



SELECTION OF PEACH GENOTYPES WITH LOW CHILLING REQUIREMENTS VIA MIXED MODELS

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Abstract: A good selection of genotypes that show proper stability and adaptability in the characters of interest is crucial to obtaining elite cultivars. In this way, the objective of this work was to study, via mixed models, the performance of advanced selections of peach trees with low chilling requirements. Sixteen advanced peach selections from the EPAGRI Drupaceae breeding program were evaluated during three crops (2017, 2018, and 2019) and at two sites with different altitudes (220 m and 360 m). The characters evaluated were: yield (t.ha⁻¹), maturation cycle (days), average fruit mass (g), soluble solids (°BRIX), and titratable acidity (%). They were analyzed via mixed models that use variance estimates obtained by the REML method (restricted maximum likelihood) by the SELEGEN – REML/BLUP program. Several genotypes showed good performance for the assessed characteristics, where sel. 0574 stood out as it obtained a good yield, high sugar content, and a good sugar/acidity ratio. Selections 0184, 0574, 0374, and 0791 present better performances for fruit yield, such as stability and adaptability (HMGV, RPGN, and HMRPGN). For the traits yield and average fruit mass, the effects of the environment do not change the behavior of the selections, making the genotypes representative of the region of interest.

Keywords: *Prunus persica* (L.) Batsch, genetic enhancement, yield, fruit quality.

Introduction

The knowledge of the crop, and the demands of the productive, market, and consumer sectors are essential for the success of the genetic improvement so cultivars that meet the objectives can be Available (Barbosa et al., 1999). In addition to guaranteeing productive and quality genotypes, they must present good climatic adaptation and guarantee the expansion of the crop in regions with the potential to be exploited (Madail and Raseira, 2008).

The peach genetic improvement program of the Empresa de Pesquisa Agropecuária e Extensão Rural de Santa Catarina (EPAGRI) at the Urussanga Experimental Station selects genotypes adapted mainly to the mild winter conditions of the Carboniferous region in the State of Santa Catarina, which present production and quality of fruit and that take over the local market and other regions of the country (Dalbó et al., 2014). This type of program requires a test protocol to validate whether



one or more genotypes have the potential to be launched as cultivars. Therefore, thorough evaluations of phytotechnical and qualitative parameters are carried out to achieve the objectives of the improvement and enhance the reliability of decisions (Madail and Raseira, 2008).

Further, how the results are interpreted influences the decision. It is known that the environment in which a genotype is cultivated affects its phenotypic expression. Thus, the greater the environmental variation, the greater the chances of the occurrence of variations, also in the expression of characters of agronomic interest in the crop. This phenomenon is known as genotype versus environment interaction (GxE) and is a complicating factor in breeding works (Resende, 2000). The cultivars should present adaptability to several environments and good stability, as well. However, their interaction with the environment makes them, in most cases, suitable for specific environments and restricted to a given environmental condition (Campbell and Jones, 2005).

Thus, the evaluation of the performance of genotypes in strategic locations and the phenotypic stability parameters allows the identification of promising peach genotypes in the region where they are evaluated.

For a good selection of genotypes that present good stability and adaptability in the characters of interest, the procedure used is the estimation through mixed models of variance components, Using the restricted maximum likelihood method (REML) and the prediction of genotypic values utilizing the best linear unbiased predictors (BLUP) (Resende, 2007). In this context, the objective of this work was to study, using mixed models, the performance of advanced selections of peach trees with a low cold requirement for southern Santa Catarina state.

Material and methods

The experiment, in particular, is the final phase of the evaluation of advanced peach tree selections under the EPAGRI genetic improvement program. At the beginning of the program, in the 1990s, crosses be-

tween cultivars from IAC ('Douradão'), EMBRAPA ('Sulina' and 'Chimarrita') and cultivars such as 'Pampeano' and the nectarine tree 'Sunraycer were carried out as a way of to obtain genotypes with low cold requirements, precocity and excellent quality fruits, aiming to serve the market of fresh fruits.

From the crosses of these parents, 16 selections advanced in the stages of the program and were in the validation phase, which was the focus of this study: 0256, 0356, 0563, 1363, 0374, 0574, 1174, 2874, 3174, 0381, 0581, 0184, 0391, 0791, 0891 and 0194.

The study was conducted in two experimental areas located in the municipality of Urussanga, in the state of Santa Catarina. One area was located at 220 m above sea level on a commercial peach orchard farm at coordinates 28°32'53.74" S and 49°19'52.84" W (Lowest altitude) and the second was at 360 m altitude, located at 28°27'51.80" S and 49°15'18.96" W (Highest altitude).

