et al. 2020b).

The breeding method commonly used in the peach crop is hybridization, with the purpose of obtaining segregating populations from which superior individuals combining traits of interest are selected (Radović et al. 2020). The main target traits in peach tree breeding for regions with mild winter are low

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need for cold to break dormancy, early maturity, fruit quality, and resistance to major diseases (Silva et al. 2014). In terms of vegetative propagation, individuals of the first generation can be selected and released as cultivars. Advancement to the S_1 generation is normally carried out for crosses in which the aim is to improve quantitative traits, such as fruit size and resistance to diseases, or the manifestation of recessive traits (Raseira and Nakasu 2002).

In breeding of perennial plants, it is relevant to predict additive genetic values for selection of parents and the total genotypic values for selection of individuals aiming at vegetative propagation (Resende 2002). If selection in clonal tests is based on an inadequate analytical procedure, it may be inefficient due to confusion among the genotypic and environmental effects (Atroch et al. 2004). According to Resende (2016), the optimal procedure for practicing selection involves estimation of variance components by the restricted maximum likelihood (REML) method (Patterson and Thompson 1971) and prediction of genotypic values by the best linear unbiased prediction (BLUP) method (Henderson 1975), also generically called the mixed model methodology.

The main advantages of using mixed model methodology are the fact that they allow incorporating kinship information; comparing individuals or varieties over time and space; correcting environmental effects, variance components estimate, and genetic values prediction simultaneously; and dealing with complex data structures. Moreover, the mixed model methodology may be applied to unbalanced data and not orthogonal designs (Alves et al. 2019). Thus, the aims of this study were to estimate genetic parameters, predict genotypic values, and analyze genotypic divergence in S_0 and S_1 peach trees evaluated in a subtropical environment by the mixed model methodology.

MATERIAL AND METHODS

Genetic material, experimental design, and traits assessed

The experiment was set up in July 2008 in a completely randomized design with 22 S_0 and S_1 peach tree clones with from one to five replications per clone at a spacing of 7.0 m between rows and 3.5 m between plants in the municipality of Viçosa (lat 20º 45' 45" S, long 42º 49' 27" W, alt 647m asl), MG, Brazil. Plants were obtained by full rift cleft grafting on Okinawa cultivar rootstock. The local climate is classified as Cwa, wet mesothermal, with rainy summers and dry winters. The plants were trained in an open-center manner, and from 3 to 5 shoots were used to form the canopy. Management practices followed the technical recommendations for the crop in subtropical regions (see Raseira et al. 2014). In periods of water deficit (especially from July to September), localized irrigation was performed.

The following traits were evaluated in the plants: percentage of bud break in mixed shoots (PBBMS), total nodes per mixed shoot (TNMS), trunk perimeter (TP), mean perimeter of new shoots (MPNS), and yield (YD). For evaluation of the PBBMS and TNMS traits, 12 shoots from the middle third of the canopy of each plant were used, four from each quadrant. The PBBMS trait was evaluated through the ratio of percentage of vegetative buds sprouted/total vegetative buds (sprouted + unsprouted). The TP trait (trunk circumference at 10 centimeters from soil level) and MPNS (mean value of the circumferences of new shoots at 10 centimeters from connection of the branches to the trunk) were evaluated using a metric tape measure, and the results were expressed in centimeters (cm). The YD trait was evaluated through counting the number of peaches per plant before beginning the harvest period.

For evaluation of the fruit traits, 15 units were collected per plant (except for six trees that did not produce a sufficient number of peaches, and, in those cases, from 3 to 14 units were collected). Two collections of fruit were made per week from the time the fruit began to ripen (1 November 2012) to the end of ripening (11 December 2012). The fruit was collected when it was at the point of harvest, with maximum development and characteristic coloring at the base of the epidermis (see Cantillano and Sachs 1984).

The following traits were evaluated in the fruit: time of harvest (TH), fruit weight (FW), mean fruit diameter (MFD); fruit length (FL), fruit pulp firmness (FPF), total soluble solids content (TSS), total titratable acidity (TTA), TSS/TTA ratio, covering of epidermis with red pigment (CERP), CIE color coordinates (L*a*b*C*h°) of the epidermis (CCE), prominence of the fruit apex (PFA), and prominence of the fruit suture region (PFSR).

