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Genetics/ Original Article

Use of the REML/BLUP methodology for the selection of sweet orange genotypes

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Abstract – The objective of this work was to select superior sweet orange (*Citrus sinensis*) genotypes with higher yield potential based on data from eight harvests, using the residual or restricted maximum likelihood/best linear unbiased prediction (REML/BLUP) methodology. The experiment was carried out from 2002 to 2008 and in 2010 in the municipality of Rio Branco, in the state of Acre, Brazil. Analyzes of deviance were performed to test the significance of the components of variance according to the random effects of the used model, and parameters were estimated from individual genotypic and phenotypic variances. A selection intensity of 20% was adopted regarding genotypic selection, i.e., only the best 11 of the 55 genotypes tested were selected. The estimates of the genetic parameters show the existence of genetic variability and the selection potential of the studied sweet orange genotypes. The genotypic correlation between harvests is of low magnitude, except for the variable average fruit mass, and, as a reflex, there is a change in the ordering of the genotypes. Genotypes 5, 48, 19, 14, and 47 stand out as being the most productive, and, therefore, are the most suitable for selection purposes. Genotypes 14 and 47 show superior performance for the character set evaluated.

Index terms: *Citrus sinensis*, genetic gain, genetic variability, productivity.

Uso da metodologia REML/BLUP para seleção de genótipos de laranjeira-doce

Resumo – O objetivo deste trabalho foi selecionar genótipos superiores de laranjeira-doce (*Citrus sinensis*) com maior potencial produtivo com base em dados de oito safras, com uso da metodologia “residual or restricted maximum likelihood/best linear unbiased prediction” (REML/BLUP). O experimento foi realizado de 2002 a 2008 e em 2010, no município de Rio Branco, no estado do Acre, Brasil. Análises de deviance foram realizadas para testar a significância dos componentes da variância de acordo com os efeitos aleatórios do modelo utilizado, e os parâmetros foram estimados a partir das variâncias genotípicas e fenotípicas individuais. Foi adotada uma intensidade de seleção de 20% em relação à seleção genotípica, ou seja, apenas os melhores 11 dos 55 genótipos testados foram selecionados. As estimativas dos parâmetros genéticos mostram a existência de variabilidade genética e o potencial de seleção dos genótipos de laranjeira-doce estudados. A correlação genotípica entre as safras é de baixa magnitude, exceto para a variável massa média dos frutos, e, como reflexo, há uma mudança na ordenação dos genótipos. Os genótipos 5, 48, 19, 14 e 47 se destacam como os mais produtivos e, portanto, são os mais adequados para fins de seleção. Os genótipos 14 e 47 apresentam desempenho superior para o conjunto de caracteres avaliados.

Termos para indexação: *Citrus sinensis*, ganho genético, variabilidade genética, produtividade.

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Introduction

Citrus is been one of the most planted, consumed, and researched fruit trees in the world due to its economic and social importance (Iglesias et al., 2007). However, although this crop presents a great diversity, few cultivars are used in commercial orchards, which affects the expansion of its genetic base and the sustainability of its productive chain (Oliveira et al., 2014).

The cultivation of sweet orange [*Citrus sinensis* (L.) Osbeck] in Brazil has been distributed throughout several regions of the country. However, there is hegemony in the Southeastern region, where the state of São Paulo is the largest producer, with a production of around 13.4 million tons (IBGE, 2021).

In the state of Acre, in the Northern region, citrus represents the second fruit tree in harvested area of approximately 1,006 ha, of which 463 ha are planted with oranges, 372 ha with lemons, and 171 ha with tangerines (IBGE, 2021). However, production does not meet local demand, requiring the importation of fruits from other states, mainly from São Paulo.

The Aquiri (Ledo et al., 1997b) and Natal and Valência (Ledo et al., 1997a) orange tree cultivars have been recommended for the Northern region. To these authors, however, their production is concentrated between April and August, which leads to a lack of availability of fruits in the market in the off-season. Therefore, research aimed at selecting individuals with superior productive characteristics is necessary to increase the supply of varieties for cultivation and extend the harvest period.

The evaluation and selection of superior genotypes comprise the main stages of a genetic improvement program, which tend to be time consuming and laborious in perennial crops (Sales et al., 2019; Azevedo et al., 2020; Ambrósio et al., 2021), such as the orange tree. Therefore, the adoption of more efficient statistical methods is essential for the genetic improvement of the species, considering the experiments involve long periods and high costs.