The climate in the region is classified as humid mesothermal with normally well-distributed rainfall and hot summer (Cfa), according to Köppen and Geiger. According to Dufloth et al. (2005), the average temperature of the coldest month is within the range of 13 to 15°C and the normal average temperature during the year varies from 17.0 to 19.3°C. The average number of hours of cold below 7.2°C in Urussanga is 234. The total normal annual rainfall may vary from 1,220 to 1,660 mm (Pola et al., 2016). Soils classified in the orders Argisol (65%) and Camisoles (31%) predominate (EMBRAPA, 2018), which, due to the terrain, vary from wavy to strongly wavy (Dufloth et al., 2005).

The sixteen advanced selections were planted in August and September 2014, at 6x-m spacing, and with the plants conducted in the "Y" system. For each selection, three seedlings were planted. The rootstock used was Okinawa (the most used cultivar in the region).

In 2017, when the selected plants were already well developed in full production, the experiment began, following the phenology and production during three seasons (2017, 2018, and 2019).

Four one-year-old branches (two on each side of the plant) were selected for each phenological cycle, two of them at 1.5 m above the ground and two at 1.8 m, with 50 cm in length and more than 4 mm in diameter. In this branch plot, the total number of flowering buds in the dormant phase was counted. Once flowering was started, the number of open flowers was quantified every four days. The total value of flowering buds and the quantification of flowers on each evaluation date allowed to determine each phenological stage and, consequently, the date of full bloom, when 50% of the flowers were open.

The fruits were harvested at the ideal point for consumption, quantified, and weighed per plant. At the end of the harvest, the production per plant was summed up and the average yield ($t. ha^{-1}$) was calculated. For this, it was multiplied by the density of plants composed in one hectare.

When over 50% of the fruits were harvested per selection, the full harvest was determined. Using the date of full bloom and the date of full harvest, the fruit maturation cycle was obtained, expressed in days.

In the most expressive harvest of each advanced selection, 10 fruits were collected per plant, to carry out the physicochemical evaluations. With a precision balance, the average fruit mass (AFM) expressed in (g) was determined. For this measurement, each fruit was weighed individually and, later, the average of the 10 fruits that make up the sample was taken.

Titrate acidity (TA) was determined through titration with sodium hydroxide (NaOH), using the formula: $\text{Titrate acidity (\%)} = (\text{ml of NaOH spent} \times \text{NaOH concentration} \times \text{Equivalent gram acid}) / \text{sample weight in g} \times 10$.

Thus, the fruits were peeled, pitted, and processed in a Black&Decker Transversal Mixer. Afterward, a sample of 6 g of pulp was removed, mixed with distilled water until completing 100 g of sample, and three drops of 0.1% phenolphthalein (indicator) were added and, finally, it was titrated with 0.1 N NaOH until the change in the color of the sample reaches a pink shade.

Soluble solids (SS) were obtained by collecting a drop of each processed pulp sample and evaluated Using a digital refractometer. Results were expressed in °Brix. In addition, the relationship between soluble solids and titratable acidity (SS/TA) was evaluated.

The experimental design was in randomized blocks in subdivided plots, where 16 advanced selections of peach trees were tested in two areas, at different altitudes in three years of evaluation (2017, 2018, and 2019), where each selection was represented by three plants, composing three repetitions.

To evaluate the characteristics of interest and select superior genotypes, the procedure that estimates the prediction of the genetic values, the BLUP (best unbiased linear prediction) or mixed models, which use variance estimates obtained by the REML method (maximum likelihood restricted), described by Resende (2007). The program used for estimation and prediction of breeding values was SELEGEN – REML/BLUP (Restricted Maximum Likelihood – Best Linear Unbiased Prediction).

The variables were analyzed following model 151 (Resende, 2007), whose equation is: $Y = X_m + Z_g + T_p + W_i + e$, where “y” is the data vector, “m” is the data vector of the effects of the measurement – repetition – location combinations (assumed to be fixed) added to the overall mean, “g” is the vector of the genotypic effects (assumed as random), “p” is the vector of the permanent environment effects (plots in this case) (random), “i” is the vector of the effects of the interaction between genotypes x locations (assumed to be random) and “e” is the vector of errors or residues (random). The capital letters represent the incidence matrices for these effects. As 16 genotypes were evaluated, the effects were considered random, according to Resende and Duarte (2007), who recommend treating genotypic effects as random when the number of treatments is equal to or greater than 10.

A Pearson correlation at 5% of significance was also performed between the variables fruit maturation cycle (days) and mean fruit mass (g), using the SigmaPlot 14.5 software.

Results and discussion

To interpret the results in the first step, the precision of the experiment must be considered because, based on this information, the reliability of the other results will be determined. The two parameters that represent this precision are the experimental coefficient of variation (CVe) and accuracy (Acgen) (Table 1). The CVe of the traits yield, average fruit mass, and maturation cycle showed values that varied from very low to low, confirming good conduction of the experiment.

