Genetics and Plant Breeding

Genotypic superiority of *Psidium Guajava* S$_1$ families using mixed modeling for truncated and simultaneous selection

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ABSTRACT: The purpose of this study was to conduct selection, genetic parameter estimation, and prediction of genetic values for 18 S$_1$ families of guava trees using mixed model methodology and simultaneous selection of traits by means of the additive selection index, multiplicative selection index, and mean rank adapted from Mulamba. All families analyzed were obtained by means of self-fertilization of superior genotypes (full siblings) from the genetic breeding program of guava trees at the Universidade Estadual do Norte Fluminense. An experimental randomized block design with 18 S$_1$ families, three replicates, and ten plants per plot was used. A total of 540 genotypes (individual plants) of guava tree were evaluated. Genetic parameter estimation and selection of the best genotypes based on the genetic value were performed using the statistical procedure, from the Selegen-REML/BLUP program. The analyses of the additive selection index, multiplicative selection index, and the sum of rank adapted from Mulamba were also performed under the Selegen program. During the evaluation by the individual BLUPs, families 1, 12, 4, 6, and 8 contributed to most of the genotypes selected for the traits under evaluation, suggesting their significant potential to generate high quality and high yield genotypes. In the selection indexes via mixed models, the multiplicative index showed higher values for genetic gains (74 %), followed by the mean rank index adapted from Mulamba (19 %), and the additive index (2 %).

Keywords: inbreeding, guava tree, mixed models, breeding

Introduction

Guava tree cultivation has been expanding in the state of Rio de Janeiro, especially in the north and northwest regions, as it presents conditions favorable to its cultivation. Under this scenario, the Universidade Estadual do Norte Fluminense Darcy Ribeiro (UENF) has been developing a genetic breeding program of guava (*P. guajava* L.) over the last nine years, achieving promising results (Pessanha et al., 2011; Campos et al., 2013; Oliveira et al., 2014; Campos et al., 2016; Quintal et al., 2017a, b; Gomes et al., 2017). This study demonstrates that obtaining inbred families is a feasible way of forming superior populations. On the basis of this assumption, the evaluation of this partial inbreeding and its relevance of various traits to the breeding of guava trees is of the utmost importance, given that a new genetic variability can be added to the program under execution.

Agronomic traits and genetic parameters estimates in S$_1$ families are a significant phase in the genetic breeding of guava trees, especially in the early stages, as they guide the choice of parents and planning of superior individuals which will be selected and later self-fertilized. As such, it is pertinent to highlight the importance of adopting accurate selection methods in the genetic breeding of perennial species. In the light of this reasoning, the mixed model methodology (REML/BLUP) has been an excellent alternative for estimating genetic parameters, for involving variance component estimates using the Restricted Maximum Likelihood method (REML) and the prediction of genotypic values using the Best Linear Unbiased Prediction (BLUP), resulting in more accurate selection (Resende et al., 2014; Gonçalves et al., 2014; Viana and Resende, 2014; Vivas et al., 2014; Santos et al., 2015).

Therefore, selection between and within families and the selection index are presented as options. Selection indexes allow for adding multiple information aimed at selection on the basis of a set of variables that gathers together a number of traits of economic interest at the same time (Cruz et al., 2014; Krause et al., 2012; Dalbosco et al., 2018). Based on the above, the objective of this study was to carry out the selecting, genetic parameter estimating, and predicting of genetic values in 18 S$_1$ families of *Psidium guajava*, by means of the mixed model methodology, and simultaneous selection of traits, using the additive selection index, multiplicative index, and mean rank adapted from Mulamba.

