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Coefficient of repeatability, stability, and adaptability estimates for *Psidium guajava* S_1 progenies via mixed models

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Abstract: This study intends to estimate the coefficient of repeatability for traits relating to yield, so as to infer what is the minimum number of evaluations required to identify superior genotypes; to verify adaptability and stability; to predict genetic gains; and to select the best families and in S_1 progenies of *Psidium guajava*. Families were obtained by means of self-fertilization of superior genotypes (full sibs) from the guava tree genetic breeding program of the UENF. The experiment was implemented at the Experimental Station of Ilha Barra do Pomba, in the municipality of Itaocara-RJ. In this case, an experimental randomized block design was used with 18 inbred families, three replicates, and ten plants per plot. Inbred families were evaluated in three harvests regarding fruit weight, number of fruits per plant, and total yield. It was then conducted an analysis of repeatability, adaptability, and stability of genotypes by means of the Selegen/REML/BLUP program. Repeatability values show that the performance of genotypes is constant among measurements, suggesting the need to perform only three evaluations for the selection of superior genotypes. There was agreement on the choice of families 1, 4, 6, and 12 as the most yielded, adaptable, and stable for the traits evaluated.

Index terms: Inbreeding; guava tree, REML/BLUP.

Estimativas do coeficiente de repetibilidade, estabilidade e adaptabilidade em progênies S_1 de *Psidium guajava* via modelos mistos

Resumo: O presente estudo tem por objetivo estimar o coeficiente de repetibilidade das características referentes à produção da goiabeira, a fim de inferir qual o número mínimo de avaliações é necessário para identificar genótipos superiores,

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além de verificar a adaptabilidade e a estabilidade, bem como prever os ganhos genéticos e selecionar as melhores famílias em progênies S_1 de *Psidium guajava*. As famílias foram obtidas por meio de autofecundações de genótipos superiores (irmãos-completos) do programa de melhoramento genético de goiabeiras da UENF. O experimento foi implementado na Estação Experimental da Ilha Barra do Pomba, no município de Itaocara-RJ. O delineamento experimental utilizado foi blocos ao acaso, com 18 famílias endogâmicas, três repetições e 10 plantas por parcela. Foram avaliadas as famílias endogâmicass em três safras, quanto ao peso dos frutos, ao número de frutos por planta e à produção total. Posteriormente, foi realizada a análise de repetibilidade, adaptabilidade e estabilidade dos genótipos através do programa Selegem/REML-BLUP. Os valores de repetibilidade demonstram que o desempenho dos genótipos é constante entre as medições, indicando a necessidade de apenas três avaliações para a seleção dos genótipos superiores. Houve concordância na escolha das famílias 1;4; 6 e 12 como as mais produtivas, adaptáveis e estáveis para os caracteres avaliados.

Index terms: Endogamia, goiabeira, REML/BLUP.

Introduction

Brazil stands out globally as the third largest guava producer (FAOSTATS, 2021), with a total yield area of 20, 294 thousand ha, which generates an average fruit yield of 26, 402 kg ha^{-1} year^{-1} (IBGE, 2021) Among all states, Rio de Janeiro ranks sixth in planted area, with an average yield of 25, 320 kg ha^{-1} year^{-1} (IBGE, 2021). A number of available cultivars have been used by farmers, including Paluma, Rica, Sassaoka, Pedro Sato, Cortibel, and Século XXI (POMMER et al., 2006; SANTOS et al., 2011). None of them, though, has been developed, tested, and recommended for Rio de Janeiro State. Hence, there is a need to develop new cultivars to meet the conditions of the consumer market and the farmer, enabling the diversification of guava cultivars in the field with different phenotypes, especially for different types of fruit, weight, size, pulp color, pulp yield, total soluble solids, pH and resistance to pests and diseases (AMBRÓSIO et al., 2021).

In this respect, the *Universidade Estadual do Norte Fluminense Darcy Ribeiro* (UENF) has been developing the genetic breeding program for guava trees over 14 years, with promising results for the breeding of the crop under examination. There is, however, a clear need for continuity of the program already in progress, which seeks to select superior individuals or to support the generation of genotypes better adapted to crop conditions of the several Brazilian yielding areas and with characteristics demanded by the consumer market (QUINTAL et at., 2017; AMBRÓSIO et al., 2021).

Accordingly, intraspecific crosses were performed in previous stages of guava breeding program of UENF to obtain segregating populations with high genetic variability (PESSANHA et al., 2011). Despite this, the success of the selection does not depend solely on genetic variability, but rather on the ability of maintaining and fixing the desirable agronomic traits in the genotypes under consideration. As such, achieving inbred families proves to be effective in this regard, in which it becomes possible the allele fixation of the agronomic traits of interest and the obtaining of plants with high yield, earliness, and homogeneity within the families, thereby providing selection success with the generation progress of guava trees under inbreeding (KRAUSE et al., 2017; KRAUSE et al., 2021; AMBRÓSIO et al., 2021).

Therefore, making more precise estimates of the genetic superiority of individuals is particularly important during the plant selection process (NEGREIROS et al., 2008). In this respect, the mixed model methodology (REML/BLUP) has demonstrated a great interest in genetic breeding of plants, as proposed in recent years (VIANA; RESENDE, 2014; RESENDE et al., 2014; RESENDE, 2016). Thereby, the individual evaluation of genotypes, the estimate of the components of variance (Restricted maximum likelihood-REML), and the prediction of individual genetic values (Best linear unbiased prediction-BLUP) are possible by means of mixed models, thus maximizing the collection of additive variances, which may enhance the required genetic gains, resulting in a more accurate selection process. In this scenario, mixed models have been applied in many perennial species to predict more accurate genetic values and estimate the repeatability of the variables, which makes it possible to estimate the minimum number of evaluations needed (FERREIRA et al., 2012; PEREIRA et al., 2013; HARDNER et al., 2016; QUINTAL et al., 2017; PAIVA et al., 2019).

Thus, the REML/BLUP analysis allows considering correlated errors within locations, as well as stability and adaptability in selecting superior genotypes, in addition to providing genetic values already discounted for instability and can be applied to any number of environments. In addition, it generates results in the unit or scale of the evaluated character, which can be directly interpreted as genetic values, which other methods do not allow. Thus, the simultaneous selection for productivity, stability and adaptability, in the context of mixed models, can be performed by the method of harmonic mean of the relative performance of genotypic predicted value (HMRPGV) (SILVA et al., 2011; ROSADO et al., 2012). In this scenario, the simultaneous selection for productivity, stability and adaptability, in the context of mixed models (REML/BLUP) has been used in several crops: cowpea (SANTOS et al., 2016); grugru palm (ROSADO et. al., 2019) maize (KRAUSE et al., 2020) and safflower (NETO et al., 2021).