The TH trait was evaluated by the number of days from the harvest date of each genotype in relation to the harvest date of the earliest genotype. The MFD trait was evaluated through the mean of the suture length (maximum

distance in the middle region from the suture line to the opposite extreme) and equatorial length (middle region perpendicular to the suture line). The FL trait was evaluated by measuring the distance between the peduncle and the fruit apex. Length measurements were obtained with a digital caliper and the results were expressed in millimeters (mm). The FPF trait was evaluated through resistance to penetration of an 8 mm rod into the pulp on one cheek of the peach, after removal of the epidermis, through a digital penetrometer, with results expressed in Newtons (N). The TSS trait was evaluated in each peach through a juice aliquot, obtained by manual compression of a piece of pulp, in a digital refractometer. The TTA trait was evaluated by titrimetry (AOAC 1990), and the results were expressed in grams of malic acid/100 g of fresh weight. The CERP trait was evaluated visually through the percentage of covering of the epidermis with tones of red pigmentation, with scores ranging from 0 to 100. The CCE traits (L*a*b*C*h°) were evaluated using a colorimeter; measurement was made on the fruit surface with the greatest pigmentation of the covering (red surface for fruit with red pigmentation; yellow or greenish yellow pigmentation for fruit without red pigment on the epidermis). The PFA and PFSR traits were evaluated by a scoring scale (1 = small, 2 = medium, and 3 = large).

Statistical analyses

The mixed model methodology was adopted to estimate the genetic parameters and to predict the genotypic values, in accordance with Resende (2016). The mixed linear model used for analysis of the plant traits (with one observation per individual) was determined by the following equation:

$$y = Xu + Zg + e,$$

where y is the phenotypic data vector, u is the scalar referring to the effect of the overall mean (fixed effect), g is the vector of the total genotypic effects (assumed as random) [$g \sim N(0, \sigma^2_g)$, where σ^2_g is the genotypic variance], and e is the residual vector (random) [$e \sim N(0, \sigma^2_e)$, where σ^2_e is the residual variance]. X and Z represent the incidence matrices for the u and g effects, respectively.

Individual phenotypic variance (σ^2_p), individual broad-sense heritability (h^2_g), accuracy of genotype selection (assuming absence of plot loss) ($r_{\hat{g}g}$), genotypic coefficient of variation (CV_g(%)), residual coefficient of variation (CV_e(%)), and relative coefficient of variation (CV_r) were estimated, respectively, by the following equations (Resende et al. 2014):

$$\sigma^2_p = \sigma^2_g + \sigma^2_e$$

$$h^2_p = \sigma^2_g / \sigma^2_p$$

$$r_{\hat{g}g} = \sqrt{h^2_g}$$

$$CV_g(\%) = (\sqrt{\sigma^2_g}/\mu) * 100$$

$$CV_e(\%) = (\sqrt{\sigma^2_e}/\mu) * 100 \text{ and}$$

$$CV_r = CV_g(\%)/CV_e(\%)$$

where μ is the overall mean.

The mixed linear model used for analysis of the fruit traits (with various observations per individual) was determined by the following equation:

$$y = Xu + Zg + Wi + Tp + e,$$

where y is the phenotypic data vector, u is the scalar referring to the effect of the overall mean (fixed effect), g is the vector of the total genotypic effects (assumed as random) [$g \sim N(0, \sigma^2_g)$, where σ^2_g is the genotypic variance], i is the vector of the effects of the genotype x measurement interaction (random) [$i \sim N(0, \sigma^2_i)$, where σ^2_i is the variance of the genotype x measurement interaction], p is the vector of the permanent effects of environment (random) [$p \sim N(0, \sigma^2_p)$, where σ^2_p is the variance of the permanent environment], and e is the residual vector (random) [$e \sim N(0, \sigma^2_e)$, where σ^2_e is the residual variance]. X, Z, W, and T represent the incidence matrices for the u, g, i, and p effects, respectively.

