



Stability and adaptability of sweet orange using mixed models

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Abstract

Evaluations with sweet oranges are usually performed in several harvests and places to verify the differential behavior according to the environmental variations. This makes the selection by traditional statistical methodologies more and more difficult since they have limitations in the case of data unbalanced, common in citrus during the experimental phase due to the possibility of plot loss over the years. The objective of this work was to estimate the temporal stability and adaptability of sweet orange genotypes cultivated in eight crops under the edaphoclimatic conditions of Rio Branco, Acre. The experimental design used was in randomized blocks containing 55 genotypes and three replications. Four agronomic characteristics were evaluated during eight harvests. The genetic parameters were estimated using the REML/BLUP methodology. After detecting the presence of significant interaction between genotypes and environments, stability and adaptability analyzes were conducted by the methods of the harmonic mean of the genotypic values (HMGV), the relative performance of the genetic values (RPGV) and the harmonic mean of the relative performance of the genotypic values (HMRPGV). The HMRPGV can be used to select stable, adapted and productive sweet orange genotypes. The number 48, 19, 5, 14, 2, 47 and 37 sweet orange genotypes can be selected for cultivation in an environment similar to the one studied, as they simultaneously present high stability, adaptability and productivity.

Keywords: Quantitative genetics, genotype x environment interaction, *Citrus sinensis* (L.)

Introduction

Evaluating the interaction of genotypes and environments (G x A) aims to verify the different behavior of genotypes in view of the environmental variations to which they are subjected (Malosetti et al., 2013). However, this analysis can generate inconsistent results and result in changes in the genotypic classification (Araújo et al., 2012) due to its complexity, especially in relation to predicting the behavior of genotypes against changes in the environment, since a genotype selected for a specific location may not be selected for another. Therefore, studies on genotypic stability and adaptability (Rosado et al., 2019) are necessary to predict the behavior of the genotype when confronted with variations in the environment in both specific and broad conditions (Cruz et al., 2014).

Long reproductive cycle, alternating production over the years, delay in expressing some characteristics

and reaching maturity have been some situations which hinder orange tree breeding and influence its interaction with the environment (Pereira et al., 2013; Viana & Resende, 2014; Cruz et al., 2014; Rodrigues et al., 2017).

There are currently several methodologies to quantify stability and adaptability which differ in conceptual terms and biometric procedures (Khalili et al., 2016; Alves et al., 2018; Rocha et al., 2017; Luz et al., 2018; Santos et al., 2018), however, they are limited in the case of data unbalanced which can be common in citrus during the experimental phase due to the possibility of plot loss over the years, in addition to not considering the effect of genotypes as random (Resende, 2007).

The mixed model methodology (REML/BLUP) has been an efficient way to analyze unbalanced data and select genotypes evaluated in different environments (Resende, 2004), through which the components of variance and genetic parameters are estimated, and

the genotypic values are predicted. Statistics based on the harmonic mean of the genotypic values (HMGV), the relative performance of the genotypic values (RPGV) and the harmonic mean of the relative performance of the genotypic values (HMRPGV) enable predicting stability, adaptability and both parameters simultaneously (Resende, 2007). Thus, genotypes are ordered simultaneously for stability, adaptability and productivity based on their genetic values, without underestimating the interaction effects (Resende, 2004).

HMRPGV has been used to interpret the genotypic stability and adaptability for fruit crops (Nascimento Filho et al., 2009; Luz et al., 2018), annual crops (Carvalho et al., 2016; Streck et al., 2019), industrial crops (Alves et al., 2018), and forestry species (Rosado et al., 2012), however, they do not exist for sweet orange trees.

In view of the above information, this study aimed to estimate adaptability and temporal stability and select genotypes of sweet orange trees through the mixed model methodology (REML/BLUP).