Furthermore, repeated measurements are made on the same individual, especially on perennial plants. Hence, multiple crop evaluations are required to select the most promising genotypes. In this manner, the analysis of observations over many harvest years permits an estimate of the coefficient of repeatability. By this estimate, it is possible to forecast how many evaluations will be needed for selection with greater reliability. Thus, estimated heritability, individual repeatability, and genotypic correlation parameters are essential during harvests for the breeder to select superior individuals (MARÇAL et al., 2016). In some studies, with perennial crops in this scenario, the authors found that to select promising genotypes with greater efficiency, it is more convenient to increase the number of years and places evaluated than the number of progenies (DANNER et al., 2010; BRUNA et al., 2012; CARGNIN, 2016; IMAI et al., 2016; RODRIGUES et al., 2017; QUINTAL et al., 2017).

Considering the above, this study intended to estimate the coefficient of repeatability for traits relating to yield, so as to infer what is the minimum number of evaluations required to identify superior genotypes; to verify adaptability and stability; to predict genetic gains; and to select the best families and individuals in S_1 progenies of *Psidium guajava.*

Material and Methods

Location, design, and population evaluated

The experiment was conducted at the experimental station of the Ilha Barra do Pomba, in the municipality of Itaocara, Rio de Janeiro State [(Northwest Region) (21º40’ south latitude, 42º04’ west longitude, and 76 m altitude)]. The soil in the experimental area is classified as Red Yellow Argisol (EMBRAPA, 2006). It was used an experimental randomized block design, with 18 inbred families, three replicates, and ten plants per plot. The 18 families evaluated originated from populations developed by Pessanha et al. (2011) with a pre-breeding work, which resulted in 17 segregating families.

This segregating population with wide genetic variability was subsequently evaluated and selected using REML/BLUP by Quintal et al. (2017), in which the most productive progenies were chosen and self-fertilized to originate the 18 inbred families that compose this experiment. Seeds from the fruits of self-fertilization were sown in tubes (three seeds per tube) and kept in a greenhouse. In July 2014, the seedlings were planted at a spacing of 5 m between rows and 1.5 m between plants. Liming and planting and top-dressing fertilization were done in accordance with the soil analysis, in line with the recommendations of Costa and Costa (2003). Drip irrigation was employed. After planting the 540 plants that are part of the experiment, it was verified they had yielded in all harvests (2016, 2017, 2018).

Traits evaluated

Observations were conducted at individual level for each of the three harvests, in which the number of fruits per plant (NF), fruit weight (FW), and total yield (TY) were evaluated. The NF was counted from the beginning of fructification until the end of the harvesting period in every individual. The FW was calculated by sampling five fruits per plant on an analytical balance, giving results in grams. The TY of individuals was calculated by multiplying the total number of fruits and fruit weight and expressed in grams (CAMPOS et al., 2013).

Analysis via mixed models

For those traits, then, the analysis of deviance, the estimate of genetic parameters, and the prediction of gains, as well as the analysis of repeatability, adaptability, and stability of genotypes were conducted. In accordance with the model described by Viana and Resende (2014), the analysis of deviance was obtained as follows:

$$D = -2ln(L)$$

$$ln(L) = -1/2ln|X'V^{-1}X| - 1/2ln|V| - 1/2(y-Xm)`V^{-1}(y-Xm),$$

in which ln(L) is the maximum point of the restricted maximum likelihood logarithm function (REML); y is the vector of the variable analyzed; m is the vector of the observation effects, considered as fixed; X is the incidence matrix of the fixed effects; and V is the variance-covariance matrix of y.

The statistical LRT (likelihood ratio test) was used for testing the meaning of the effects as shown below:

$$LRT: |-2ln(L_{we}) + 2ln(L_{mf})|,$$

in which L_{we} is the maximum point of the maximum likelihood function for the reduced model (without the effects) and L_{mf} is the maximum point of the maximum likelihood function for the complete model. Variables were analyzed by the Selegen-REML/BLUP software (Resende, 2016) utilized for obtaining the components of variance by means of the restricted maximum likelihood (REML), and the individual genotypic values using the best linear unbiased predictor (BLUP).

For the REML/BLUP approach, adaptability, and stability, the model 62 of the Selegen-REML/BLUP computer program was adopted, which evaluated one location and various harvests (Resende, 2016). The prediction of genetic values was performed using the mixed model approach, and the model was adopted according to the equation described:

$$y = Xm + Za + Wp + Qi + Ts + e,$$

in which y is the vector of data; m is the vector of measurement-replicate combination effects (considered as fixed) added to the overall mean; a is the vector of the individual additive genetic effects (considered as random); p is the vector of plot effects (random); i is the vector of the effects of genotypes x measurements interaction (random); s is the vector of permanent effects (random); and e is the vector of errors or residues (random); X is the incidence matrix of fixed effects; Z is the incidence matrix of individual genetic effects; W is the incidence matrix of plot effects; Q is the incidence matrix of the effects of genotype x measurement interaction; and T is the incidence matrix of permanent effects. Vector m comprises all measurements in all replicates and simultaneously adjusts them for replicate, measurement effects, and replicates x measurements interaction.

The mixed model equations were given by:

$$\begin{bmatrix} X'X & X'Z & X'W & X'Q & X'T \\ Z'X & Z'Z + A^{-1}\lambda_1 & Z'W & Z'Q & Z'T \\ W'X & W'Z & W'W + I\lambda_2 & W'Q & W'T \\ Q'X & Q'Z & Q'W & Q'Q + I\lambda_3 & Q'T \\ T'X & T'Z & T'W & T'Q & T'T + I\lambda_4 \end{bmatrix} \begin{bmatrix} \hat{m} \\ \hat{a} \\ \hat{p} \\ \hat{\imath} \\ \hat{s} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \\ W'y \\ Q'y \\ T'y \end{bmatrix}$$

in which:

$$h^2 = \frac{\sigma_g^2}{\sigma_a^2 + \sigma_p^2 + \sigma_i^2 + \sigma_s^2 + \sigma_e^2},$$

individual heritability;

$$p = \frac{\sigma_c^2}{\sigma_a^2 + \sigma_p^2 + \sigma_i^2 + \sigma_s^2 + \sigma_e^2},$$

coefficient of determination of plot effects;

$$i = \frac{\sigma_i^2}{\sigma_a^2 + \sigma_p^2 + \sigma_i^2 + \sigma_s^2 + \sigma_e^2},$$

coefficient of determination of effects of genotype x measurement interaction;

$$s = \frac{\sigma_s^2}{\sigma_a^2 + \sigma_p^2 + \sigma_i^2 + \sigma_s^2 + \sigma_e^2},$$

coefficient of determination of permanent effects; and

A, additive relationship coefficient matrix among individuals.