Individual phenotypic variance (σ^2_p), individual broad-sense heritability (h^2_g), coefficient of determination of the genotype x measurement effects (c^2_i), coefficient of determination of the permanent environment effects (c^2_{pe}), individual

repeatability coefficient (p), and genotypic correlation through measurements ($r_{g\,med}$), were estimated, respectively, by the following equations(Resende et al. 2014):

$$\sigma^2_p = \sigma^2_g + \sigma^2_i + \sigma^2_{pe} + \sigma^2_e$$

$$h^2_g = \sigma^2_g / \sigma^2_p$$

$$c^2_i = \sigma^2_i / \sigma^2_p$$

$$c^2_{pe} = \sigma^2_{pe} / \sigma^2_p$$

$$p = (\sigma^2_g + \sigma^2_p) / \sigma^2_p$$

$$r_{g\,med} = \sigma^2_g / (\sigma^2_g + \sigma^2_i)$$

Genotypic divergence among clones was calculated based on the mean genotypic Euclidean distances of the predicted genotypic values, and clustering was performed by the Tocher method (Rao 1952). The genotypic correlations (Pearson correlation) and the multivariate analysis of principal components were estimated/made using the predict genotypic values. All statistical analyses were performed using the Selegen-REML/BLUP software (Resende 2016).

RESULTS AND DISCUSSION

The estimates of the variance components and of the genetic and non-genetic parameters for the plant traits are shown in Table 1. Based on the standard deviations of the individual broad-sense heritabilities, there was genotypic variability among clones for all the plant traits. The PBBMS and YD traits had coefficients of genotypic variation and coefficients of relative variation higher than those of the other traits. The PBBMS, TNMS, and YD traits had relative coefficients of variation higher than one, indicating a scenario favorable to selection. The TP and MPNS traits had residual coefficients of variation higher than the genotypic coefficients of variation, a fact that indicates greater difficulty in identification of superior genotypes.

According to Resende (2015), the PBBMS, TNMS, and YD traits have individual broad-sense heritabilities of high magnitudes ($h^2_g \geq 0.50$), whereas the TP and MPNS traits have individual broad-sense heritabilities of moderate magnitudes ($0.15 < h^2_g < 0.50$). According to Resende and Duarte (2007), the PBBMS, TNMS, and YD traits have high accuracies ($0.70 < r_{\hat{g}g} < 0.89$), whereas the YD and MPNS traits have moderate accuracies ($0.50 < r_{\hat{g}g} < 0.69$).

Clustering by the Tocher method for the plant traits resulted in the formation of two mutually exclusive groups, and only one clone (C4) was in group II. The C4 clone had a genotypic value for PBBMS near the overall mean and relatively high genotypic values for TNMS (22.68), TP (52.64 cm), MPNS (28.55 cm), and YD (261.07 peaches plant^{-1}). Considering

Table 1. Estimates of variance components and of genetic and non-genetic parameters for the plant traits: percentage of bud break in mixed shoots (PBBMS), total nodes per mixed shoot (TNMS), trunk perimeter (TP); mean perimeter of new shoots (MPNS), and yield (YD) evaluated in S_0 and S_1 peach trees

Component/parameter	**PBBMS** (%)	**TNMS**	**TP** (cm)	**MPNS** (cm)	**YD**
σ^2_g	82.76	6.84	15.48	7.55	5444.54
σ^2_e	52.13	5.56	37.60	13.21	2135.03
σ^2_p	134.89	12.40	53.08	20.76	7579.56
h^2_g	0.61±0.27	0.55±0.26	0.29±0.19	0.36±0.21	0.72±0.30
$r_{\hat{g}g}$	0.78	0.74	0.54	0.60	0.85
CV_g(%)	23.80	13.71	8.39	11.06	54.94
CV_e(%)	18.89	12.36	13.08	14.64	34.40
CV_r	1.26	1.11	0.64	0.76	1.60
μ	38.22	19.08	46.89	24.83	134.30

σ^2_g: genotypic variance, σ^2_e: residual variance, σ^2_p: individual phenotypic variance, h^2_g: individual broad-sense heritability (total genotypic effects), $r_{\hat{g}g}$: accuracy of genotype selection (assuming absence of plot loss), CV_g(%): genotypic coefficient of variation, CV_e(%): residual coefficient of variation, CV_r: relative coefficient of variation and μ: overall mean.

the YD trait and selection of the five best clones (C4, C21, C12, C15, and C5), predicted gain from selection was 70.68%, and that shows the possibility of considerable genetic progress from clonal selection.