For a long time, the most used method for plant breeding was the analysis of variance, where all effects are fixed, except for the experimental error, however, this methodology has been considered inadequate due to the assumption of an independence of errors in cases of data imbalance and when each plot provides various data in different sites and years, being, therefore, correlated (Freitas, 2013). In addition, it is essential to verify an individual's genetic superiority during the selection process using true genotypic values and not only phenotypic averages (Borges et al., 2010), since the estimates of genetic parameters subsidize the planning of efficient improvement strategies (Rosado et al., 2019).

The residual or restricted maximum likelihood/best linear unbiased prediction (REML/BLUP) methodology is currently considered the standard in the selection of perennial species, showing accuracy in the selection process, besides enabling the modeling of fixed and random effects (Resende, 2002; Carias et al., 2014). In this methodology, the components of variance from which genetic parameters are estimated are obtained by REML and the genotypic values are predicted by BLUP (Resende, 2002; Bezerra et al., 2020).

Therefore, the REML/BLUP methodology has been used in genotypic selection and to promote an increase in the genetic gain of several perennial crops such as coffee (*Coffea canephora* Pierre ex A.Froehner) (Carias et al., 2016; Silva et al., 2018), passion fruit (*Passiflora* spp.) (Santos et al., 2015; Silva et al., 2017), bacuri (*Platonia insignis* Mart.) (Maia et al., 2016), and eucalyptus (*Eucalyptus* spp.) (Rosado et al., 2012). However, the application of this methodology to sweet oranges is still scarce.

The objective of this work was to select superior sweet orange genotypes with higher yield potential based on data from eight harvests, using the REML/BLUP methodology.

Materials and Methods

The experiment was carried out from 2002 to 2008 and in 2010 in the municipality of Rio Branco, in the state of Acre, Brazil (9°58'29"S, 67°49'44"W, at 160 m altitude). The climate of the region is Aw, hot and humid, according to the Köppen-Geiger classification, with an annual dry period of three months, an average annual rainfall of 1,700 mm, an annual average relative humidity of 83%, and maximum and minimum annual temperatures of 30.9 and 20.8°C, respectively (Agritempo, 2019). Temperature and precipitation data during the experimental period are shown in Figure 1 (Inmet, 2019).

The soil of the experimental area is an Argissolo Vermelho-Amarelo distrófico, according to the Brazilian soil classification system (Santos et al., 2018), i.e., an Oxisol, with a medium/clayey texture, good drainage, and a flat topography. The chemical analysis of the soil, carried out at the beginning of the experiment, at 20 cm depth, showed: pH 5.2, 0.17 $\text{cmol}_c\ \text{kg}^{-1}$ K, 3.70 $\text{cmol}_c\ \text{kg}^{-1}$ Ca, 1.49 $\text{cmol}_c\ \text{kg}^{-1}$ Mg, 0.14 $\text{cmol}_c\ \text{kg}^{-1}$ Al, 2.57 $\text{cmol}_c\ \text{kg}^{-1}$ H + Al, sum of bases of 5.36 $\text{cmol}_c\ \text{kg}^{-1}$, cation exchange capacity of 5.5 $\text{cmol}_c\ \text{kg}^{-1}$, and base saturation of 68% (Negreiros et al., 2014).

A total of 55 genotypes of sweet orange were obtained from the state of Acre, Brazil: 54 in production; and a local cultivar, Aquiri (Table 1). The genotypes came