The components of the variance to calculate the coefficient of repeatability were estimated according to the procedure of restricted maximum likelihood (REML), being repeatability at plot level (ρ) estimated by:

$$\rho = \frac{V_g + V_{perm}}{Vp}$$

$$\rho = \frac{\sigma_a^2 + \sigma_p^2 + \sigma_i^2 + \sigma_s^2}{\sigma_a^2 + \sigma_p^2 + \sigma_i^2 + \sigma_s^2 + \sigma_e^2}$$

in which V_g is the genetic variance among plants, V_{perm} is the permanent effects variance, and V_p is the phenotypic variance.

The other parameters were estimated as heritability in the broad sense at individual level (h_g^2), in other words, genotypic effects; coefficient of determination of permanent effects (c_{perm}^2); coefficient of determination of plot effects (c_{plot}^2); coefficient of determination of effects of genotype x harvest interaction (c_{gm}^2); genetic determination (R_2); and selective accuracy after various measurements.

Stability estimate was obtained by the HMGV (Harmonic Mean of Genetic Values) method given by the estimator:

$$HMGV = \frac{n}{\sum_{j=1}^{n}\left(\frac{1}{Vg_{ij}}\right)}$$

in which n is the number of environments or harvests ($n = 3$ harvests); i is the genotype evaluated; and $V_{g_{ij}}$ is the genotypic value i in environment j.

Adaptability was measured by RPGV values (relative performance of genotypic values), as the expression:

$$RPGV = \frac{1}{n} x \left(\frac{\sum_{j=1}^{n} Vg_{ij}}{M_j}\right)$$

in which M_j the mean of the variable analyzed (fruit mass, number of fruits, and guava yield) in the environment j.

By the HMRPGV (harmonic mean of relative performance of genotypic values) method, the selection of the best individuals within each progeny in which they distinguished themselves was carried out based on three aspects: selection based on the genetic value predicted, assuming the average performance in all harvests (with no interaction effect); selection based on the genetic value predicted, assuming the average performance in each harvest (with the effect of the average interaction) and without interaction effect; and simultaneous selection for yield, stability (HMGV), and adaptability (RPGV). This combined selection is determined by:

$$HMRPGV = \frac{{}^{n}/\left(\sum_{j=1}^{n} x\ 1\right)}{Vg_{ij}}$$

in which n is the number of environments or harvests (n = 3 harvests); and $V_{g_{ij}}$ is the value of genotype i in the environment j expressed as a proportion of the average in the said environment.

The Selegen software was employed for the REML/BLUP approach and for adaptability and stability (RESENDE, 2016). Families were ranked in line with the genotypic values found. On the basis of these values, it was applied the selection of the best families for each trait in the three-year evaluation.

RESULTS AND DISCUSSION

Analysis via mixed models

It was possible to see in the analysis of deviance that the effects of the genotypes were significant only for fruit weight (Table 1), which demonstrates variability among the genotypes evaluated, with possibilities of genetic gain by the selection of superior individuals for this trait. The low genetic variability shown for the other variables may be attributed to the high degree of relationship between and within inbred families, making the traits of the genotypes more homogeneous because of the first generation of self-fertilization performed in the population. For the variables number of fruits and total yield, there was a considerable difference of 1% for plot effect, pointing out significant genetic variability within the plot.

This result is due to the fact that these traits are highly affected by the environment, that is, a small environmental variation affects their behavior within the blocks (SOUZA et al., 2020). Therefore, the absence of significant effects for the source genotype variation between the traits evaluated denotes that selection between families will provide lower gains due to the low variability present between families. Significances for plot effects indicate significant genetic variability within the plot. In this way, it is not interesting to select between, but within, families (BORÉM; MIRANDA, 2017).

For all variables analyzed, though, the effects of genotype x measurement interaction were highly significant. This was because of the environmental effects that confirmed the genotype x measurement interaction to be significant. This may cause problems when selecting, given that little coincidence exists among the best genotypes in the harvests under evaluation. A further element of the different response of the genotypes in the different agricultural years (measurement/harvest) was the important increase in the number of fruits and yield from one harvest to the other.

To avoid these factors, it is required to employ a model that considers this genotype x harvest interaction, accurately recommending the promising genotypes. Hence, the major advantages of using the REML/BLUP methodology in this study were the com-

Table 1. Analysis of deviance for fruit weight, number of fruits, and total yield in inbred families of *P. guajava*, evaluated in four harvests (*Universidade Estadual do Norte Fluminense Darcy Ribeiro*, municipality of Campos dos Goytacazes, Rio de Janeiro State, 2022).

Effect	FW(g)		NF		TY (kg)	
	Dev	LRT	Dev	LRT	Dev	LRT
Genotype	4379.91	**7.14****	4146.70	0.61ns	9899.71	0.67ns
Plot	4372.92	0.15ns	4156.38	**10.29****	9910.20	**11.16****
Genotype × Measurement	4394.46	**21.69****	4151.66	**5.57***	9908.16	**8.92****
Permanent environment	4593.64	**220.87****	4367.64	**221.55****	10130.06	**230.82****
Complete model	4372.77		4146.09		9899.24	

NF: number of fruits; FW: fruit weight; TY: total yield * significant at 5%, ** significant at 1%. ns = not significant.

parison of individuals or varieties regarding time (generations, years) and space (locations, blocks); simultaneous correction for environmental effects, estimate of components of variance, and prediction of genetic values; dealing with complex data structures (repeated measurements, different years, locations, and designs); implementation in unbalanced data; and non-orthogonal designs (VIANA; RESENDE, 2014).

It can be seen in the results of the components of variance that the phenotypic variance was divided into genetic variance, genotype x measurement interaction variance, permanent effect variance, and temporary residual variance. The contribution of genetic variance was low for the variables fruit weight (384.18), number of fruits (52.91), and total yield (1515625.22), with predominance of environmental effects, highlighting the permanent effects, evidencing that the traits were greatly influenced by environmental conditions, proven by low heritability (Table 2). As Cruz et al. (2012) points out, the lower the genetic variance and the greater the environmental effect, the lower the heritability of the trait, which can be proved by the results obtained. The expression of these traits is complex within this scenario, given the large number of segregating locus controlling the trait, while suffering the influence of environmental effects. Consequently, understanding the heritability and the determining components of their variation are vital in the study of quantitative traits (FALCONER, 1987; SOUZA et al., 2017).