According to Resende and Duarte (2007), accuracy is the best parameter to measure experimental precision as it considers the level of genotypic variation and the number of repetitions. It is assumed that in the selection processes in plant breeding, accuracy values greater than 70% should be sought. Therefore, the values of this study are considered very good, since the lowest accuracy value was 80% (high) for the yield, 93% (very high) for the average fruit weight, and 97% (very high) for the fruit maturation cycle.

Another important factor to be considered is the repeatability coefficient of individual plots (r). This parameter refers to the neces-

sary number of evaluated repetitions of the same characteristic so that the accuracy of the experiment is adequate (Resende, 2002). In practice, it is very important to use more accurate selection procedures with fewer repetitions as it reduces the costs and the time required to complete a selection process in breeding programs for perennial crops such as peach (Della Bruna et al., 2012).

For yield, average fruit mass, and maturation cycle evaluated in three seasons, the repeatability coefficients were 0.93, 0.83, and 0.88, respectively. Considering the pattern of two measurements, Resende (2002) proposes the following classification for the repeatability coefficient: high ($r \geq 0.60$); medium ($0.30 < r < 0.60$), and low ($r \leq 0.30$). According to this classification, the coefficients of the experiment are considered high. High estimative values of the repeatability coefficient of the evaluated character indicate that it is possible to predict the real value of individuals with a relatively small number of measurements (Cornacchia et al., 1995), indicating that there will be a small gain in accuracy with the increase in the number of measurements (Falconer and Mackay, 1997; Della Bruna et al., 2012). High values of r and ac-

Table 1. Analysis of variance, repeatability of individual plots, coefficients of determination, coefficients of variation, and accuracy of genotype selection for the traits yield (kg.ha⁻¹), average fruit mass (g), and maturation cycle (days) of advanced selections at the two sites and three years of evaluation. Urussanga, SC, 2023.

| | Yield | Average fruit mass | Maturation cycle |
|---------------------|-------------------|--------------------|-------------------|
| Vg | 9483677.72 | 330.50 | 183.22 |
| Vperm | 29542818.11 | 275.17 | 0.19 |
| Vint | 253351.23 | 1.65 | 20.23 |
| Ve | 3073758.65 | 124.17 | 27.12 |
| Vf | 42353605.71 | 731.50 | 230.75 |
| h2g | 0.223917 ± 0.0790 | 0.451821 ± 0.1122 | 0.794019 ± 0.1488 |
| R | 0.93 | 0.83 | 0.88 |
| Acgen | 0.80 | 0.93 | 0.97 |
| Rgloc | 0.97 | 1.00 | 0.90 |
| c2int | 0.01 | 0.00 | 0.09 |
| CVgi% | 18.78 | 13.19 | 12.32 |
| CVe% | 33.43 | 12.48 | 1.97 |
| Overall mean | 16398.89 | 137.86 | 109.83 |

Vg.: genotypic variance; Vperm.: permanent environment variance; Vint.: variance of the genotypes x locations interaction; Ve.: residual variance; Vf.: individual phenotypic variance; h2g: individual heritability; r: repeatability of individual plots; Acgen.: genotype selection accuracy; rgloc.: genotypic correlation between performance in different environments; c2int: coefficient of determination of the effects of the genotypes x locations interaction; CVgi%.: coefficient of genotypic variation; CVe%.: residual or experimental coefficient of variation.

curacy demonstrate the regularity of superiority of individuals from one crop to another, also, the expression of these traits has good genetic control.

The coefficient of determination of the effects of the genotypes and locations interaction (c^2_{int}) were of low magnitude in both experimental areas (Table 1), indicating the non-permanence of environmental heterogeneity within the blocks. In other words, the variations in climatic and environmental conditions that occurred in the locations did not reflect any significant change in the behavior of the evaluated genotypes. The genotypic correlation between the performance of the selections for the different areas shows high values, confirming the low interaction between the genotype and location.

The genotypic variance was observed for yield, average fruit mass, and maturation cycle, indicating the presence of variability among the tested selections. However, heritability was differentiated for the traits, largely because of the participation of genetic variance in phenotypic variance, which will be discussed later.

Regarding the yield, the environmental variance was high, showing a difference between the environments. This can be seen in the averages of the locations, where the highest altitude area presented $18.54 \text{ t}\cdot\text{ha}^{-1}$ and the lowest $14.25 \text{ t}\cdot\text{ha}^{-1}$. However, the variance of the interaction between genotype and environment was low, demonstrating that environment does not affect behavior between genotypes. That is, yield showed a difference between the environments, nevertheless, this difference is strictly due to the environmental factor and not because a genotype expresses this characteristic differently. In practical terms, the tested selections show the same behavior in both locations, that is, the variability between them will be the same and their ranking will not show any changes, according to the environment.