Material and Methods

The experiment was conducted in the experimental field of Embrapa Acre, in the municipality

of Rio Branco, Acre, between 2002 and 2010. The municipality is located at 9° 58' 29" latitude S and 67° 49' 44" longitude W, at 160 m of altitude. The predominant climate of the region is AW according to the Köppen classification (hot and humid, with an annual dry period of 3 months), with a maximum temperature of 30.9 °C and a minimum of 20.8 °C, annual precipitation of 1,700 mm and relative humidity around 83%. The data referring to temperature and rainfall during the experiment are available in Figure 1 (INMET, 2019).

The soil in the experimental area had the following characteristics: pH: 5.2; K: 0.17 cmolc kg⁻¹; Ca: 3.70 cmolc kg⁻¹; Mg: 1.49 cmolc kg⁻¹; Al: 0.14 cmolc kg⁻¹; H + Al: 2.57 cmolc kg⁻¹; sum of bases: 5.36 cmolc kg⁻¹; organic carbon: 7.27 g kg⁻¹; CTC: 5.5 cmolc kg⁻¹ and base saturation 68%.

The buds that gave rise to the clones were collected in the period from March to June 1999 in areas of settlement projects of the National Institute of Colonization and Agrarian Reform (INCRA). A total of 54 sweet orange tree seedlings still in the production phase from the Mesoregion of Vale do Acre, as well as the local 'Aquiri' cultivar (recommended by Embrapa Acre), were selected, totaling 55 genotypes (Table 1) (Gondim et al., 2001).

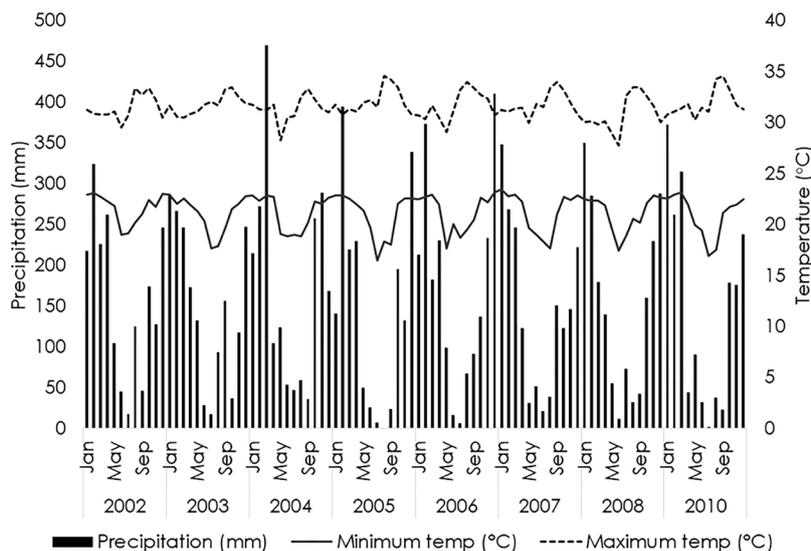


Figure 1. Temperature (°C) and rainfall (mm) during the experimental period (2002 to 2010) in Rio Branco, Acre State.

Table 1. Collection sites of sweet orange genotypes [*Citrus sinensis* (L.) Osbeck] in the State of Acre.

Collection site	Geographic coordinates	Genotypes
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

¹Local 'Aquiri' cultivar.

Five branches were collected from each genotype each containing ten buds with the help of pruning shears. Two vegetative buds were removed from each branch and grafted onto Rangpur lime rootstock (*Citrus limonia* (L.) Osbeck) (Gondim et al., 2001).

The selected matrices came from free-standing plants (produced from seeds), were vigorous, apparently healthy with an average age of 22 years, productive and producing quality fruits to meet the consumer market demands. The harvest season of most of these genotypes is distributed from February to October, with a concentration in April to July (Gondim et al., 2001).

The genotypes were planted in February 2000, adopting the spacing of 8 x 8 m and the 'Aquiri' orange cultivar was used as a border. The experimental design was in randomized blocks with 55 treatments (54 genotypes collected in different counties of Acre State, in addition to the 'Aquiri' cultivar) and 3 replicates, being considered one plant per plot (Gondim et al., 2001).