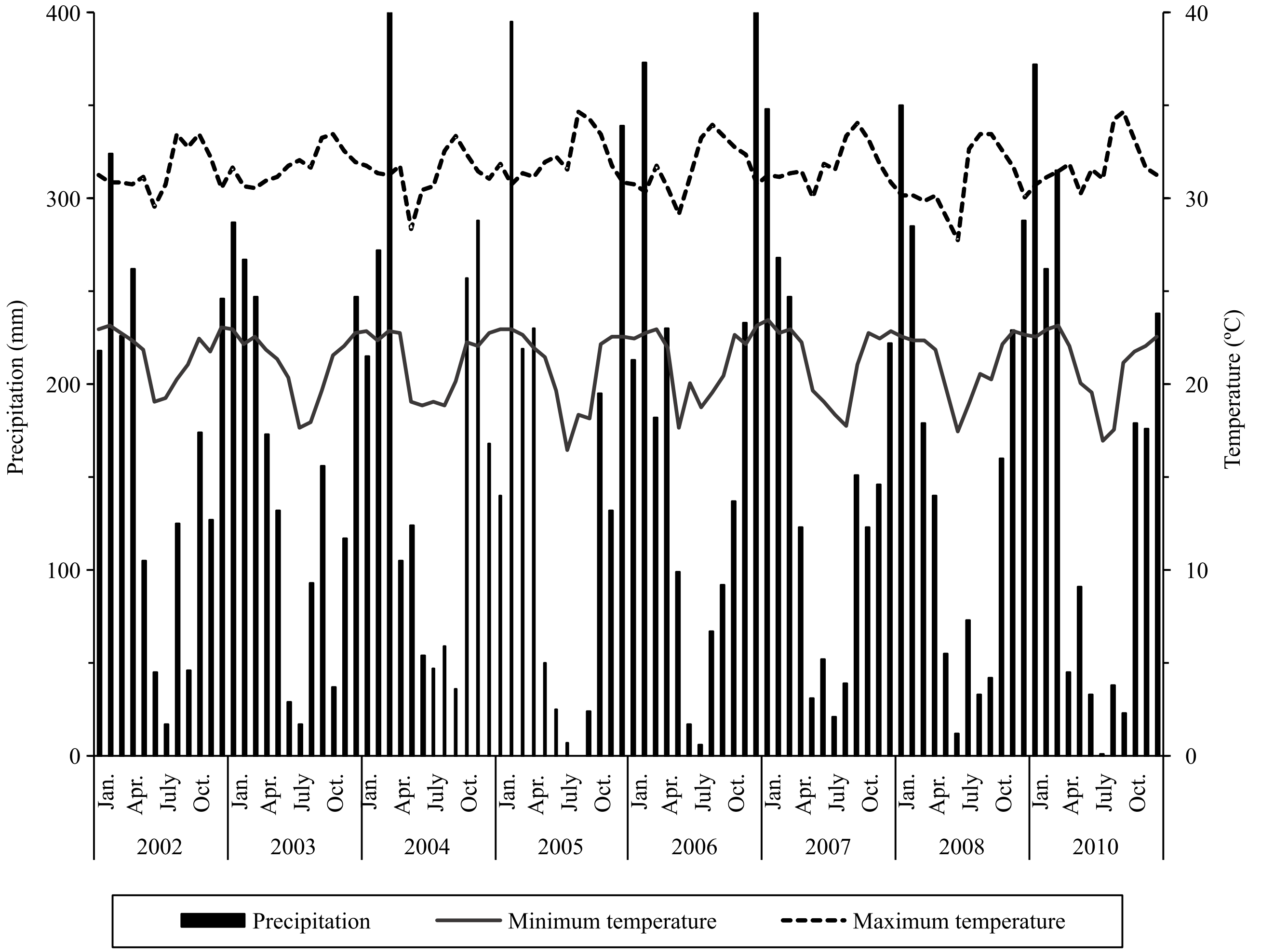

Figure 1. Precipitation and maximum and minimum monthly air temperatures from 2002 to 2008 and in 2010 in the experimental area in the municipality of Rio Branco, in the state of Acre, Brazil. Source: Inmet (2019).

Table 1. Collection sites (municipalities) of sweet orange (*Citrus sinensis*) genotypes in the state of Acre, Brazil.

Collection site	Geographic coordinates	Genotype
Plácido de Castro	10°19'43"S, 67°10'44"W	1, 2, 3, 4, 5, 6, 7, 8
Senador Guiomard	10°09'03"S, 67°44'13"W	9, 10, 11, 12, 13, 14, 15, 16
Capixaba	10°34'29"S, 67°40'38"W	17, 18,19, 20, 21, 22, 23
Xapuri	10°39'11"S, 68°30'03"W	24, 25, 26, 27, 28, 29, 30, 31
Sena Madureira	09°04'10"S, 68°39'30"W	32, 33, 34, 35, 36, 37, 38
Brasiléia	11°00'01"S, 68°44'59"W	39, 40, 41, 42
Epitaciolândia	11°01'56"S, 68°43'54"W	43, 44, 45, 46, 47
Porto Acre	09°35'42"S, 67°32'36"W	48, 49, 50, 51, 52
Rio Branco	09°58'29"S, 67°49'44"W	53, 54, 55(1)

(1)Local Aquiri cultivar. Fonte: Gondim et l., 2001; Negreiros et al., 2014.

from plants from vigorous and apparently healthy seeds, with an average age of 22 years, which were productive and producing quality fruits and the genotype seedlings were produced by budding, using the Rangpur lime (*Citrus limonia* Osbeck) rootstock (Gondim et al., 2001).