The estimation of genotypic correlation coefficients is a key requirement for progress in plant breeding, since the genetic correlations may cause correlated responses to genetic selection (Resende 2015). The TP and MPNS traits, and TNMS and YD traits had strong positive correlation (0.79 and 0.73, respectively) (0.70 to 0.90); the TP and YD traits, PBBMS and MPNS traits, and MPNS and YD traits had weak positive correlation (0.41, 0.31 and 0.30, respectively) (0.30 to 0.50); the PBBMS and TP traits, and TNMS and TP traits had negligible positive correlation (0.22 and 0.01, respectively) (0.00 to 0.30); the PBBMS and YD traits, and TNMS and MPNS traits had negligible negative correlation (-0.07 and -0.10, respectively) (0.00 to -0.30); and the PBBMS and TNMS traits had weak negative correlation (-0.39) (-0.30 to -0.50).

The estimates of the variance components and of the genetic and non-genetic parameters for the fruit traits are shown in Table 2. Based on the standard deviations of the individual broad-sense heritabilities, there was genotypic variability among clones for all the fruit traits. The TH, TTA, TSS/TTA, CERP, and CCE (L*a*b*C*hº) traits had higher genotypic variance than environmental variance. These results indicate a scenario favorable to genetic selection. In contrast, the FW, MFD, FL, FPF, TSS, PFA, and PFSR traits had relative coefficients of variation less than one, which indicates greater difficulty in identification of superior genotypes.

According to Resende (2015), the TH, TTA, TSS/TTA, L*, b*, C*, and hº traits had individual broad-sense heritabilities of high magnitudes ($h_g^2 \geq 0.50$); the FW, DF, FL, TSS, CERP, a*, and PFA traits had individual broad-sense heritabilities of moderate magnitudes ($0.15 < h_g^2 < 0.50$); and the FPF and PFSR traits had individual broad-sense heritabilities of low magnitudes ($h_g^2 \leq 0.15$).

The coefficients of determination of the effects of the genotype *x* measurement interaction and of the effects of the permanent environment ranged from 0.002 (TTA) to 0.064 (TH) and from 0.02 (TSS/TTA) to 0.21 (CERP), respectively.

Table 2. Estimates of variance components and of genetic and non-genetic parameters for the fruit traits: time of harvest (TH), fruit weight (FW), mean fruit diameter (MFD); fruit length (FL), fruit pulp firmness (FPF), total soluble solids content (TSS), total titratable acidity (TTA), TSS/TTA ratio, covering of the epidermis with red pigment (CERP), CIE color coordinates (L*a*b*C*h°) of the epidermis (CCE), prominence of the fruit apex (PFA), and prominence of the fruit suture region (PFSR) evaluated in S_0 and S_1 peach trees

Component/ parameter	TH	FW	MFD	FL	FPF	TSS	TTA	TSS/TTA	CERP	CCE					PFA	PFSR
										L*	a*	b*	C*	h°		
σ_g^2	82.01	213.34	11.58	12.20	42.43	0.91	0.07	458.32	173.13	26.38	16.25	51.64	27.79	341.46	0.17	0.03
σ_i^2	6.23	13.77	1.11	2.07	2.01	0.01	0.00	2.29	4.58	0.13	0.17	0.41	0.42	1.73	0.00	0.01
σ_{pe}^2	5.29	31.19	1.62	1.18	23.96	0.23	0.00	13.82	79.62	6.00	4.72	15.41	7.95	95.07	0.01	0.01
σ_e^2	4.15	235.78	13.13	19.07	257.32	0.95	0.01	93.97	126.65	11.31	13.72	18.28	12.19	156.70	0.23	0.20
σ_p^2	97.69	494.08	27.45	34.51	325.73	2.10	0.09	568.41	383.98	43.82	34.86	85.75	48.35	594.97	0.42	0.25
h_g^2	0.84 (0.08)	0.43 (0.06)	0.42 (0.06)	0.35 (0.05)	0.13 (0.03)	0.43 (0.06)	0.83 (0.08)	0.81 (0.08)	0.45 (0.06)	0.60 (0.07)	0.47 (0.08)	0.60 (0.07)	0.57 (0.07)	0.57 (0.07)	0.40 (0.06)	0.11 (0.03)
c_i^2	0.06	0.03	0.04	0.06	0.01	0.01	0.00	0.00	0.01	0.00	0.01	0.01	0.01	0.00	0.01	0.05
c_{pe}^2	0.05	0.06	0.06	0.03	0.07	0.11	0.05	0.02	0.21	0.14	0.14	0.18	0.16	0.16	0.04	0.04
p	0.89 (0.09)	0.49 (0.07)	0.48 (0.07)	0.39 (0.06)	0.20 (0.04)	0.54 (0.07)	0.87 (0.09)	0.83 (0.08)	0.66 (0.08)	0.74 (0.08)	0.60 (0.09)	0.78 (0.08)	0.74 (0.08)	0.73 (0.08)	0.44 (0.06)	0.15 (0.04)
$r_{g\,med}$	0.93	0.94	0.91	0.85	0.95	0.99	1.00	1.00	0.97	0.99	0.99	0.99	0.99	0.99	0.98	0.70
CV_g (%)	82.01	19.92	6.76	6.62	14.24	8.00	49.99	65.22	105.74	8.86	56.90	30.13	20.18	24.98	27.08	8.39
CV_e (%)	18.46	20.94	7.20	8.28	35.07	8.20	19.36	29.53	90.44	5.80	52.28	17.93	13.37	16.92	31.76	22.39
CV_r	4.44	0.95	0.94	0.80	0.41	0.98	2.58	2.21	1.17	1.53	1.09	1.68	1.51	1.48	0.85	0.37
μ	11.04	73.33	50.31	52.76	45.74	11.90	0.53	32.83	12.44	57.96	7.09	23.85	26.12	73.97	1.51	2.00