These data are very important for the best choice regarding the potential selections in a breeding program, because when advanced selections are tested in different environments, one of the objectives of the program

is to check their behavior and if there is some prominence, regardless of the place that it is being cultivated. This information is crucial on the assumption that the selection chosen as a cultivar is representative, adaptable and stable for the study region.

As for the fruit maturation cycle character, a low environmental variance was observed, showing that there was no difference between the environments for this trait. This can be seen in the means for each environment, where in the highest altitude area, the cycle was 109.86 days and in the lower altitude area, it was 109.78 days, from flowering to fruit maturation. The interaction between genotype and environments was low, conferring, as well as the other characters, the same behavior of the selections in relation to the environments.

Yield and average fruit mass showed low heritability. Production is a characteristic that is influenced by soil and climate issues and also management, such as plant nutrition, climatic factors that affect effective fruiting, the incidence of diseases and pests, and pruning and thinning management. The average fruit mass is also strongly influenced by climatic and nutritional factors and also by management practices. Low effective fruiting is caused by several environmental factors or incidence of diseases, providing a smaller amount of fruit which causes a higher average mass per fruit (Nava et al., 2009). In addition, practices such as fertilization and thinning result in fruits of good quality and sizes that are interesting to the preferences of the consumers (Oliveira et al., 2017).

On the other hand, the fruit maturation cycle showed high heritability, which may be a trait easily worked on in the improvement program, resulting in a high genetic gain. In addition, it is a character linked to the size of the fruit, therefore, it may improve this characteristic as well.

It can be seen in Table 2 the order of the selections considering the two locations for the yield character, where their results refer to the predicted genotypic effects (g) and values ($u + g$), free from any interaction with environments. The quantity ($u + g + gem$) refers to

the average genotypic value in the various environments and capitalizes on an average interaction with all evaluated environments (Resende, 2002). Thus, the five best selections with genetic effects were 0184, 0574, 0374, 0791, and 0256. The genetic gain of the best selection (0184) in relation to the experimental mean was 4.26 t.ha⁻¹, that is, it corresponds to 26% above the average of 16.4 t.ha⁻¹. The other selections, 0574, 0374, 0791, and 0256 obtained a gain of 20.11%, 17.41%, 15.96%, and 14.83%, respectively, in relation to the experiment mean. This information is of paramount importance as a basis for the breeding program to decide the elite selections that may become the cultivars.

The average genotypic value in the various environments (u+g+gem) capitalizes on an average interaction with all environments, and this interaction capitalization is intrinsic to the genotypes that were chosen as they are more stable and better adapted to the range of environments to which the experimental designs were set. In this work, the genotypes chosen through the genotypic average are repeated, free of interaction (Table 2) and their recommendation can be extrapolated for being planted in various environments, respecting the pattern of interaction of the experimental sites (Resende, 2007).

Because they present a low genotype x location interaction (Table 1), the ranking seen in Table 2 of the selections by the productivity character does not change if we separate the means of the two locations of the experiment. So, it can be inferred that the effects of the environment do not change the behavior of the selections. In other words, in practical terms, the selections present the same behavior in both experimental areas, regardless of the management practice and/or edaphoclimatic factors. Also, it may be indicated, if there is a potential selection, for both experimental areas. This also shows the best representativeness of these selections for the different conditions imposed. This is what is searched in a breeding program; that the selected genotypes are representative and adapted so that they can be grown under different conditions in the region of interest.

Unlike the results obtained in this study, Della Bruna et al. (2012) obtained a high environmental variance of the yield character of peach tree selections grown in three different locations on the south coast of Santa Catarina state, where it was observed that some selections did not have the same behavior in the different evaluation sites.

Table 2. Estimates of the mean components (individual BLUP), for the character yield of the peach tree selections. Urussanga, SC, 2023.