Materials and Methods

Local, design, and evaluated population

The experiment was conducted at the experimental station of Ilha Barra do Pomba, in the municipality of Itaocara, in the state of Rio de Janeiro (northwest region), Brazil (21°40′ S, 42°04′ W, altitude of 76 m). The soil in the experimental area is classified as Red-Yellow Argisol (Embrapa, 2006). An experimental randomized block design with 18 S$_1$ families, three replicates, and ten plants per plot was

used. The 18 inbred families evaluated came from populations developed by Pessanha et al. (2011) in a pre-breeding study, in which 20 *Psidium* ssp. accesses were collected in the municipalities of São João da Barra (21° 38′ 56″ S, 41° 3′ 9″ W, 12 m altitude) and Bom Jesus do Itabapoana (21° 8′ 23″ S, 41° 39′ 48″ W, 88 m altitude), in the state of Rio de Janeiro, Brazil, to evaluate genetic diversity, via RAPD markers, with the objective of studying genetic divergence of these accesses for guiding crosses. After molecular analysis, intraspecific crosses of *Psidium guajava* accesses were engineered between the seven superior and contrasting parents, found via RAPD molecular analysis, resulting in 17 segregating families.

This segregating population of wide genetic variability was further evaluated and selected by Quintal et al. (2017a, b) using REML/BLUP, in which the most productive progenies were selected and self-fertilized to originate the 18 inbred families that comprise the experiment. Seeds from the fruits of self-fertilization were sown in tubettes (three seeds each tubette) and maintained in a greenhouse. Seedlings were planted, in July 2014, with spacing of 4-m between rows and 1.5-m between plants. Liming, planting and covering fertilizers were implemented according to soil analysis, following the recommendations of Costa and Costa (2003). Drip irrigation was also used. From the experiment, 540 (individual plants) guava trees were evaluated employing the descriptors determined for the *P. guajava* L. species, as defined by the UPOV (1987) (International Union for the Protection of New Varieties of Plants) and described in Campos et al. (2013).

Phenotyping

The following traits were evaluated:

Total fruit weight per plant (TFW) – this was determined by weighing all the fruits of each genotype from the beginning to the end of the harvest; total number of fruits per plant (TNF) – each individual was counted from the beginning to the end of the harvest.

For the other traits, the following sampling approach of five fruits collected from each genotype was used: fruit mass (FM) – five fruits collected from each genotype were weighed using a semi-analytical scale in g; transversal fruit diameter (FD) – for the five fruits sampled, the equatorial region of the fruits, was identified using a caliper and expressed in mm; fruit length (FL) – the longitudinal region of the fruit was measured with a caliper and expressed in mm; peel thickness (PT) – a measurement covering the region from the fruit peel to the beginning of the pulp was taken using a caliper and was expressed in mm; ratio of fruit length/width (FL/W) – obtained by the ratio of fruit length to fruit diameter (dimensionless); placental mass (PM) – this consisted of the endocarp region and was determined using the semi-analytical scale; pulp yield (PY) – calculated by the following formula:

$$1 - \frac{(PF - PP)}{PF} * 100 \, ;$$

mesocarp thickness (MT) – derived from two measurements on both sides in the median region of the fruit using a caliper with the results in mm; endocarp thickness (ET) – this consisted of the region in which the seeds are concentrated.

The region of the placenta was measured with a digital caliper and expressed in mm; pulp mass (PM) – this was the mesocarp region and was determined by subtracting the total mass and the placental mass; total soluble solids (TSS) – measurements by means of juice extracted from a sample of fruit pulp tissue by hand press extraction, taken in a portable refractometer, in the range from 0 to 32° Brix; pH (pH) – this was obtained by using the pH meter expressed in pH values.

Mixed model in plant selection and genetic parameter estimate

Two different selection strategies were used to check whether there was an increase in genetic gain. The first one was the REML/BLUP procedure, by which individuals were ranked according to the genotypic values for each trait. On the basis of these values, a selection of the 30 best individuals for each trait was made. For the second, a simultaneous selection of traits was used via the additive selection index (AI), multiplicative selection index (MI), and mean rank adapted from Mulamba (MR).