The evaluations were carried out during the 2002, 2003, 2004, 2005, 2006, 2007, 2008 and 2010 harvests. The orange trees were cultivated without irrigation, and fertilizations were performed according to the soil analysis. The characteristics evaluated were total number of fruits per plant, number of fruits per m², average fruit mass (kg) and productivity (kg m⁻²).

The genetic-statistical analyzes were performed using the mixed model methodology, in which the genetic parameters were estimated using the Restricted Maximum Likelihood (REML) method and the genotypic values were predicted by the best linear unbiased prediction (BLUP) method (Resende, 2016).

The data were submitted to individual and joint analyzes of variance. The statistical model adopted for the analysis of individual variance is represented in the following equation:

$$y = Xb + Zg + e$$

In which: y : data vector; b : vector of the effects of the blocks (assumed as fixed) added to the general average; g : data vector of random genotype effects; e : randomized vector errors; X and Z : represent the incidence matrices for vectors b and g .

The data was standardized using the obtained correction factor for cases in which the variation in heritability coefficients was verified in the broad-sense, according to the following expression described by Resende (2007):

$$\frac{\sqrt{h_{ik}^2}}{\sqrt{h_t^2}}$$

In which: h_{ik}^2 : individual broad-sense heritability for character i in the k evaluation; h_t^2 : average of individual broad-sense heritability of the k evaluation for character i .

After standardizing the data, a joint analysis of variance was performed considering the genotypes and harvests, according to the following statistical model:

$$y = Xb + Za + Wc + e$$

In which: b : vector of the effects of the blocks (assumed as fixed) added to the general average; a : vector of the individual genotypic effects (assumed as random); c : vector of the effects of the plot (randomized); e : vector of errors (random); X , Z and W represent the incidence matrices for the referred effects above.

Analyzes of deviance (ANADEV) were performed to test the significance of the components of variance according to the random effects of the model. The likelihood ratio test (LRT) was used implementing the components of variance, in which the significance of the model was assessed by the chi-squared test with one degree of freedom (Resende, 2007).

The classification of genotypes simultaneously considering productivity and stability was performed by the harmonic mean of the genetic values (HMGV), obtained as follows:

$$HMGV_i = \frac{n}{\sum_{j=1}^n \frac{1}{GV_{ij}}}$$

In which: n : number of years/harvests ($n = 8$) in which genotype i was evaluated; GV_{ij} : is the genetic value of genotype i in the year/harvest j expressed by the ratio of the average in this year/harvest.

The genotypes simultaneously considering productivity and adaptability were selected through the relative performance of genotypic values (RPGV) over the years/harvests, obtained by:

$$RPGV_i = \frac{1}{n} \left(\frac{\sum_{j=1}^n GV_{ij}}{M_j} \right)$$

In which: M_j : average fruit productivity in the year/harvest j .

The sweet orange genotypes were simultaneously classified for productivity, stability and adaptability by the harmonic mean of the relative performance of the genotypic values (HMRPGV), obtained according to the expression:

$$HMRPGV_i = \frac{n}{\sum_{j=1}^n \frac{1}{RPGV_{ij}}}$$

The $RPGV_{\mu}$ and $HMRPGV_{\mu}$ values were obtained by multiplying $RPGV$ and $HMRPGV$ by the general average of each characteristic considering all years/harvest. Thus, the mean genotype values were provided,

penalized by instability and capitalized by adaptability. The selective accuracy and the gains with the selection were obtained according to Resende (2016).

The statistical model 20 was adopted for individual analyzes, which refers to evaluating unrelated genotypes obtained in randomized blocks containing one plant per plot. Furthermore, model 55 was used in the joint analysis for genotypes in a randomized block design with stability

and temporal adaptability in one place and at different harvests using the Selegen REML/BLUP software program (Resende, 2016).