| Order | Genotype | g ¹ | (u + g) ² | Gain | New Mean | (u+g+gem) ³ |
|-------|----------|----------------|----------------------|---------|----------|------------------------|
| 1 | 0184 | 4265.83 | 20664.72 | 4265.83 | 20664.72 | 20721.7 |
| 2 | 0574 | 2330.96 | 18729.85 | 3298.4 | 19697.29 | 18760.98 |
| 3 | 0374 | 1970.32 | 18369.21 | 2855.7 | 19254.6 | 18395.53 |
| 4 | 0791 | 1906.64 | 18305.53 | 2618.44 | 19017.33 | 18331 |
| 5 | 0256 | 1689.01 | 18087.9 | 2432.55 | 18831.44 | 18110.46 |
| 6 | 0563 | 1317.21 | 17716.1 | 2246.66 | 18645.55 | 17733.7 |
| 7 | 3174 | 628.58 | 17027.47 | 2015.51 | 18414.4 | 17035.87 |
| 8 | 0194 | 485.32 | 16884.21 | 1824.23 | 18223.12 | 16890.69 |
| 9 | 1174 | -238.53 | 16160.37 | 1595.04 | 17993.93 | 16157.18 |
| 10 | 1363 | -357.18 | 16041.72 | 1399.82 | 17798.71 | 16036.94 |
| 11 | 0581 | -624.93 | 15773.96 | 1215.75 | 17614.64 | 15765.61 |
| 12 | 0381 | -1030.52 | 15368.37 | 1028.56 | 17427.45 | 15354.6 |
| 13 | 0391 | -1342.48 | 15056.41 | 846.17 | 17245.06 | 15038.48 |
| 14 | 0356 | -2081.19 | 14317.7 | 637.07 | 17035.97 | 14289.9 |
| 15 | 0891 | -2481.3 | 13917.59 | 429.18 | 16828.07 | 13884.45 |
| 16 | 2874 | -6437.74 | 9961.16 | 0 | 16398.89 | 9875.16 |

1: predicted genotypic effects; 2: predicted genotypic means; 3: average genotypic value in the various environments and capitalizes on an average interaction with all evaluated environments.

The values of HMGV (harmonic mean of genotypic values) for the 16 evaluated genotypes are the productivity values themselves, penalized by instability. This mean indicates predictability, that is, the maintenance of productivity in the face of different environments. Thus, the selection based on this criterion contemplates both attributes simultaneously, productive and stable genotypes. According to this criterion, the five genotypes that best associate these two characteristics in decreasing order are 0184, 0574, 0374, 0791, and 0256 (Table 3). According to Vencovsky and Torres (1988), for the farmer, it is of fundamental importance that a cultivar remains stable over the years.

The adaptability of genetic values can be predicted using the Relative Performance of Genetic Values (RPGN) method. The adaptability evaluates the level of response to environmental stimuli, that is, the ability of the genotypes to respond advantageously to the improvement of the environment (Mariotti et al., 1976). Table 3 classifies the genotypes that showed greater adaptive synergism in the different environments for yield. Using the product of the RPGN by the overall mean (OM), the column RPGN*OM was obtained,

which classifies the genotypes in the following decreasing order: 0184, 0574, 0374, 0791, and 0256, indicating that such genotypes respond with an advantage to the improvement of environments.

Regarding the simultaneous selection for yield, adaptability, and stability, in the context of mixed models, Resende (2004) remarks that it can be performed using the Harmonic Mean of the Relative Performance of Genetic Values (HMRPGN) method. This method is based on predicted genotypic values, via mixed models, and it places stability, adaptability, and productivity in a single statistic, which facilitates the selection of higher genotypes (Regitano Neto et al., 2013). Applying the aforementioned HMRPGN method, the genotypes 0184, 0574, 0374, 0791, and 0256 are highlighted in Table 4 as the five best, with performances for peach yield, equal to that observed for HMGV and RPGN.

According to Zeni-Neto et al. (2008), the values of RPGN and MHPRVG indicate accurately the average superiority of the genotype in relation to the average of the environment in which it was tested, so selection 0184 has a superiority of as many as 1.27 times the average of the places where it was

Table 3. Stability of genotypic values (HMGV), adaptability of genotypic values (RPGN), mean genotypic values capitalized through interaction (RPGN*OM), stability and adaptability of genotypic values (HMRPGN), and mean genotypic values at the sites (HMRPGN*OM) for productivity (t.ha⁻¹) of 16 peach tree selections evaluated for three seasons (2017, 2018 and 2019) in two areas (220 m and 360 m altitude). Urussanga, SC, 2023.