It is worth noting that in relation to the reproduction of the guava tree, this culture has a rate (60%) of self-fertilization, thus being higher than that of cross-fertilization. In this way, guava is classified as an autogamous-allogamous mixed reproduction system (MEDINA, 1988). Therefore, obtaining partially endogamous families is a feasible possibility for the formation of superior populations. When carrying out the first (S_1) generation of self-fertilization, it causes an increase in homozygosity (50%) and a decrease (50%) in heterozygosity in the offspring, which is a viable alternative for obtaining homogeneous fruits in commercial guava orchards, with consequent allelic fixation (FALCONER; MACKAY, 1996).

Table 2. Components of variance obtained by the individual REML for fruit weight (FW), number of fruits per plant (NF), and total yield (TY) of the fruits in inbred families of *P. guajava* evaluated in three harvests (*Universidade Estadual do Norte Fluminense Darcy Ribeiro*, municipality of Campos dos Goytacazes, Rio de Janeiro State, 2022).

Components of Variance	FW (g)	NF	TY (kg)
V_g	384.18	52.91	1515625.22
V_{plot}	28.95	159.14	5568714.40
V_{gm}	62.28	20.84	878287.64
V_{perm}	883.48	597.55	20692330.46
V_e	462.29	305.99	10096552.55
V_p	1821.19	1136.45	38751510.29
h^2_g	0.21	0.05	0.04
c^2_{plot}	0.015	0.14	0.14
c^2_{gm}	0.03	0.01	0.02
c^2_{perm}	0.48	0.52	0.53
r	0.71	0.71	0.72
r_{gmsm}	0.86	0.71	0.63
Overall mean	**186.21**	**58.40**	**10519.95**

V_g: genotypic variance among progenies (1/4 of additive variation); V_{plot}: environmental variance among plots; V_{gm}: genotype x measurement interaction variance; V_{perm}: permanent effect variance; V_e: temporary residual variance; V_p: individual phenotypic variance; h^2_g: heritability among individual progeny; r: individual repeatability; c^2_{plot}: coefficient of determination of plot effects; c^2_{gm}: coefficient of determination of the effects of genotype x measurement interaction; c^2_{perm}: coefficient of determination of permanent effects; r_{gmsm}: genotypic correlation by measurements; overall mean of the experiment.

The individual heritability obtained for the variables studied was 0.21 for fruit weight, 0.05 for number of fruits, and 0.04 for total yield (Table 2). For Resende (2009), heritability is classified as low ($h < 0.15$), median ($0.15 < h < 0.50$), and high magnitude ($h > 0.50$). Considering this, the values found herein are considered as low and median magnitude for individual heritability, thereby validating the results of other perennial crops, like guarana (0.06%) (ATROCH et al., 2004) and coffee (0.07%) (PEREIRA et al., 2013). But it should be noted that values of small and medium magnitude for heritability are expected, mostly because it is a quantitative trait in perennial species, which are susceptible to climate variations along the years. Within this context, states that individual heritabilities of low magnitude are common for quantitative traits and, moreover, the use of procedures for selection via mixed models is worthwhile, considering that even with traits of low heritability, favorable genetic gains are predicted, and genotypes have potential for selection (RESENDE, 2009; VIANA; RESENDE 2014).

In addition to the high influence of the environment on the expression of traits related to production, the low magnitude of individual heritability may also be associated with the narrow genetic base of the population used, as these are inbred families that were obtained through families of full siblings (QUINTAL et al., 2017; AMBRÓSIO et al., 2021).

The coefficient of repeatability based on the three measurements showed high magnitude, with values of (0.71), (0.71), and (0.72) for fruit weight, number of fruits, and total yield, respectively (Table 2). According to Resende (2009) values of repeatability equal to or less than 0.30 are considered low, and median values between 0.30 and 0.60 and above 0.60 are considered high. Accordingly, the high values of estimate of the coefficient of repeatability with respect to the traits studied suggest that it is possible to predict the real value of individuals with a relatively small number of measurements pointing out that there will be little gain in accuracy with the increase in the number of measurements (FALCONER, 1987; CORNACCHIA et al., 1995; (SANCHÉZ et al., 2017). Yet, when repeatability is low, a considerable number of replicates are required so that a satisfactory determination value is met. As a result, knowledge of the coefficient of repeatability makes it possible for the evaluation phase to be executed efficiently, but with a minimum amount of time and workforce.

The values relating to the estimate of the genetic coefficient of determination, accuracy, and efficiency gain of selection, which would be obtained by performing up to ten measurements in each individual, indicated that it is possible to predict the efficiency of m measurements in situations in which only one measurement is carried out (Table 3). Results show that there was little increase in genetic determination from one harvest to the other because the repeatability value is of high magnitude for three traits, causing small values of increase in accuracy and efficiency among the measurements.

Table 3. Efficiency of the repeated measurements predicted by BLUP for fruit weight, number of fruits, and total yield in inbred guava tree families evaluated in three harvests. (*Universidade Estadual do Norte Fluminense Darcy Ribeiro*, municipality of Campos dos Goytacazes, Rio de Janeiro State, 2022).

m	Fruit weight (g)				Number of fruits				Total yield (kg)			
	h^2_{avg}	R^2	A_{cm}	Ef	h^2_{avg}	R^2	A_{cm}	Ef	h^2_{avg}	R^2	A_{cm}	Ef
1	0.21	0.71	0.45	1.00	0.05	0.71	0.22	1.00	0.04	0.72	0.20	1.00
2	0.24	0.83	0.49	1.08	0.05	0.83	0.24	1.08	0.04	0.83	0.21	1.07
3	**0.26**	**0.88**	**0.51**	**1.11**	**0.06**	**0.88**	**0.24**	**1.11**	**0.04**	**0.88**	**0.22**	**1.10**
4	0.26	0.90	0.51	1.13	0.06	0.91	0.25	1.13	0.05	0.91	0.22	1.12
5	0.27	0.92	0.52	1.14	0.06	0.92	0.25	1.14	0.05	0.92	0.22	1.13
6	0.27	0.93	0.52	1.14	0.06	0.93	0.25	1.14	0.05	0.93	0.22	1.14
7	0.27	0.94	0.52	1.15	0.07	0.94	0.25	1.15	0.05	0.94	0.22	1.14
8	0.28	0.95	0.53	1.15	0.07	0.95	0.25	1.15	0.05	0.95	0.23	1.15
9	0.28	0.95	0.53	1.16	0.07	0.96	0.25	1.16	0.05	0.95	0.23	1.15
10	0.28	0.96	0.53	1.16	0.07	0.96	0.26	1.16	0.05	0.96	0.23	1.15

Coefficient of determination of repeatability (R^2), accuracy of permanent phenotypic values based on m years of evaluation (A_{cm}), and efficiency of the m evaluations in comparison with the situation in which only one evaluation is conducted (Ef).