Data analysis was conducted following descriptions by Viana and Resende (2014), in which biometric models are adequate for species with a mixed reproductive system and cross-fertilization species under self-fertilization, as the species under study has a reproductive system considered mixed. The authors believe that, in addition to this genetic model being based on additive and dominance models, disregarding epistasis, it is also appropriate when a population where p = q = 0.5 is self-fertilized and selection is carried out in a segregating population.

In accordance with the Viana and Resende model (2014), the analysis of deviance was obtained as follows:

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

$$\ln(L) = -1/2\ln|X´V-1X| - 1/2\ln|V| - 1/2(y-Xm)´V-1(y-Xm),$$

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

The LRT statistical test (likelihood ratio test) was applied to test the significance of effects in the following way:

LRT: $|-2\ln(L_{se}) + 2\ln(L_{fm})|$,

in which L_{se} is the maximum point of the maximum likelihood function for the reduced model (without the effects) and L_{fm} the maximum point of the maximum likelihood function for the complete model.

For the analysis of the variables, the Selegen-REML/BLUP software computational application (Resende, 2016) was applied to obtain the variance components by means of the restricted maximum likelihood (REML) and also the individual genotypic values by using the best linear unbiased predictor (BLUP).

Model 107, proposed by Viana and Resende (2014), was chosen for this study: model y = Xr + Za + Wp + e, in which: y is the data vector; r the vector of repetition effects (assumed as fixed) added to the overall mean; a the vector of individual additive genetic effects (assumed as random); p the vector of plot effects; and the vector of errors or residues (random). Capital letters represent the incidence matrices for these effects.

The components of variances and parameters were estimated as follows: σ_g^2 : genetic variance among families, in which components of the additive genetic variance and dominance genetic variance depend on the rate of self-fertilization; σ_{parc}^2: environmental variance between plots; σ_e^2: residual variance; σ_f^2 : individual phenotypic variance; h_a^2: total individual heritability (using 3/2 of the additive genetic variance in the numerator, when S = 0) in the narrow sense; C^2par = coefficient of determination of plot effects; h_{mp}^2 : heritability of the progeny mean, assuming complete survival; Acprog: accuracy of the progeny selection, assuming complete survival; h_{ad}^2: additive heritability within plot (using 1/2 of the additive genetic variance in the numerator, where S = 0); and overall mean of the experiment.

Individual heritability in the restricted sense in the block; $h^2 = \dfrac{\sigma_a^2}{\sigma_a^2 + \sigma_e^2}$,

Phenotypic variance; $\sigma_f^2 = \sigma_a^2 + \sigma_e^2$

Additive genetic variance;

$\sigma_a^2 = \left[\hat{a}'A^{-1}\hat{a} + \sigma_e^2 tr(A^{-1}C^{22}) \right] / q$,

in which
tr: matrix trace operator;
C^{22} derives from:

$C^{-1} = \begin{bmatrix} C_{11} C_{12} \\ C_{21} C_{22} \end{bmatrix} - 1 = \begin{bmatrix} C^{11} C^{12} \\ C^{21} C^{22} \end{bmatrix}$

C: coefficient matrix of mixed model equations accuracy of prediction of genetic value;

$r_{\hat{a}a}^2 = \left[1 - PEV / \sigma_a^2 \right]^{1/2}$

Simultaneous selection of traits via additive selection index, multiplicative selection index, and mean rank adapted from Mulamba

The selection indexes aiming at generating gain in a genotypic aggregate composed of a number of traits were produced by the Selegen software application (Resende, 2016) by means of three alternative approaches using model 101: (a) additive index, in which relative economic importance or trait weights are provided; (b) multiplicative index, in which genotypic aggregate relates to the trait product; and (c) mean rank adapted from Mulamba, in which genotypic values are classified for each trait, and the ranking mean of each genotype for all traits presented as a final result. From the genotypic values predicted, the additive index (AI), multiplicative index (MI), and mean rank adapted from Mulamba (MR) were applied, which were constructed from the REML/BLUP methodology, being presented, in brief, as follows:

AI = (p*C1)*(VG*C1)) + ...