The experiment was implemented with the plants in a 8x8 m spacing in a randomized complete block design with 55 treatments and 3 replicates. The evaluations were carried out in the harvests between April and August from 2002 to 2008 and in 2010. Orange trees were cultivated without irrigation, and fertilization was performed according to the soil analysis carried out annually (Ledo et al., 1997a, 1997b; Mattos Júnior et al., 2005). The assessed characteristics were: total number of fruits per plant, number of fruits per square meter, average fruit mass (kg), and productivity (kg m^{-2}).

Individual analyzes were carried out for each harvest, in order to verify the heterogeneity of variances using the following statistical model: y = Xb + Zg + e, where y is the data vector, b is the data vector of the fixed block effects added to the general average, g is the data vector of random genotype effect, e is the vector of random errors, and X and Z represent the incidence matrices for vectors b and g, respectively (Resende, 2002).

The data were standardized according to Resende (2007) for the cases in which variation coefficients of broad-sense heritability were observed even as a joint analysis was carried out after standardization, considering genotypes and harvests, according to the following statistical model: y = Xb + Za + Wi + e, where y is the data vector; b is the vector of the block effects (assumed as fixed) added to the general average; a is the vector of individual genotypic effects (assumed as random); i is the vector of the effects of the genotype/environment interaction (with the environment corresponding to years); e is the vector of errors (random); and X, Z, and W represent the incidence matrices for the referred effects.

Analyzes of deviance were performed to test the significance of the components of variance according to the random effects of the model. The likelihood ratio test was used, implementing the components of variance in which the significance of the model was assessed by the chi-squared test with a degree of freedom. Therefore, deviances with the complete and reduced models were obtained. Next, the deviance of the reduced model of each effect was subtracted from the full deviance and compared with the chi-squared value with a degree of freedom at 1 and 5% probability (Resende, 2007).

The following genetic parameters were estimated from the genotypic and phenotypic variances according to Resende (2007): individual broad-sense heritability (h^2_g), heritability of genotype average in eight harvests (h^2_{mg}), selective accuracy, coefficient of determination of permanent effects (c^2_{perm}), coefficient of determination of effects of the genotype x harvests (environment) interaction (c^2_{gm}), and genotypic correlations over long harvests (r_{gmed}).

A selection intensity of 20% was adopted regarding genotypic selection, i.e., only the best 11 of the 55 genotypes tested were selected, aiming to simplify the presentation and discussion of the results.

For the individual analyzes, the statistical model 20 was adopted, referring to the evaluation of unrelated genotypes obtained in the randomized complete blocks containing one plant per plot. Lastly, the 55 model was used for the conjoint analysis, being related to the genotypes in a randomized complete block design, with temporal stability and adaptability in one site and at various times, using the SELEGEN-REML/BLUP genetic-statistical computational application (Resende, 2016).

Results and Discussion

The effects of genotypes were highly significant ($p<0.01$) for all analyzed variables (Table 2). This result is desirable, as it reflects the existence of genetic variability between genotypes, which indicates the possibility of selection.

The different responses of the genotypes according to the evaluated environment (harvest years) show that productivity differed from one harvest to another (Table 2). Productivity was lower in some years, mainly because orange is a fruit plant that presents alternating production, but also because of climatic variations throughout the experimental period, among other causes (Figure 1).

The effects of the genotype x environment (GxE) interaction were significant ($p<0.01$) for all evaluated variables (Table 2). However, this interaction is undesirable for the breeder, as it is difficult to predict how the genotypes will behave in relation to changes in the environment, which could lead to different performances in each year of production, a characteristic of orange trees. Although the presence of the GxE interaction is undesirable, when looking for superior individuals, it is necessary to assess their behavior in different environments. Moreover, evaluations restricted to just one environment (year or location) are inefficient given the strong influence of the other factors that determine such interaction (Carias et al., 2014).

Therefore, genotypes with satisfactory performance in one harvest may not show the same performance in the next one (Cruz et al., 2012). This observation allows indicating in which crop the genotypes were more productive and then conducting the selection process. However, some genetic parameters should be estimated for genotype selection to be reliable (Rosado et al., 2019).

The variance resulting from environmental effects represents the highest percentage (80%) of the phenotypic variance for number of fruits per plant (NFP) and shows that the contribution of the genetic variance (Vg) was small (6.6%) (Table 3). This indicates that the environmental variation from one year to the next had a great influence on this characteristic, mostly because the variables assessed are quantitative and

Table 2. Analysis of deviance of number of fruits per plant (NFP), number of fruits per square meter (NF m^{-2}), fruit mass (FM), and productivity of 55 genotypes of sweet orange (*Citrus sinensis*) in eight harvest years (environment), from 2002 to 2008 and in 2010, in the municipality of Rio Branco, in the state of Acre, Brazil.