σ_g^2: genotypic variance, σ_i^2: variance of the genotype *x* measurement interaction, σ_{pe}^2: variance of the permanent environment, σ_e^2 : residual variance, σ_p^2: individual phenotypic variance, h_g^2: individual broad-sense heritability (total genotypic effects), c_i^2: coefficient of determination of the genotype *x* measurement effects, c_{pe}^2: coefficient of determination of the permanent environment effects, p: individual repeatability coefficient, $r_{g\,med}$: genotypic correlation through measurements, CV_g (%): genotypic coefficient of variation, CV_e (%) : residual coefficient of variation, CV_r: relative coefficient of variation, and μ: overall mean.

Therefore, this implies that the contribution of the genotype *x* measurement interaction was small for phenotypic variance. According to Resende and Alves (2020), the TH, TTA, TSS/TTA, CERP, L*, a*, b*, C*, and hº traits had individual repeatability coefficients of high magnitudes ($p \geq 0.60$); the FW, DF, FL, TTA, and PFA traits had individual repeatability coefficients of medium magnitudes ($0.30 < p < 0.60$); and the FPF and PFSR traits had individual repeatability coefficients of low magnitudes ($p \leq 0.30$). Thus, for the FPF and PFSR traits, the evaluation of more peaches per plant is necessary to obtain greater selective accuracy.

Clustering by the Tocher method for the fruit traits resulted in formation of five groups. The groups I, II, III, IV, and V contain 11 (C3, C4, C5, C9, C12, C13, C14, C15, C18, C19, and C21), 7 (C1, C2, C6, C7, C8, C17, and C20), 2 (C11, and C22), 1 (C10), and 1 (C16) clones, respectively. This therefore implies that there was greater genetic divergence among clones when the fruits traits were considered. The genotypic correlation coefficients among the fruit traits are shown in Table 3. The FW and DF, FW and FL, DF and FL, TSS and TSS/TTA, and TTA and TSS/TTA traits had strong (> ± 0.70) or very strong (> ± 0.90) correlations. In addition, the CCE traits (L*a*b*C*hº) had a high degree of linear association.

Results concerning multivariate analysis of principal components involving the seven more important traits for the peach breeding are presented in Table 4. The eigenvalues inform about the variation associated with each principal component. The first four principal components explained 80.62% (Table 4) of the total variability explained by the seven

Table 3. Genotypic correlation coefficients among the fruit traits: time of harvest (TH), fruit weight (FW), mean fruit diameter (MFD); fruit length (FL), fruit pulp firmness (FPF), total soluble solids content (TSS), total titratable acidity (TTA), TSS/TTA ratio, covering of the epidermis with red pigment (CERP), CIE color coordinates (L*a*b*C*h°) of the epidermis (CCE), prominence of the fruit apex (PFA), and prominence of the fruit suture region (PFSR) evaluated in S_0 and S_1 peach trees