| Ord | Sel. | HMGV | Sel. | RPGN | RPGN*OM | Sel. | HMRPGN | HMRPGN*OM |
|-----|------|----------|------|------|----------|------|--------|-----------|
| 1 | 0184 | 20510.29 | 0184 | 1.27 | 20803.71 | 0184 | 1.26 | 20784.84 |
| 2 | 0574 | 18514.91 | 0574 | 1.14 | 18801.48 | 0574 | 1.14 | 18796.39 |
| 3 | 0374 | 18143.01 | 0374 | 1.12 | 18428.79 | 0374 | 1.12 | 18425.28 |
| 4 | 0791 | 18078.22 | 0791 | 1.12 | 18363.49 | 0791 | 1.11 | 18360.14 |
| 5 | 0256 | 17840.42 | 0256 | 1.10 | 18131.28 | 0256 | 1.10 | 18129.89 |
| 6 | 0563 | 17471.95 | 0563 | 1.08 | 17755.55 | 0563 | 1.08 | 17753.98 |
| 7 | 3174 | 16785.55 | 3174 | 1.04 | 17057.47 | 3174 | 1.04 | 17055.87 |
| 8 | 0194 | 16594.59 | 0194 | 1.03 | 16886.98 | 0194 | 1.02 | 16886.93 |
| 9 | 1174 | 15874.78 | 1174 | 0.98 | 16154.04 | 1174 | 0.98 | 16154.00 |
| 10 | 1363 | 15741.13 | 1363 | 0.97 | 16026.12 | 1363 | 0.97 | 16025.70 |
| 11 | 0581 | 15482.84 | 0581 | 0.96 | 15758.94 | 0581 | 0.96 | 15758.77 |
| 12 | 0391 | 15050.61 | 0381 | 0.93 | 15334.25 | 0381 | 0.93 | 15332.67 |
| 13 | 0381 | 14722.42 | 0391 | 0.91 | 15010.01 | 0391 | 0.91 | 15006.86 |
| 14 | 0356 | 14001.43 | 0356 | 0.87 | 14268.33 | 0356 | 0.87 | 14266.43 |
| 15 | 0891 | 13557.21 | 0891 | 0.84 | 13842.35 | 0891 | 0.84 | 13834.89 |
| 16 | 2874 | 9402.43 | 2874 | 0.59 | 9759.40 | 2874 | 0.59 | 9679.28 |

grown, followed by the sel. 0574 with 1.14 compared to the local average.

For the average fruit mass character, the ranking of the 16 selections presented the sel. 1363 in the first place, followed by sel. 3174, then sel. 1174, 0563, 0791, and so on until sel. 2874, which was ranked in last place (Table 4). The sel. 1363 showed a genetic gain of 25.56g in relation to the average of the experiment, that is, it obtained 18.54% above the average of 137.86g. The other selections, such as 3174, 1174, 0563, and 0791, present a gain of 17.39%, 15.35%, 13.6%, and 12.54%, respectively, in relation to the average.

Similar to the yield, these pieces of information are also important as a basis for the breeding program to decide which elite selections can become cultivars since the characteristic high average fruit mass is one of the main objectives. The correlation between average fruit mass (g) and fruit maturation cycle (days) showed a positive correlation of 0.949 for these two characteristics. That is, the longer the maturation cycle, the greater the average fruit mass.

Della Bruna (2007) evaluated the fruit growth curve of different short-cycle (77 to 85 days), medium cycle (86 to 109 days), and long cycle (more than 109 days) cultivars, where all

cultivars showed a relative very high initial growth rate, which was reduced until fruit maturation for short and medium cycle varieties. On the other hand, for long-cycle varieties, at the end of the cycle, an increase in relative growth occurred once more. It can be seen that genotypes with a longer maturation cycle have one more growth phase, culminating in a higher average fruit mass.

The length of the maturation cycle varied by 54 days from the shortest cycle (sel. 2874 with 80 days) to the longest cycle (sel. 3174 with 134 days) selection. For this characteristic, this ranking is relative because the selection with the longest cycle has positive or negative factors, as well as the one with the shortest cycle. In other words, having a shorter cycle leads to precocity, lower costs with pesticide applications, and lower risk of residues, however, it also has a lower average fruit mass. On the other hand, selections with a longer cycle may have a later harvest and larger fruits, but with higher costs to the producer because of the greater demand for phytosanitary treatments on the plants and greater risks, in case of damage caused by the weather (strong winds or hailstorms). Thus, the use of ranking for the maturation cycle will be valid when separating the selections per harvest period, where the objectives are different.

Table 4. Estimates of the mean components (individual BLUP), for the character average fruit mass (g) of the peach tree selections. Urussanga, SC, 2023.