Results and Discussion

It was found that the genotype and the $G \times A$ interaction effects were significant ($p < 0.01$) by LRT for all variables, in contrast to the permanent environment whose effect was only significant for productivity (Table 2).

Table 2. Deviance analysis (ANADEV) of the number of fruits per plant, number of fruits per m², average fruit mass and productivity of sweet orange genotypes evaluated in eight harvests.

FV	Number of fruits per plant		Number of fruits per m ²		Mean fruit mass (kg)		Productivity (kg/m ²)	
	Deviance	LRT	Deviance	LRT	Deviance	LRT	Deviance	LRT
		(χ^2)		(χ^2)		(χ^2)		(χ^2)
Genotype (G)	15331.43	16.16**	4710.66	17.28**	-7122.92	22.37**	409.63	9.7**
G x Years	15331.31	16.04**	4715.89	22.51**	-7135.22	10.07**	423.33	23.4**
Permanent environment	15315.44	0.17 ^{ns}	4694.91	1.53 ^{ns}	-7141.8	3.49 ^{ns}	409.73	9.8**
Complete model	15315.27		4693.38		-7145.29		399.93	

^{ns} e **: not significant and significant at 1% probability through the analysis of deviance based on the LRT test (χ^2) with 1 degree of freedom (table 1^o: 6.63 for the level of significance at 1%).

The significant results for genotypes, environments and their interaction indicate that the genotypes suffered different influences from the environments and present different performances, which makes it difficult to recommend only one cultivar for the entire region.

The presence of the genotype x year interaction reinforces the need to have genotype performance evaluated in different environments and with harvests also being considered in biometric models (Rosado et al., 2019), and indicates that evaluations restricted to only one environment (year or location) are inefficient due to several factors that determine such interaction (Valério et al., 2009; Carías et al., 2016). Because the experiment was conducted in different years/harvests, it was already assumed that the interactions would be significant.

The different responses of the genotypes according to the agricultural years evaluated show that productivity was different from one harvest to another. Productivity was lower in some years, mainly because it is a crop that presents alternating production (Duarte et al., 2011), combined with climatic variations throughout the experimental period (Figure 1).

Peixoto et al. (2018) observed a significant $G \times A$ interaction in physic nuts (*Jatropha curcas*) evaluated in five years of production. According to the authors, the performance of the genotype can be attributed to climatic factors during the years since the evaluated environments were the production years, and these

factors consequently resulted in the significance of the interaction. Therefore, in these cases and as observed in this work, adaptability and temporal stability studies are necessary so that superior genetic materials are selected with greater precision.

For the purpose of presenting and simplifying the results, 20% of the genotypes were exposed. Thus, Table 3 shows the ordering of 11 superior orange genotypes (G) of the 55 tested in eight harvests, referring to stability (HMGV - harmonic mean of the genotypic values), adaptability (RPGV - relative performance of the genotypic values) and simultaneous adaptability, stability and productivity (HMRPGV - harmonic mean of relative performance of the genotypic values) by the REML/BLUP methodology for characteristics related to production and productivity.

From the HMGV results, it was found that those which best associate productivity with stability among the genotypes considering the number of fruits per plant in decreasing order are 20, 21, 35, 22, 5, 48, 43, 2, 54, 33 and 37 (Table 3). The most stable genotypes for the number of fruits per m² were 5, 48, 37, 2, 19, 43, 33, 47, 31, 4 and 46. In addition, genotypes 22, 10, 12, 15, 14, 16, 1, 52, 32, 13 and 28 stood out for the average fruit mass, while for productivity it was found that the 11 most stable genotypes were: 19, 48, 5, 31, 2, 46, 14, 47, 13, 1 and 37. These genotypes stood out because in addition to having the highest productivity among the 55 genetic materials tested, they also demonstrated low sensitivity to climate

change. Greater stability is necessarily associated with greater productivity. In addition, as HMGV penalizes the genotypic values of each genotype for instability, this ensures greater precision and accuracy in ordering genotypes within and between locations (Resende, 2007).