The evaluation of three harvests shows the value of genetic determination of 0.88 for both traits. Consequently, the use of three measurements is adequate to estimate the real value of the individuals, with reliability above 80%. Viana and Resende (2014) highlight those values of coefficient of determination above 80% can be considered appropriate when selecting a group of individuals. This result is of great relevance for the breeding of this population. as it saves time and resources for the selection of superior individuals. On the other hand, in the study conducted by Quintal et al. (2017) with a guava tree segregating population, the authors consider the values of the coefficients of repeatability for FW (0.25), NF (0.14), and YIE (0.29) as low, suggesting that, for the population under study, the three harvests were not enough to select the best individuals with the highest accuracy. For variables FW and YIE, from five measurements, it would be possible to get more precise estimates of genetic coefficient of determination and accuracy for the selection of genotypes with greater reliability (QUINTAL et al., 2017).

In this regard, one purpose of the coefficient of repeatability is exactly to determine how many phenotypic observations should be performed in each individual to optimize the selection of genotypes, reducing cost and workforce (CRUZ et al., 2012). Considering this, the traits evaluated by this study presented high regularity in the measurements and, for being highly repeatable, they optimized the phenotyping processes, requiring lower cost in workforce and time. Thus, knowing the coefficient of repeatability of traits of interest enables the evaluation of the amount of time spent to select genetically superior individuals with the accuracy sought by the researcher (BRUNA et al., 2012). Therefore, the repeatability coefficient serves exactly to measure the high or low capacity that the plants have to repeat the expression of the character. Thus, the use of the repeatability coefficient in traits related to productivity, associated with vegetative propagation, is an efficient breeding strategy (RESENDE, 2016).

In this sense, the low estimates of heritability obtained may have contributed to low and median selective accuracy values for number of fruit (0.24), total yield (0.22), and fruit weight (0.51). They were, however, effective in directing the minimum number of evaluations that should be performed on the population. Based on the classification of Resende and Duarte (2007), the values of accuracy in individual selection ranged from low to moderate. And in line with Sturion and Resende (2004), and Resende and Duarte (2007) number of factors influence the value of selective accuracy; among them, heritability, repeatability of trait, quality of information, and procedures used in the estimate of genetic values can be pointed out. In a general way, the use of three measurements enabled an increase in selective efficiency (Ef) of 10% for total yield and 11% for fruit weight and number of fruits. Having the values of Ef, the selection of superior individuals can be made with three measurements in traits with high repeatability, achieving an ideal value of genetic determination.

For the most promising inbred families, the predicted genetic gains were satisfactory for fruit weight (31% to 2%), total yield (9% to 0.23%) and number of fruits (6% to 0.33%). The seven best families selected for the traits total yield and number of fruits were coincident, particularly 1, 4, 6, 12, 8, and 2. The same did not occur, however, with the variable fruit weight, since only families 1, 6, 4 and 12 were selected for both variables (Table 4).

Of the total number of individuals evaluated, 100% presented new means with a higher performance than the general mean for both variables. This would suggest that there is great probability of finding promising new genotypes among and within the best inbred families. The genetic gains estimated by BLUP are equivalent to the mean of the predicted genetic values for the selected genotypes, and the new mean refers to the general mean of the trait added to the gain, resulting in an increase in the mean of the population for that trait (SANTOS et al., 2015).

Table 4: Order, predicted gain, and new mean for fruit weight, number of fruits, and total yield of the best inbred families of *P. guajava*, evaluated in three harvests (*Universidade Estadual do Norte Fluminense Darcy Ribeiro*, municipality of Campos dos Goytacazes, Rio de Janeiro State, 2022).

Ord.	Fruit weight (g)			Number of fruits			Total yield (kg)		
	Family	Mean	Gain (%)	Family	Mean	Gain (%)	Family	Mean	Gain (%)
1	1	217.65	31.44	4	65.28	6.88	1	11506.40	9.38
2	10	212.60	26.38	8	64.23	5.83	4	11438.12	8.73
2	6	210.17	23.95	12	63.17	4.77	6	11322.32	7.63
4	7	204.67	18.45	1	62.50	4.10	12	11217.06	6.63
5	11	200.48	14.27	6	61.85	3.45	8	11115.29	5.66
6	12	197.57	11.36	2	61.25	2.85	2	10999.48	4.56
7	4	194.84	8.62	17	60.79	2.39	17	10901.45	3.63
8	17	192.75	6.54	9	60.36	1.95	7	10806.88	2.73
9	2	191.10	4.8	7	59.82	1.42	9	10723.19	1.93
10	9	188.88	2.66	11	59.05	0.65	10	10624.60	0.99
11	8	186.21	1.33	10	58.40	0.33	11	10519.95	0.23

It should be noted, therefore, that some families that presented the best values for fruit weight differed from the most promising regarding number of fruits and total yield. This is because plants with a greater fruit mass generally produce less fruit and thus lower yield. That the increase in the average fruit weight is connected to the number of fruits yielded per plant, so a greater quantity of fruits in the plant may induce it to yield smaller fruits in weight and size because the available reserves would be used to fill more fruits, limiting the size achieved by each one of them. However, the selection of different progenies for fruit mass is not a problem for this population, because the entire population already has an average mass (186 grams) higher than the 'Paluma' cultivar (140 grams) (GONZAGA NETO et al., 2001; CARDOSO et al., 2011).

Regarding the difference between the highest and the lowest new mean of the genotypes in the ranking, a low amplitude is observed for all traits, which is due to the narrowing of the means predicted caused by the REML/BLUP, which makes the differences among the genotypes smaller and result more from genetic than environmental effects (VIANA; RESENDE, 2014; RESENDE, 2016).

Therefore, it is worth mentioning that through these results it is possible to verify, among families and within them, the presence of promising genotypes for traits associated with production, that is, prioritizing gains in traits that obtained the highest values of genetic variance, heritability and consequently great accuracy for selecting individuals with precision and obtaining greater gains (AMBRÓSIO et al., 2021).