| Order | Genotype | g ¹ | (u + g) ² | Gain | New mean | (u+g+gem) ³ |
|-------|----------|----------------|----------------------|-------|----------|------------------------|
| 1 | 1363 | 25.56 | 163.42 | 25.56 | 163.42 | 163.48 |
| 2 | 3174 | 22.40 | 160.26 | 23.98 | 161.84 | 160.31 |
| 3 | 1174 | 15.56 | 153.42 | 21.17 | 159.03 | 153.46 |
| 4 | 0563 | 11.46 | 149.31 | 18.75 | 156.60 | 149.34 |
| 5 | 0791 | 11.45 | 149.31 | 17.29 | 155.14 | 149.33 |
| 6 | 0374 | 9.86 | 147.72 | 16.05 | 153.91 | 147.75 |
| 7 | 0574 | 7.79 | 145.64 | 14.87 | 152.72 | 145.66 |
| 8 | 0356 | 5.07 | 142.92 | 13.64 | 151.50 | 142.94 |
| 9 | 0256 | 0.72 | 138.57 | 12.21 | 150.06 | 138.57 |
| 10 | 0581 | 0.35 | 138.21 | 11.02 | 148.88 | 138.21 |
| 11 | 0891 | -9.10 | 128.76 | 9.19 | 147.05 | 128.73 |
| 12 | 0194 | -14.56 | 123.30 | 7.21 | 145.07 | 123.26 |
| 13 | 0184 | -15.89 | 121.97 | 5.44 | 143.29 | 121.93 |
| 14 | 0381 | -16.48 | 121.38 | 3.87 | 141.73 | 121.34 |
| 15 | 0391 | -18.90 | 118.96 | 2.35 | 140.21 | 118.91 |
| 16 | 2874 | -35.30 | 102.56 | 0.00 | 137.86 | 102.47 |

1: predicted genotypic effects; 2: predicted genotypic means; 3: average genotypic value in the various environments and capitalizes on an average interaction with all evaluated environments.

For the fruit quality characteristics (sugar content and titratable acidity), all selections presented accuracies greater than 80% (Table 5), demonstrating adequate reliability in the results.

Table 5. Analysis of variance, repeatability of individual plots, coefficients of determination, coefficients of variation, and accuracy of genotype selection for the characters soluble solids (SS), titratable acidity (TA), and SS/TA ratio of the fruits of the 16 advanced selections in both locations and the three years of evaluation. Urussanga, SC, 2023.

| | SS | TA | SS/TA ratio |
|---------------------|---------------|---------------|----------------|
| Vg | 0.2510 | 0.0268 | 64.2696 |
| Vperm | 0.1812 | 0.0058 | 11.5020 |
| Vint | 0.0882 | 0.0075 | 3.3770 |
| Ve | 0.5923 | 0.0026 | 9.9188 |
| Vf | 1.1127 | 0.0426 | 89.0675 |
| R | 0.4677 | 0.9396 | 0.8886 |
| Acgen | 0.8371 | 0.9201 | 0.9692 |
| Rgloc | 0.7399 | 0.7816 | 0.9501 |
| CVgi% | 5.0501 | 31.4218 | 35.2956 |
| CVe% | 5.3334 | 15.1714 | 15.9685 |
| Overall mean | 9.9204 | 0.5207 | 22.7134 |

Vg.: genotypic variance; Vperm.: permanent environment variance; Vint.: genotypes x locations interaction variance; Ve.: residual variance; Vf.: individual phenotypic variance; r: repeatability of individual plots; Acgen.: genotype selection accuracy; rgloc.: genotypic correlation between performance in different environments; CVgi%.: coefficient of genotypic variation; CVe%.: residual or experimental coefficient of variation.

For the SS character only, the repeatability coefficient was low (0.4677), which can be demonstrated by a high error variance. This means that between the repetitions during the harvests, a variation was observed. According to Corelli Grappadelli and Marini (2008), this trait is strongly influenced by climatic factors, such as temperature range between day and night, water availability in the soil, and incident radiation on the fruit. Thus, it can be considered common, over the year, to have differences in the sugar content of the genotypes. However, for this trait, it would be interesting to carry out further observations in later years to increase the reliability of the results.

Another important factor shown in Table 5 is the interaction variance (genotype x environ-

ment) which was low for all traits, meaning that regardless of the environment, the genotypes show the same behavior.

Table 6 shows the ranking of the 16 peach tree selections according to the characteristics that give flavor to the fruit, such as soluble solids (SS), titratable acidity (TA), and the relationship of the two parameters (SS/TA). For SS, the best selection was 0574 with 10.68°BRIX, followed by 0563 with 10.5°BRIX, the 0791 in third with 10.50, and so on until reaching the sixteenth position, given to selection 0381, with 8.67°BRIX. According to Bassi and Monet (2008), the sugar content in peaches (or TTSS) can reach up to 20°BRIX, or even higher, although the average values found in commercial cultivars range from 9 to 15°BRIX. In tropical producing regions, values greater than 10°BRIX are considered satisfactory. In this way, the first eight selections (0574, 0563, 0791, 3174, 2874, 1174, 0194, and 1363) present average values, according to this pattern.

According to the attractiveness pattern of Brazilian consumers, they prefer sweet fruits with low acidity (Trevisan et al., 2010). Thus, the acidity ranking is from the lowest value to the highest, where 2874 ranked first place (0.29), followed by 0574 (0.31) and 0391 (0.35) in third place, and finally, selection 0891 in the sixteenth position with the highest acidity of 0.78.