One of the ways used to capitalize the response capacity of each genotype is through the relative performance of the genotypic values (RPGV) (Borges et al., 2010; Regitano Neto et al., 2013). Thus, the most adapted genotypes in decreasing order for number of fruits per plant were: 5, 48, 43, 2, 37, 33, 4, 39, 14, 47 and 19, while the best genotypes for number of fruits per m² were: 5, 48, 37, 2, 43, 47, 19, 4, 33, 31 and 46. Regarding the average fruit mass, superior performance was presented by the number 10, 22, 14, 12, 15, 16, 1, 52, 28, 32 and 13 genotypes. Moreover, greater adaptability for productivity was observed for genotypes 48, 19, 5, 31, 46, 14, 2, 37, 47, 1 and 13.

The RPGV shows that at least nine genotypes (5, 48, 43, 2, 37, 4, 47 and 19) coincided considering three characteristics (number of fruits per plant, number of fruits per m² and productivity), although the ordering was not the same.

The average genotypic values capitalized by the interaction (RPGV μ) were obtained using the RPGV product by the general average of each variable. Thus, RPGV values for productivity were multiplied by 1.4768 kg/m² and thus RPGV μ was obtained. According to these results, it was found that genotype 48 had the greatest genotypic adaptability associated with fruit productivity among the 55 evaluated, responding positively to the improved environment. In addition to this genotype, numbers 19, 5, 31, 46, 14, 2, 37, 47, 1 and 13 also stood out, which are among the 11 most stable along with the greater adaptability.

The majority of citrus farmers who have small orchards do not adopt the appropriate management technologies (Andrade Neto et al., 2011), mainly due to the high price of inputs which can influence the performance of the cultivars. Therefore, the results presented by these genotypes in terms of genotypic adaptability and stability provide greater security for farmers in planting these materials because producers can trust the stability and adaptability of cultivars for the cultivation location when it is not possible to control the environment through cultural treatments (Melo et al., 2018).

Mean genotypic values of each genotype in the evaluated environments are provided through the

HMRPGV μ , being penalized for instability and capitalized for adaptability (Borges et al., 2010). The genotypes which simultaneously showed greater adaptability, stability and quantity of fruits per plant were: 10, 5, 48, 43, 2, 37, 33, 4, 39, 14 and 47 (Table 3). It is observed that the ordering based on the number of fruits per plant did not coincide in any of the tested methodologies, however genotypes 5, 48, 43, 2, 37 and 33 were among those selected in all of them.

The number of fruits per plant for genotype selection did not coincide by the HMGV, RPGV and HMRPGV criteria, and therefore it is possible to demonstrate the importance of these attributes for decision making in the selection. Thus, it can be inferred that the genotypes showed low stability for this variable, or had an unpredictable behavior in facing environmental variations. According to Carvalho et al. (2016), the change in ordering can occur due to the complex fraction of the G x A interaction which favors selecting more specific adaptation genotypes. Therefore, the selection based on the RPGV criteria (and mainly HMRPGV) is more appropriate in this case.

Some studies have shown that HMGV, RPGV and HMRPGV criteria are not coincident (e.g., Rosado et al. (2012) and Santos et al. (2015) for Eucalyptus clones; Atroch et al. (2013) for guaranazeiro clones; and Moreto et al. (2017) for cassava clones). On the other hand, Carvalho et al. (2016) and Rosado et al. (2019) observed agreement between the HMGV, RPGV and HMRPGV criteria in discriminating the most productive genotypes and with high adaptability and stability. Regarding the number of fruits per m², the number 5, 48, 37, 2, 43, 47, 19, 33, 4, 46 and 31 genotypes stood out for their HMRPGV (Table 3). It is noted that genotypes 5, 48, 37 and 2 coincided by the three methodologies, indicating that these present higher productivity, adaptability and genotypic stability.