With regard to the analysis of phenotypic stability and adaptability, there is coincidence in the order of the most yielded families by the criteria of adaptability (RPGV), stability (HMGV), and both simultaneously (HMRPGV) (Table 5). As Pinto Júnior et al. (2006) and Resende (2009) state, HMGV, RPGV, and HMRPGV methods are concordant in the order of genetic materials, and the utilization of these attributes or selection criteria leads to a refinement in the selection, in the conclusion of reliable predictions about genetic values and, simultaneously, for yield, stability, and adaptability. The values of HMRPGV show the mean superiority of the genotype over the mean of the environment where it is grown, that is, in accordance with Resende (2009), it is an inference on the expected yield. These estimates of HMRPGV can be used when considering planting in several locations with varying patterns of G X A interaction.

For number of fruits and total yield, the first families selected (1, 4, 6, 8, and 12) presented adaptability, stability, and high yield, which means that these attributes predominate in the various harvests. By contrast, some families that distinguished themselves for number of fruit and total yield differed from the most promising ones in terms of fruit weight (10, 7, and 11). Families 1, 6, 4 and 12, however, were superior to three traits evaluated, demonstrating their high yield potential.

Table 5. Analysis of phenotypic stability and adaptability in inbred families of *P. Guajava* (*Universidade Estadual do Norte Fluminense Darcy Ribeiro*, municipality of Campos dos Goytacazes, Rio de Janeiro State, 2022).

Fruit weight (g)

Orderm	Family	HMGV	RPGV	RPGV*MG	HMRPGV	HMRPGV*MGG
1	1	219.13	1.18	219.69	1.17	219.54
2	10	208.41	1.17	208.96	1.12	208.86
3	6	205.90	1.10	208.96	1.10	206.44
4	7	186.58	1.10	187.88	1.00	187.61
5	11	182.94	0.98	183.58	0.98	183.58
6	12	180.72	0.97	182.32	0.97	181.86
7	4	177.50	0.95	178.05	0.95	178.04
8	17	176.87	0.95	177.63	0.95	177.60
9	2	176.09	0.95	177.14	0.95	176.99
10	9	167.62	0.95	168.07	0.90	168.03
11	8	158.08	0.85	158.52	0.84	158.21

Number of fruits

Order	Family	HMGV	RPGV	RPGV *MG	HMRPGV	HMRPGV*MGG
1	4	51.82	1.11	65.19	1.11	65.08
2	8	49.98	1.07	62.87	1.07	62.76
3	12	49.98	1.05	61.47	1.05	61.46
4	1	49.94	1.04	61.09	1.04	61.08
5	6	48.07	1.01	59.26	1.01	59.26
6	17	47.41	0.99	58.13	0.99	58.13
7	2	47.01	0.99	58.10	0.99	58.10
8	9	46.85	0.98	57.38	0.98	57.38
9	7	44.96	0.94	55.22	0.94	55.22
10	10	42.92	0.88	51.86	0.88	51.77
11	11	42.57	0.88	51.79	0.88	51.76

Total yield (kg)

Order	Family	HMGV	RPGV	RPGV *MG	HMRPGV	HMRPGV*MGG
1	1	9563.10	1.09	11556.50	1.09	11537.13
2	4	9446.10	1.07	11311.08	1.07	11275.26
3	6	9274.02	1.05	11078.78	1.05	11066.46
4	12	9194.68	1.05	11078.26	1.05	11049.70
5	8	8820.22	1.00	10581.96	1.00	10532.26
6	2	8788.13	0.98	10410.17	0.98	10408.84
7	17	8666.10	0.98	10363.53	0.98	10355.99
8	7	8629.18	0.96	10145.51	0.96	10134.07
9	9	8478.94	0.95	10015.09	0.95	10013.09
10	10	8336.89	0.92	9736.63	0.92	9719.11
11	11	8101.59	0.89	9441.89	0.89	9419.68

HMGV: Harmonic Mean of Genetic Values; HMRPGV: Harmonic Mean of Relative Performance of Genotypic Values; HMRPGV*MG: Harmonic Mean of Relative Performance of Genotypic Values related of genotypic values; RPGV*MG: Relative Performance of Genotypic Values multiplied; RPGV: Relative Performance of Genotypic Values; RPGV*MG: Relative Performance of Genotypic Values multiplied by the overall mean.

These results point out that the most yielded families are also those with the most stable and adaptable response, particularly when the first five families are selected. In this way, the characterization of inbred families regarding their relative patterns of adaptability and stability after the selection process for yield capacity is truly relevant for selecting inbred families to be used to continue the breeding program. On the basis of the adaptability, stability, and yield patterns, it could be identified the superior S_1 families, which were self-fertilized to obtain the S_2 families.

Conclusion

High values of repeatability prove that the performance of genotypes is constant among measurements, suggesting the need for only three evaluations for the selection of superior genotypes with greater reliability.

Families 1, 4, 6, 12, and 8 are indicated as the best ones as the genotypes were promising for number of fruits and total yield.

There was agreement in choosing families 1, 4, 6 and 12 as the most yielded, adaptable, and stable for the traits fruit weight, number of fruits, and total yield.

Hence, the findings suggest that the population under study is promising, and the families selected have potential to be used as parents to obtain new inbred families, leading to the continuity of the breeding program.

Conflict of Interest

The authors declare no conflict of interest.

Availability of Data and Materials

The data that support the fndings of this study are available on request from the corresponding author.

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References

AMBRÓSIO, M.V.A.P.; RIBEIRO, R.M.; PREISIGKE, S.C.; CAVALCANTE, N.R.; SILVA, F.A. da; TORRES, G.X.; SOUSA, C.M.B. Genotypic superiority of Psidium Guajava S1 families using mixed modeling for truncated and simultaneous selection. **Scientia Agricola**, Piracicaba, v.78, p.1-9, 2021.

ATROCH, A.L.; RESENDE, M.; NASCIMENTO FILHO, F.J. Seleção clonal em guaranazeiro via metodologia de modelos lineares mistos (REML/BLUP). **Revista de Ciências Agrárias**, Belém, v.41, p.193-201, 2004.

BRUNA, D. E.; MORETO, A.L.; DALBÓ, M. A. 2012. Uso do coeficiente de repetibilidade na seleção de clones de pessegueiro para o litoral sul de Santa Catarina. **Revista Brasileira de Fruticultura**, Jaboticabal, v.34, n.1, p.206-15, 2012.

BORÉM, A.; MIRANDA, G.V.; FRITSCHE-NETO, R. **Melhoramento de plantas.** 7.ed. Viçosa: Editora UFV, 2017. 543p.

CAMPOS, B. M.; VIANA, A. P.; QUINTAL, S.S.R.; GONÇALVES, L.S A.; PESSANHA, P.G.O. Quantificação da divergência genética entre acessos de goibeira por meio da estratégia Ward-MLM. **Revista Brasileira de Fruticultura**, Jaboticabal, v.35, p.571-8, 2013.