However, for most connoisseurs of the fruit, the balance between sugar and acidity is what gives the fruit a good flavor, that is, it needs to be sweet, but with a slight acidity to balance the flavor (Trevisan et al., 2010). Thus, selections such as 2874, followed by 0574 and 0391 are genotypes that present a good sugar/acidity ratio.

The selection of superior genotypes through the evaluation of the characteristics of interest using the mixed models, despite being not much used, becomes a very effective method. This is because of the reliability of the results, the range of available information, such as stability and adaptability of individuals, ranking of genotypes, and genetic gain, which are fundamental for decisions in a breeding program.

Table 6. Ranking of peach tree selections according to soluble characteristics (SS), titratable acidity (TA), and SS/TA ratio. Urussanga, SC, 2023.

| Order | SS | | TA | | SS/TA | |
|-------|-----------|-------|-----------|------|-----------|-------|
| | Selection | Mean | Selection | Mean | Selection | Mean |
| 1 | 0574 | 10.68 | 2874 | 0.29 | 2874 | 36.14 |
| 2 | 0563 | 10.51 | 0574 | 0.31 | 0574 | 35.02 |
| 3 | 0791 | 10.50 | 0391 | 0.35 | 0391 | 28.58 |
| 4 | 3174 | 10,45 | 3174 | 0.37 | 3174 | 28.42 |
| 5 | 2874 | 10.40 | 0194 | 0.37 | 0194 | 27.71 |
| 6 | 1174 | 10.36 | 0791 | 0.38 | 0791 | 27.35 |
| 7 | 0194 | 10.29 | 0256 | 0.42 | 0256 | 22.96 |
| 8 | 1363 | 10.28 | 0356 | 0.44 | 0356 | 21.92 |
| 9 | 0581 | 9.78 | 1363 | 0.50 | 1363 | 20.41 |
| 10 | 0184 | 9.77 | 0563 | 0.53 | 0563 | 19.72 |
| 11 | 0356 | 9.73 | 0581 | 0.66 | 0581 | 14.84 |
| 12 | 0256 | 9.71 | 0374 | 0.68 | 1174 | 13.68 |
| 13 | 0391 | 9.37 | 0184 | 0.73 | 0184 | 13.41 |
| 14 | 0891 | 9.24 | 0381 | 0.75 | 0374 | 13.32 |
| 15 | 0374 | 9.06 | 1174 | 0.76 | 0891 | 11.85 |
| 16 | 0381 | 8.67 | 0891 | 0.78 | 0381 | 11.55 |

Moreto et al. (2017) evaluated through mixed models, the performance of cassava genotypes in the state of Santa Catarina and considered clone 269 as the one with the best performance among the genotypes evaluated for all statistics used in the work (HMGV, RPGN, and HMRPGN), providing significant gains with their selection.

Moreto and Della Bruna (2014) evaluated 84 peach clones that presented high productivity, adaptability, and genotypic stability evaluated through mixed models. The authors found that clones 57 and 51 stood out among the others and that the HMGV, RPGN, and HMRPGN statistics are good alternatives to be used as criteria for the selection of superior clones and that the average fruit mass character was little influenced by the environment.

Because of the different characteristics evaluated, each one obtained different rankings, which showed that some selections showed potential for one character, but not for others. However, some selections were in the first ranks, thus, potential genotypes for launching as cultivars. This commonly occurs in breeding programs, where the researcher must consider the traits as a whole, and the most productive does not always become a potential selection.

The selection 0574A stood out as it was in the best position for most characteristics. It presented good productivity of 18.51 t.ha⁻¹ (second place in the ranking), with an average fruit mass of 145.64 g (seventh place), a good total soluble solids content of 10.68 °BRIX (first place), and an excellent sugar and acidity ratio, 35.02 (second position). Therefore, the selection 0574 has great potential to be made available as a cultivar.

However, others also stood out and they should be investigated for other parameters. A better way to interpret the data would be to split the selections into groups, according to the harvest season, as the objectives in each period of the harvest are different. Thus, a selection that did not obtain a good position in the ranking of the 16 selections may have potential, if compared to a smaller group. So, the results of the analyses via mixed models allied to the phenological characteristics are fundamental to corroborate even more for the decisions to select genotypes in a breeding program.

Conclusions

Several genotypes showed good performance for the evaluated traits in which sel. 0574 stood out which obtained good produc-

tivity, high sugar content, and a good sugar/ acidity ratio.

Selections 0184, 0574, 0374, and 0791 present better performances for fruit yield, such as stability and adaptability (HMGV, RPGN, and HMRPGN).

Regarding the yield and average fruit mass, the effects of the environment do not change the behavior of the selections, making the

genotypes representative of the region of interest.

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