Source	NFP		NF m^{-2}		Fruit mass (kg)		Productivity (kg m^{-2})	
	Deviance	LRT (χ^2)	Deviance	LRT (χ^2)	Deviance	LRT (χ^2)	Deviance	LRT (χ^2)
Genotype (G)	15,331.43	16.16**	4,710.66	17.28**	-7,122.92	22.37**	409.63	9.70**
Environment (E)	15,315.44	0.17^{ns}	4,694.91	1.53^{ns}	-7,141.80	3.49^{ns}	409.73	9.80**
GxE	15,331.31	16.04**	4,715.89	22.51**	-7,135.22	10.07**	423.33	23.40**
Complete model	15,315.27		4,693.38		-7,145.29		399.93	

**Significant at 1% probability through the analysis of deviance based on the likelihood ratio test (LRT) distributed chi-squared (χ^2) with 1 degree of freedom (χ^2 tabulated: 6.63 for a significance level of 1%). ^{ns}Nonsignificant.

Table 3. Estimation of variance components and genetic parameters of number of fruits per plant (NFP), number of fruits per square meter (NF m^{-2}), fruit mass (FM), and productivity of sweet orange (*Citrus sinensis*) genotypes evaluated in eight harvest years, from 2002 to 2008 and in 2010, in the municipality of Rio Branco, in the state of Acre, Brazil.

Variance component(1)	NFP	NF m^{-2}	Fruit mass (kg)	Productivity (kg m^{-2})
V_g	7498.9478**	1.4316**	0.00011**	0.0335**
V_{perm}	634.4612^{ns}	0.3428^{ns}	0.00003^{ns}	0.0277**
V_{gm}	13549.2255**	2.4821**	0.00009**	0.0718**
V_e	91539.7184**	13.4521**	0.00076**	0.3747**
V_f	113222.3528	17.7233	0.00095	0.5077
Parameter(2)				
h^2_g	0.0662**	0.0808**	0.1138**	0.0659**
h^2_{mg}	0.5673	0.5924	0.6787	0.4975
Ac	0.7228	0.7697	0.8238	0.7053
c^2_{perm}	0.0056^{ns}	0.0193^{ns}	0.0321^{ns}	0.0546**
c^2_{gm}	0.1197**	0.1403**	0.0911**	0.1415**
r_{gmed}	0.3562	0.3655	0.5554	0.3180
General mean	614.6123	8.2951	0.1802	1.4768

(1)V_g, genetic variance; V_{perm}, variance of permanent effects; V_{gm}, variance of genotype x measurement interaction; V_e, temporary residual variance; and V_f, phenotypic variance. (2)h^2_g, individual broad-sense heritability; h^2_{mg}, heritability of the average genotypes; Ac, accuracy of genotype selection; c^2_{perm}, coefficient for determining permanent effects; c^2_{gm}, coefficient for determining the effects of genotypes and enviroment (harvest years); and r_{gmed}, genotypic correlation through measurements over harvests. **Significant at 1% probability. ^{ns}Nonsignificant.

highly influenced by the environment. In addition, the predominance of environmental variance is common in young perennial plants since they are subjected to different annual weather conditions, contributing to the phenotypic potentials being expressed in different magnitudes over the years (Pereira et al., 2013).

The lowest proportion of phenotypic variance for NFP was 0.56%, being calculated through the relationship between the variance of the permanent portion (V_{perm}) and phenotypic variance (V_f), and observed through the V_{perm}, i.e., genotype/block (Table 3). For number of fruits (NF) per square meter, fruit mass (FM), and productivity, a similar performance was observed, with the lowest proportion of phenotypic variance being 1.93, 3.16, and 5.46%, respectively. This indicates that there was little variation in the environment of the experimental plot, and, therefore, the number of blocks was adequate to accurately predict the individual's real value in the experiment, in alignment with Araújo et al. (2015).

Genetic parameters are essential for the correct selection of superior individuals (Pereira et al., 2013). According to Lucius et al. (2014), heritability (h^2) is one of the most important genetic parameters for the breeder and quantifies the fraction of phenotypic variance that is inheritable, i.e., genotypic nature (Rodrigues et al., 2013).