CARDOSO, E.A.; COSTA, J. T.A.; SOARES, I.S.; SILVA, R.M.; MARACAJÁ, P.B. Produtividade da goiabeira 'Paluma' em função da adubação mineral. **Revista Verde de Agroecologia e Desenvolvimento Sustentável**, Pombal, v.6, p.149-53, 2011.

CARGNIN, A. Repetibilidade e número de colheita de características para seleção de clones de variedades viníferas. **Ciência Rural**, Santa Maria, v.46, n.2, p.221-6, 2016.

COSTA, A.F.S.; COSTA, A.N. **Tecnologias para produção de goiab**a. Vitória: Instituto Capixaba de Pesquisa e extensão Rural, 2003.

CORNACCHIA, G.; CRUZ, C.D.; LOBO, P.R.; PIRES, I.E. Estimativas do coeficiente de repetibilidade para características fenotípicas de procedências de Pinus tecunumanii (Schw.) Eguiluz, Perry e Pinus caribaea var. hondurensis Barret, Golfari. **Revista Árvore**, Viçosa, MG, v.19, n. 3, p.333-45, 1995.

CRUZ, C.D.; REGAZZI A.J.; CARNEIRO, P.C.S. **Modelos biométricos aplicados ao melhoramento genético**. 4.ed. Editora UFV, Viçosa, 2012. v.1, 514 p.

DANNER, M.A.; RASEIRA, M.C.B.; SASSO, S.A.Z.; SCARIOT, I.C.; SCARIOT, S. Repetibilidade de caracteres de fruto em araçazeiro e pitangueira. **Ciência Rural**, Santa Maria, v.40, n. 10, p.2086-91, 2010.

EMBRAPA. **Sistema brasileiro de classificação de solos**. 2.ed. Rio de Janeiro: Centro Nacional de Pesquisa do Solo, 2006. 306p.

FALCONER, D.S. **Introdução a genética quantitativa**. Viçosa: UFV, 1987. p. 279.

FALCONER, D.S.; MACKAY, T.F.C **Introduction to quantitative genetics**. 4.ed. Edinburgh: Longman Group Limited, 1996. 464 p.

FAOSTAT. **Agriculture organization of the United Nations.** Rome: FAO Retrieved, 2021. Disponível em: *http://faostat3.fao.org/faostatgateway/go/to/download/Q/QC/S*. Acesso 19 jan. 2021.

FERREIRA, F.M.; NEVES, L.G.; BRUCKNER, C.H.; VIANA, A.P.; CRUZ, C.D.; BARELLI, M.A.A. Formação de supercaracteres para seleção de famílias de maracujazeiro amarelo. **Acta Scientiarum. Agronomy**, Maringá, v.32, n.2, p.247-54, 2012.

GONZAGA NETO, L.; SOARES, J.M.; TEIXEIRA, A.H.C.; MOURA, M.S.B. **Goiaba**: produção: aspectos técnicos. Petrolina: Embrapa Semi-Árido; Brasília: Embrapa Informação Tecnológica, 2001, p.72 (Frutas do Brasil, 17).

HARDNER, C. M.; HEALEY, A. L.; DOWNES, G.; HERBERLING, M.; GORE, P.L. Improving prediction accuracy and selection of open-pollinated seed-lots in Eucalyptus dunnii Maiden using a multivariate mixed model approach. **Annals of Forest Science**, Paris, v.73, n.4, p.1035-46, 2016.

IMAI, A.; KUNIGA, T.; YOSHIOKA, T.; NONAKA, K.; MITANI, N.; FUKAMACHI, H.; HAYASHI, T. Evaluation of the best linear unbiased prediction method for breeding values of fruit-quality traits in citrus. **Tree Genetics & Genomes**, Heidelberg, v.12, n. 6, p.119, 2016.

IBGE - Instituto Brasileiro de Geografia e Estatística. **Lavoura permanente e temporária**. Rio de Janeiro, 2021. Disponível em: *http://www.sidra.ibge.gov.br/bda/tabela/listabl.asp?z=t&o=11&i=P&c=1181*. Acesso 28 dez. 2021.

KRAUSE, W.; CAVALCANTE, N.R.; VIANA, A.P.; AMBROSIO, M.; SANTOS, E.A.; VIERA, H.D. Genetic variability in inbred guava families mediated by agronomic traits. **Functional Plant Breeding Journal**, v.3, n.5, p.61, 2021.

KRAUSE, M.D.; DIAS, K.O.G.; SANTOS, J.P.R; OLIVEIRA, A.A.; GUIMARÃES, L.J.M.; PASTINA, M.M.; MARGARIDO, G.R.A.; GARCIA, A.A.F.Aumentando a capacidade preditiva de híbridos de milho tropical via interação genótipo por ambiente sob modelos multivariados GBLUP. **Crop Science,** New York, v.60, p.3049-65, 2020.

KRAUSE, W.; VIANA, A.P.; CAVALCANTE, N.R.; AMBRÓSIO, M.; SANTOS, E.A.; VIEIRA, H.D. Digital phenotyping for quantification of genetic diversity in inbred guava (Psidium guajava) families. **Genetics and Molecular Research**, Ribeirão Preto, v.16, p.1-11, 2017.

MARÇAL, T.S.; GUILHEN, J.H.S.; OLIVEIRA, W.B.S.; FERREIRA, M.F.S.; RESENDE, M.D.V.; FERREIRA, A. Repeatability of biometric characteristics of Juçara palm fruit Repetibilidade de características biométricas de frutos de palmito Juçara. **Bioscience Journal**, Uberlândia, v.32, p.50-60, 2016.

NEGREIROS, J.R.S.; SARAIVA, L.L.; OLIVEIRA, T.K.de; ÁLVARES, V.S.; RONCATTO, G. Estimativas de repetibilidade de caracteres de produção em laranjeiras-doces no Acre. **Pesquisa Agropecuária Brasileira,** Brasília, DF, v.43, n.12, p.1763-8, 2008.

NETO, S.S.O.; ZEFFA, D.M.; EBERTZ, O.F.; ZANOTTO, T. M. Genetic variability, adaptability and, stability of safflower genotypes developed for the Brazilian conditions by REML/BLUP. **Agronomy Journal**, Madison, v.113, n. 4, p.3100-9, 2021.

PAIVA, C.L. de.A.; VIANA, A.P.; SANTOS, E.A.; QUINTAL, S.S.R. Repetibility in guava: how many evaluations is necessary for selection the best guava tree?. **Functional Plant Breeding Journal**, Campos dos Goytacazes, v.1, p.51-60, 2019.