	FW	MFD	FL	FPF	TSS	TTA	TSS/TTA	CERP	L*	a*	b*	C*	h°	PFA	PFSR
TH	0.27	0.32	0.15	0.20	0.03	-0.40	0.30	-0.35	0.16	-0.26	0.20	0.12	0.26	-0.19	0.14
FW		0.99	0.86	0.22	-0.26	-0.03	-0.14	-0.15	0.09	-0.08	0.03	0.00	0.16	-0.07	0.12
MFD			0.84	0.25	-0.24	-0.06	-0.10	-0.22	0.15	-0.12	0.10	0.07	0.22	-0.09	0.15
FL				0.13	-0.27	-0.01	-0.17	-0.19	0.15	-0.12	0.18	0.17	0.20	0.38	0.31
FPF					0.38	-0.44	0.53	-0.42	0.29	-0.25	0.21	0.16	0.36	-0.18	0.23
TSS						-0.53	0.73	-0.37	0.46	-0.36	0.33	0.33	0.42	-0.03	-0.30
TTA							-0.90	0.39	-0.38	0.39	-0.27	-0.22	-0.40	0.11	0.15
TSS/TTA								-0.36	0.38	-0.29	0.25	0.23	0.34	-0.13	-0.25
CERP									-0.93	0.88	-0.92	-0.87	-0.96	-0.13	-0.10
L*										-0.88	0.96	0.95	0.96	0.19	0.04
a*											-0.87	-0.80	-0.94	-0.13	-0.10
b*												0.99	0.93	0.30	0.13
C*													0.88	0.33	0.14
h°														0.11	0.04
PFA															0.46

Table 4. Results concerning to multivariate analysis of principal components referring to traits: percentage of bud break in mixed shoots (PBBMS), yield (YD), time of harvest (TH), fruit weight (FW), fruit pulp firmness (FPF), total soluble solids content/total titratable acidity (TSS/TTA) ratio, and covering of the epidermis with red pigment (CERP) evaluated in S_0 and S_1 peach trees

Principal Component	Explained ratio	Accumulated	Correlation between traits and principal components						
			PBBMS	YD	TH	FW	FPF	TSS/TTA	CERP
1	0.3193	0.3193	-0.40	0.02	-0.57	-0.26	-0.74	-0.73	0.78
2	0.1834	0.5027	0.44	0.46	-0.28	-0.82	-0.18	0.27	-0.17
3	0.1644	0.6671	0.40	-0.80	-0.51	-0.08	0.19	0.16	0.16
4	0.1391	0.8062	0.63	0.05	-0.03	0.37	-0.35	-0.45	-0.33
5	0.0969	0.9030	-0.14	0.30	-0.55	0.17	0.43	-0.17	-0.18
6	0.0577	0.9608	0.22	0.24	-0.04	0.26	0.01	0.24	0.41
7	0.0392	1.0000	-0.15	-0.03	-0.18	0.16	-0.29	0.28	-0.17

traits. Thus, these four new variables (the principal components) can be used for practical inferences. This is because when the principal components, cumulatively, explain more than 70% of the total variation, all the available information can be summarized in these components (Ferreira 2008).

The correlations between each trait and the principal components is an alternative approach to the eigenvectors with the weighting coefficients of the traits in the principal components (Resende 2007). The three traits with the highest correlations with the last three principal components were FPF, CERP, and TH (Table 4). Thus, these three traits could be excluded from genetic evaluation and do not need to be evaluated in future studies. The retained traits are those with high variability between clones and with low or zero correlations with the other traits.

Regarding the fruit ripening period (1 November to 11 December), the clones evaluated are classified as medium maturity (Barbosa et al. 1990). None of the clones evaluated were superior in relation to all the traits evaluated; nevertheless, some were quite prominent for some traits.

Traits of polygenic inheritance are highly affected by changes in the environment. The yield trait in fruit trees fluctuates from year to year. Excess production in one crop season can cause reduction in production in the following crop season. In peach trees, a common practice is thinning the fruit for the purpose of promoting an increase in the size of the remaining fruit and stabilizing production over crop years, avoiding a biennial fluctuation in production. Finally, it is important to highlight that for greater accuracy in clonal selection, evaluation of genotypes in more years and more locations is recommended.

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