According to Resende (2002), h^2 in perennial species can be classified as low (h^2 <0.15), median (0.15 <h^2 <0.50), or high (h^2> 0.50). Therefore, high heritability values have been associated with a greater genetic variance and/or a lower environmental influence (Pompeu Junior et al., 2013), and their magnitude shows the importance of genotype selection based on predicted genotypic value instead of on observed phenotype (Santos et al., 2015).

The estimates of h^2_g, calculated through the relationship between V_g and V_f, for the evaluated variables, were of low magnitude, with values ranging from 0.0662 (6.6%) for NFP to 0.1138 (11.38%) for FM (Table 3). According to Santos et al. (2015), this might be due to the association between a low genetic variance and a high phenotypic variance, as observed in the present work. Resende (2002), however, found values of individual heritability around 20% for most of the quantitative characters of economic importance.

According to Zhou & Joshi (2012), h^2_g has been an important parameter in vegetatively propagated crops such as citrus, since genetic variability is released only once in these species, and the genotype of a plant is fixed after crossing with no opportunity for segregation in future phases.

Individual heritabilities of low magnitude have also been observed for other perennial crops, with values of: 0.08% for physic nut (*Jatropha curcas* L.) (Cardoso et al., 2018), 0.07% for coffee (*Coffea arabica* L.) (Pereira et al., 2013), 0.01% for guava (*Psidium guajava* L.) (Almeida, 2017), and 0.1% for papaya (*Carica papaya* L.) (Moreira et al., 2019), confirming the results of the present study.

The estimates of the h^2_{mg} of the genotypes ranged from 0.50 to 0.68 for productivity and FM, respectively (Table 3). These values indicate a great potential for the selection of individuals to compose a population with the possibility of satisfactory gains for these variables. According to this estimate, the experimental arrangement is classified as highly accurate due to the decrease in experimental errors (Rosado et al., 2012).

The estimates of the heritability coefficient of h^2_{mg} showed that the experimental arrangement and the number of replicates used in the present study were adequate to isolate environmental effects, resulting in a greater precision in estimating the parameter. This is favorable for selecting plants that will be propagated vegetatively.

It was observed that the heritability coefficients based on the average of the genotypes presented higher values than the estimates at the individual level (h^2_g) for all variables (Table 3). Similar results have been found in the literature, for example, for coffee (Rodrigues et al., 2013) and guava (Almeida, 2017). As both of these are perennial species, the obtained results are in agreement with those of the present work and allow to infer that selection based on the average of the families can be more efficient than that based on the estimates within them.

In the genotypic evaluation, the most important statistical parameter to assess the quality of the experiment and the individual's predicted genetic value is selective accuracy (Pompeu Junior et al., 2013). This parameter refers to the correlation between the predicted and true genetic values of individuals and is dependent on the heritability and repeatability of the evaluated trait (Resende & Duarte, 2007). Accuracy reflects the quantity and quality of the information and procedures used in the prediction of genetic values;

furthermore, it measures reliability in the selection of the best genotypes (Resende, 2002).

According to the classification of Resende (2002), the accuracy found in the present study was of high magnitude, ranging from 0.70 to 0.82 (Table 3). Resende & Duarte (2007) concluded that an accuracy above 0.70 is desirable for selecting superior genotypes at the beginning of a breeding program when it is possible to select many genotypes, although an accuracy greater than 50% already indicates a good precision in genotype selection. Therefore, the accuracy observed in the present work proves that selection was adequate, indicating the possibility of greater gains and a high reliability in the prediction of genotypic values.

A possible explanation for the high accuracy values obtained is the number of harvests assessed. The greater the number of harvests in each plant, the greater the accuracy of the predictions, and, consequently, the greater the confidence in the evaluation, the more accurate the inferences (Sturion & Resende, 2005).

The c^2_{perm} quantifies the environmental variation that remains from one harvest to the next (Mrode, 2014; Resende, 2015). With the exception of the productivity variable, whose significance was high, the coefficients for determining the permanent effects were not significant (Table 3), revealing that the environmental variation from one year to the next was not important. According to Resende (2002), good experiments with perennial crops have coefficients of determination around 10% of all phenotypic variation within blocks, since values of up to 10% do not interfere in the estimation of genetic parameters.

The c^2_{gm} was about 14% for NF per square meter and productivity, and 11 and 9% for NFP and FM, respectively (Table 3). These coefficients indicate how much each component contributes to the total phenotypic variance (Borges et al., 2010).