PEREIRA, T.B.; CARVALHO, J.P.F.; BOTELHO, C.E.; RESENDE, M.D.V.; REZENDE, J.C.; MENDES, A.N.G. Eficiência da seleção de progênies de café F4 pela metodologia de modelos mistos (REML/BLUP). **Bragantia**, Campinas, v.72, n.3, p.230-6, 2013.

PESSANHA, P.G. de O.; VIANA, A.P; AMARAL JÚNIOR, A.T.; SOUZA, R.M.DE.; TEIXEIRA, M.C.; PEREIRA, M.G. Avaliação da diversidade genética em acessos de Psidum ssp.via marcadores RAPD. **Revista Brasileira de Fruticultura**, Jaboticabal, v.33, p.129-36, 2011.

PINTO JÚNIOR, J.E.; STURION, J.A.; RESENDE, M.D.V.; RONZELLI JÚNIOR, P. Avaliação simultânea de produtividade, adaptabilidade e estabilidade genotípica de Eucalyptus grandis em distintos ambientes do estado de São Paulo. **Boletim de Pesquisa Florestal**, Colombo, v.53, p.79-108, 2006.

POMMER, C.V.K.R.N.; MURAKAMI, F. Watlington: goiaba no mundo. **O Agronômico**, Campinas, v.58, n.1, p.22-6, 2006.

QUINTAL, S.S.R.; VIANA, A. P.; CAMPOS, B.M.; VIVAS, M.; AMARAL JÚNIOR, A.T. DO. Analysis of structures of covariance and repeatability in guava segregant population. **Revista Caatinga**, Mossoró, v.30, n.4, p.85-9, 2017.

RESENDE, M.A.V.; FREITAS, J.A.DE.; LANZA, M.A.; RESENDE, M.D.v.DE., AZEVEDO, C.F. Divergência genética e índice de seleção via BLUP em acessos de algodoeiro para características tecnológicas da fibra. **Pesquisa Agropecuária Tropical**, Goiânia, v.44, p.334-40, 2014.

RESENDE, M.D.V. **Genética biométrica e estatística no melhoramento de plantas perenes.** Brasília: EMBRAPA, 2009. p.975.

RESENDE, M.D.V. Software Selegen-REML/BLUP: a useful tool for plant breeding. **Crop Breeding and Applied Biotechnology**, Londrina, v.16, p.330-9, 2016.

RESENDE, M.DV.; DUARTE, J.B. Precisão e controle de qualidade em experimentos de avaliação de cultivares. **Pesquisa Agropecuária Tropical**, Goiânia, v.37, p.182-94, 2007.

RODRIGUES, H.S.; CRUZ, C.D.; MACÊDO, J.L.V.; RESENDE, M.D.V., LOPES, R. BORÉM, A. Genetic variability and progeny selection of peach palm via mixed models (REML/BLUP). **Acta Scientiarum. Agronomy**, Maringá, v.39, n.2, p.165-73, 2017.

ROSADO, A.M.; ROSADO, T.B.; ALVES, A.A.; LAVIOLA, B.G.E.; BHERING, L.L. Seleção simultânea de clones de eucalipto de acordo com produtividade, estabilidade e adaptabilidade. **Pesquisa Agropecuária Brasileira**, Brasília, DF, v.47, p.964-71, 2012.

ROSADO, R.D.S.; ROSADO, T.B.; CRUZ, C.D.; FERRAZ, A.G.; CONCEIÇÃO, L.D.H.C.S. da; LAVIOLA, B.G. Parâmetros genéticos e seleção simultânea para adaptabilidade e estabilidade da macaúba. **Scientia Horticulturae**, New York, v.248, p.291-6, 2019.

SANCHÉZ, C.F.B.; ALVES, R.S.; GARCIA, A.D.P.; TEODORO, P.E.; PEIXOTO, L.A.; SILVA, L.A., BHERING, L.L.; RESENDE, M.D.V. Estimates of repeatability coefficients and the number of the optimum measure to select superior genotypes in Annona muricata L. **Genetics and Molecular Research**, Ribeirão Preto, v.16, p.1–8, 2017.

SANTOS, C.A.F.; CORRÊA, L.C.; COSTA, S.R. Genetic divergence among Psidium accessions based on biochemical and agronomic variables. **Crop Breeding and Applied Biotechnology**, Londrina, v.11, n.2, p.149-56, 2011.

SANTOS, E.A.; VIANA, A.P.; FREITAS, J.C.O.; RODRIGUES, D.L.; TAVARES, R.F.; PAIVA, C.L.; SOUZA, M.M. Genotype selection by REML/BLUP methodology in a 62 segregating population from an interspecific Passiflora spp.crossing. **Euphytica**, Dordrecht, v.204, p.1-11, 2015.

SANTOS, A.; CECCON, G.; TEODORO, P.E.; CORREA, A.M.; ALVAREZ, R.C.F.; SILVA, J.F. da; ALVES, V.B. Adaptabilidade e estabilidade de genótipos de feijão caupi ereto via REML/BLUP e GGE Biplot. **Bragantia**, Campinas, v.75, n. 3, p.299-306, 2016.

SILVA, G.O.; CARVALHO, A.D.F.; VEIRA, J.V.E.; BENIN, G. Verificação da adaptabilidade e estabilidade de populações de cenoura pelos métodos AMMI, GGE biplot e REML/BLUp. **Bragantia**, Campinas, v.70, p.494-501, 2011.

STURION, J.A.; RESENDE, M.D.V. Eficiência do delineamento experimental e capacidade de teste no melhoramento genético da erva-mate (Ilex paraguariensis St. Hil.). **Boletim de Pesquisa Florestal**, Colombo, v.50, p.3-10, 2004.

SOUZA, Y.P.; DAHER, R.F.; PEREIRA, A.V.; SILVA, V.B.; FREITAS, R.S.; GRAVINA, G.A. Repeatability and minimum number of evaluations for morphoagronomic characters of elephant-grass for energy purposes. **Revista Brasileira de Ciências Agrárias**, Recife, v.12, p.391-7, 2017.

SOUZA, C.M.B.; VIANA, A. P.; RIBEIRO, R.M.; CAVALCANTE, N.R.; ALVES, F.; AMBROSIO, M.; AMARAL JUNIOR, A.T. Guava breeding via full-sib family selection: conducting selection cycle and divergence between parents and families. **Crop Breeding and Applied Biotechnology**, Ribeirão Preto, v.20, p.1-9, 2020.

VIANA, A.P.; RESENDE, M.D. V. de. **Genética quantitativa do melhoramento de fruteiras**. Rio de Janeiro: Interciência, 2014. p.282.