Regarding the average fruit mass, the ordering of genotypes by HMRPGV was 10, 22, 14, 12, 15, 16, 1, 52, 28, 32 and 13, in decreasing order (Table 3). It is observed that there was agreement among all genotypes for the three evaluated methodologies for this characteristic, with a difference in the ordering.

According to the HMRPGV for productivity, number 48, 19, 5, 14, 31, 46, 2, 47, 13, 37 and 1 genotypes stood out (Table 3). These genotypes are highlighted for simultaneously presenting greater stability, adaptability and productivity among the 55 genotypes of sweet oranges tested. Considering productivity, there was also agreement of the superior genotypes by the three tested

methodologies, although with different orders.

It is generally observed that the number 48, 19 and 5 genotypes showed better behavior than the others due to productivity, adaptability and stability. This indicates that these genotypes have high value for future commercial crops. Number 48 and 19 genotypes alternated between the 1st and 2nd positions in the different criteria, while the number 5 genotype was the only one which maintained its position in occupying 3rd, regardless of the methodology studied. This indicates that these genotypes showed adaptability and phenotypic stability in the eight years/harvests analyzed, in addition to being productive, meaning that the genotypes remained productive regardless of the year/harvest.

For number of fruits per m², average fruit mass and productivity by the three methods (HMGV, RPGV and HMRPGV), it was observed that there was a small change in the ordering, but all genotypes coincided among the best. Therefore, although the selection is not the same according to the evaluated methods, it is observed that the estimates classified the genotypes in a similar way when using each of the three parameters obtained by the Blup procedure for productivity, showing that the selected genetic materials stand out for presenting high stability and adaptability for the evaluated character. These results corroborate the studies by Candido et al. (2018); Carvalho et al. (2016); Regitano Neto et al. (2013); Torres et al. (2015);

Santos et al. (2018); Coan et al. (2018) and Rosado et al. (2019), who also verified a similar ordering of the superior genetic materials according to the evaluated criteria. According to Torres et al. (2015), superior genetic materials which stand out for having adaptability and stability have greater adaptive synergism.

The REML/BLUP methodology does not group environments, so the results provided were directly interpreted as genetic values, and were already penalized or capitalized by adaptability and stability estimates. In comparing studies of adaptability and stability in physic nuts, Peixoto et al. (2018) concluded that HMRPGV is the most efficient method to maximize the genetic gain and the most adequate to select superior genotypes of perennial crops.

Finally, it is observed that HMGV, RPGV and HMRPGV are efficient tools to assist the breeder in selecting the best genotypes in orange breeding programs.

Although the local 'Aquiri' cultivar is the most used in the region, it was not listed in the list of the 20% best genotypes by HMGV, RPGV and HMRPGV, demonstrating that it can be replaced by other clones which have better adaptability and productive stability characteristics. Thus, the selected genotypes can better compose the citrus production system in the region, as they can promote greater security for the producer and possibilities for diversifying their orchards.

Table 3. Stability (HMGV), adaptability (RPGV and RPGV μ) and simultaneous adaptability, stability and productivity (HMRPGV and HMRPGV μ) for number of fruits per plant, number of fruits per m², average fruit mass (kg) and productivity (kg/m²) obtained for 55 genotypes of sweet orange.

Order	Number of fruits per plant							
	Stability		Adaptability			Stability, adaptability, and productivity		
	G	HMGV ¹	G	RPGV ²	RPGV μ ³	G	HMRPGV ⁴	HMRPGV μ ⁵
1	20	3566.39	5	1.70	1047.29	10	2.17	1332.35
2	21	2126.03	48	1.56	956.45	5	1.53	939.44
3	35	1796.34	43	1.40	860.06	48	1.44	888.08
4	22	848.75	2	1.38	847.69	43	1.33	818.90
5	5	379.38	37	1.36	835.15	2	1.30	799.18
6	48	347.39	33	1.35	830.11	37	1.29	795.13
7	43	301.88	4	1.34	825.13	33	1.28	786.03
8	2	301.01	39	1.30	800.03	4	1.26	772.24
9	54	294.13	14	1.30	796.06	39	1.25	767.69
10	33	292.86	47	1.29	791.86	14	1.25	767.14
11	37	286.72	19	1.26	774.96	47	1.23	756.68