The r_{gmed} for FM was 55% (Table 3), indicating that the interaction is not of a complex nature, i.e., the relative position of the genotypes is not changed over the years (Vencovsky & Barriga, 1992). However, the genotypic correlation for NFP, NF per square meter, and productivity was 36, 37, and 32%, respectively, being considered of low magnitude and indicating complex interaction levels. Therefore, the classification of the genotypes in the different years is not the same, that is, the genotypes did not behave similarly in the different years evaluated.

In mixed models, tests are not performed to compare means as the effect of genotypes is considered random (Resende, 2002). Therefore, in this methodology, a decreasing order of the genotypes is obtained according to their genetic values (Duarte & Vencovsky, 2001).

Genotypes 5, 48, 19, 47, 14, 39, 2, and 43 stood out for NFP, NF per square meter, and productivity, while genotypes 5 and 48 remained in the same order considering these three variables (Table 4). This result can be explained by a high positive correlation between the genotypic behavior of the clones in the different harvests (Rodrigues et al., 2013).

The ranking of the 11 genotypes follows the same order, based on two criteria: predicted genotypic values (u + g) and average genotypic values in the different environments (u + g + gem) (Table 4). The values obtained for the genotypes are higher by the criterion u + g + gem due to the capitalization of the average interaction. However, the original mean of the genotypes showed higher values than those of u + g and u + g + gem, likely due to the effect of the environment and its interaction with the genotypes. Borges et al. (2010) emphasized that genotypic values must be preferred by researchers, as they are the true values to be predicted. The new average is obtained of predictions made by BLUP, meaning that these are the values that the genotypes probably produce in commercial crops.

The u + g for all variables were very close to the new average, which reflected a relative performance (quotient between genotypic values and the new average) above 94%, which is evidence of the accuracy selection of the REML/BLUP methodology (Freitas et al., 2013).

The average FM was 0.2052 kg (Table 4), being close to that of 0.207 kg found by Beber et al. (2018). Genotypes 10, 22, 14, 12, 15, 1, 16, 28, 52, 32, and 47 had the highest FM, although genotypes 14 and 47 also stood out in terms of produced quantity. In addition, the selection of the 11 sweet orange genotypes based on the average FM provides a gain of 1.13%.

For productivity, the genetic gain when selecting the 11 best genotypes was of 0.1584 kg m^{-2} and the new average became 1.6352 kg m^{-2} with a u + g of 1.5856 kg m^{-2} (Table 4). Therefore, the selection of the 11 most productive sweet orange genotypes provides a gain of 9.69%.

With u + g, it is possible to recommend cultivars for sites that were not part of the experimental network, as

Table 4. Selection of the 11 best (20%) of 55 genotypes of sweet orange (*Citrus sinensis*) according to number of fruits per plant (NFP), number of fruits per square meter (NF m^{-2}), fruit mass (FM), and productivity, evaluated in eight harvest years, from 2002 to 2008 and in 2010, in the municipality of Rio Branco, in the state of Acre, Brazil[(1)].

Order	Genotype	g	u + g	Gain	New average	u + g + gem
Number of fruits per plant (NFP)						
1	5	157.8704	772.4827	157.8704	772.4827	808.1380
2	48	115.2073	729.8195	136.5388	751.1511	755.8393
3	43	88.0099	702.6221	120.3625	734.9748	722.4994
4	4	83.8497	698.4619	111.2343	725.8466	717.3996
5	39	83.0565	697.6688	105.5987	725.8466	716.4272
6	2	75.0725	689.6848	100.5110	715.1233	706.6401
7	33	74.1234	688.7357	96.7414	711.3537	705.4766
8	14	71.7250	686.3373	93.6143	708.2266	702.5365
9	47	71.7250	681.1024	90.6005	705.2128	696.1193
10	37	63.3332	677.9455	87.8738	702.4861	692.2494
11	19	50.6044	665.2166	84.4857	699.0979	676.6457
Number of fruits per square meter (NF m^{-2})						
1	5	2.4756	10.7706	2.4756	10.7706	11.3079
2	48	1.5869	9.8819	2.0312	10.3263	10.2263
3	4	1.2174	9.5124	1.7599	10.0550	9.7766
4	47	1.2146	9.5096	1.6236	9.9186	9.7732
5	37	1.1066	9.4017	1.5202	9.8153	9.6419
6	39	1.0935	9.3886	1.4491	9.7441	9.6259
7	2	1.0931	9.3881	1.3982	9.6933	9.6254
8	43	1.0558	9.3508	1.3554	9.6505	9.5800
9	33	0.8777	9.1728	1.3024	9.5974	9.3633
10	14	0.8371	9.1322	1.2558	9.5509	9.3139
11	19	0.8349	9.1299	1.2176	9.5126	9.3111
Fruit mass (FM, kg)						
1	10	0.0228	0.2029	0.0228	0.2029	0.2052
2	22	0.0184	0.1986	0.0206	0.2008	0.2005
3	14	0.0133	0.1935	0.0182	0.1983	0.1948
4	12	0.0126	0.1928	0.0168	0.1970	0.1940
5	15	0.0111	0.1913	0.0156	0.1958	0.1924
6	1	0.0093	0.1894	0.0146	0.1948	0.1904
7	16	0.0092	0.1894	0.0138	0.1940	0.1903
8	28	0.0078	0.1880	0.0131	0.1932	0.1888
9	52	0.0074	0.1876	0.0124	0.1926	0.1883
10	32	0.0070	0.1872	0.0119	0.1921	0.1879
11	47	0.0059	0.1861	0.0113	0.1915	0.1866
Productivity (kg m^{-2})						
1	5	0.2213	1.6981	0.2212	1.6981	1.7574
2	48	0.2184	1.6952	0.2198	1.6966	1.7537
3	19	0.1879	1.6647	0.2092	1.6860	1.7151
4	14	0.1793	1.6562	0.2017	1.6785	1.7042
5	47	0.1606	1.6374	0.1935	1.6703	1.6805
6	39	0.1437	1.6205	0.1852	1.6620	1.6590
7	31	0.1407	1.6175	0.1788	1.6556	1.6552
8	2	0.1340	1.6108	0.1732	1.6500	1.6467
9	46	0.1335	1.6103	0.1688	1.6456	1.6461
10	43	0.1144	1.5913	0.1634	1.6402	1.6219
11	13	0.1088	1.5856	0.1584	1.6352	1.6147

[(1)] g, effect of genotypes; u + g, predicted genotypic values; and u + g + gem, average genotypic values in the different environments (harvest years).

the performance of the materials is free of interaction (GxE) (Borges et al., 2012). These same authors found that the recommendation of these genetic materials is based on u + g + gem, since they capitalize the average interaction in all environments, and is limited to sites where the experiment is carried out or that present the same interaction pattern (GxE) as that of the site where the experiment was evaluated. According to the mentioned authors, otherwise, the recommendation based on the criterion of values (u + g) is more reliable.

From the values of the new average, it was observed that the average productivity was around 1.70 kg m^{-2} or 17 Mg ha^{-1} sweet oranges (Table 4), higher than that of 15.18 Mg ha^{-1} in the Northern region, but lower than the national average of 27.64 Mg ha^{-1} (IBGE, 2021). This value is relatively good, since the experiment was carried out in dry conditions with unfavorable climatic conditions in some years due to the occurrence of water deficits in the critical stages of fruit formation and maturation (Figure 1), causing a low yield. In addition, the used spacing (8.0x8.0 m), resulting in a lower density of plants, also contributed to this productivity.

Another factor that may have interfered in the average productivity of sweet orange was the alternation in production caused by endogenous factors, such as low carbohydrate reserves and hormonal imbalances, as well as by exogenous factors as climate conditions (Agustí et al., 2014; Bons et al., 2015). This alternation in production is characterized by a high production in one year/harvest, known internationally as a “year on”, followed by a year/harvest with an absence of or low fruit production, characterized as a “year off” (Efrom & Souza, 2018). Therefore, the low quantity of fruits produced in certain harvests interfered in the average productivity. This shows that the relationship between orange productivity and environmental variations is quite complex, since these variations can affect plant growth and development in different ways at different crop stages.

Although productivity has been the main variable sought in the genotype selection process, it is also necessary to take into account other characters. In the present study, the other evaluated characteristics showed a behavior similar to that of productivity. However, there was a change in the ordering of genotypes regarding genetic gains due to the low magnitude of the genotypic correlation, as observed by Maia et al. (2014).

Conclusions

1. Estimates of genetic parameters reveal the existence of genetic variability and indicate the potential for the selection of some of the studied sweet orange (*Citrus sinensis*) genotypes in the state of Acre, Brazil.
2. The genotypic correlation between harvests is of low magnitude, except for the variable average fruit mass, and there is a change in the ordering of the genotypes as a reflex.
3. Genotypes 5, 48, 19, 14, and 47 stand out as the most productive, being, therefore, the most suitable for selection purposes.
4. Genotypes 14 and 47 show superior performance for the character set evaluated by the conjoint selection for all characters.

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