Order	Number of fruits per m ²							
	Stability		Adaptability			Stability, adaptability, and productivity		
	G	HMGV ¹	G	RPGV ²	RPGV μ ³	G	HMRPGV ⁴	HMRPGV μ ⁵
1	5	6.10	5	1.55	12.83	5	1.48	12.30
2	48	5.59	48	1.41	11.70	48	1.37	11.35
3	37	5.18	37	1.33	11.01	37	1.27	10.55
4	2	5.05	2	1.29	10.68	2	1.26	10.43
5	19	4.84	43	1.26	10.42	43	1.23	10.22
6	43	4.77	47	1.25	10.38	47	1.22	10.16
7	33	4.74	19	1.24	10.28	19	1.21	10.02
8	47	4.74	4	1.24	10.27	33	1.20	9.99

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9	31	4.63	33	1.23	10.17	4	2.00	9.95
10	4	4.62	31	1.20	9.99	46	1.18	9.78
11	46	4.57	46	1.20	9.93	31	1.19	9.78
Average fruit mass (kg)								
Order	Stability		Adaptability			Stability, adaptability, and productivity		
	G	HMGV ¹	G	RPGV ²	RPGV μ^3	G	HMRPGV ⁴	HMRPGV μ^5
1	22	0.15	10	1.21	0.22	10	1.20	0.22
2	10	0.14	22	1.17	0.21	22	1.15	0.21
3	12	0.14	14	1.10	0.20	14	1.10	0.20
4	15	0.14	12	1.10	0.20	12	1.10	0.20
5	14	0.14	15	1.10	0.20	15	1.09	0.20
6	16	0.13	16	1.08	0.19	16	1.08	0.19
7	1	0.13	1	1.07	0.19	1	1.07	0.19
8	52	0.13	52	1.06	0.19	52	1.06	0.19
9	32	0.13	28.00	1.06	0.19	28	1.06	0.19
10	13	0.13	32.00	1.05	0.19	32	1.05	0.19
11	28	0.13	13.00	1.05	0.19	13	1.05	0.19
Productivity (kg/m ²)								
Order	Stability		Adaptability			Stability, adaptability, and productivity		
	G	HMGV ¹	G	RPGV ²	RPGV μ^3	G	HMRPGV ⁴	HMRPGV μ^5
1	19	1.01	48	1.26	1.86	48	1.25	1.85
2	48	0.99	19	1.25	1.85	19	1.23	1.81
3	5	0.95	5	1.23	1.81	5	1.19	1.76
4	31	0.95	31	1.19	1.76	14	1.18	1.74
5	2	0.93	46	1.19	1.75	31	1.17	1.73
6	46	0.93	14	1.18	1.75	46	1.17	1.73
7	14	0.92	2	1.17	1.73	2	1.15	1.70
8	47	0.90	37	1.17	1.72	47	1.14	1.68
9	13	0.90	47	1.16	1.71	13	1.14	1.68
10	1	0.89	1	1.15	1.70	37	1.13	1.67
11	37	0.89	13	1.15	1.69	1	1.13	1.67

¹HMGV - harmonic mean of the genotypic values; ²RPGV - relative performance of the genetic values; ³RPGV μ - Relative Performance of genotypes based on genetic means free of interaction, where μ is the general mean of the experiment; ⁴HMRPGV - Harmonic mean of relative performance of the genotypic values; ⁵HMRPGV μ - Harmonic mean of genotype performance based on genetic means free from interaction

Conclusions

HMRPGV can be used to select stable, adapted and productive sweet orange genotypes.

The number 48, 19, 5, 14, 247 and 37 sweet orange genotypes can be selected for cultivation in environments similar to the one studied as they simultaneously present high stability, adaptability and productivity.

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