MI = (VG*C1) + ...

SMR = (r*VG*C1) + ...,

in which * is the multiplication sign; p the economic weight set for the trait; VG the genotypic value predicted; r the rank of the genotype; C1 the trait of interest, it being possible to add as many as needed into the equation (Viana and Resende, 2014). In the additive index, analyses were conducted with random economic weights of different magnitudes for the main traits TNF, TFW, FM, PM: arbitrary weight (100, 100, 80, 70). All other traits had a weight of 1. For the application of the mean rank index adapted from Mulamba, the trends of increase and decrease used for the additive index were maintained, but no economic weights were attributed.

Results and Discussion

Genetic evaluation of the 18 S$_1$ families of *Psidium guajava* using mixed models

Results show a significant difference for fruit mass, fruit length, fruit diameter, mesocarp thickness, total soluble solids (Brix), and placental weight traits according to the Chi-square test at 1 % probability (Table 1). For endocarp thickness, length/diameter ratio, total number of fruits, and total fruit weight traits, there is a significance of 5 %. Thus, the existence of genetic variability in the genotypes under evaluation was verified, which enabled the successful selection of superior genotypes on the basis of these traits and high precision in the variance component estimates. For the number of fruits, total weight of fruit, endocarp thickness traits, a significant difference of 1 % was observed for plot effect, highlighting the significant genetic variability within the plot.

The highest values for genotypic variance (σ_g^2) observed refer to the total fruit weight (4059786.00), total number of fruits (166.62), fruit mass (474.78), and mass of pulp (295.13) traits, and highlight the considerable genetic variability in the families evaluated in terms of these particular traits (Table 2). As such, knowing genotypic variance is essential to breeding programs, given that it indicates the extent of genetic variation in a specific trait, especially in view of the possibility of its enhancement (Cruz et al., 2014).

Table 1 – Deviance estimates for morphoagronomic traits of 18 S_1 families of *Psidium guajava* (Campos dos Goytacazes municipality, Rio de Janeiro state, Brazil, 2019).

Effect	Fruit mass		Fruit length		Fruit diameter	
	Deviance	LRT (χ^2)	Deviance	LRT (χ^2)	Deviance	LRT (χ^2)
Genotype	3815.77	25.29**	2576.51	20.56**	1963.38	16.79**
Plot	3791.45	0.97 ns	2556.32	0.37 ns	1949.81	3.22 ns
Complete model	3790.48		2555.95		1946.59	

Effect	Endocarp thickness		Mesocarp thickness		Peel thickness	
	Deviance	LRT (χ^2)	Deviance	LRT (χ^2)	Deviance	LRT (χ^2)
Genotype	1809.92	5.22*	1181.23	6.78**	–178.46	1.27 ns
Plot	1817.56	12.86**	1174.52	0.07 ns	–176.22	3.51 ns
Complete model	1804.70		1174.45		–179.73	

Effect	Pulp Mass		Brix		pH	
	Deviance	LRT (χ^2)	Deviance	LRT (χ^2)	Deviance	LRT (χ^2)
Genotype	3661.15	20.76**	872.07	10.64**	1074.85	0.01 ns
Plot	3642.32	1.93 ns	862.58	1.5 ns	1074.87	0.03 ns
Complete model	3640.39		861.43		1074.84	

Effect	Diam/ Length Ratio		Pulp yield		Placental weight	
	Deviance	LRT (χ^2)	Deviance	LRT (χ^2)	Deviance	LRT (χ^2)
Genotype	–1364.27	5.21*	–2158.82	3.78 ns	2740.10	15.63**
Plot	–1368.39	1.09 ns	–2162.19	0.41 ns	2725.48	1.01 ns
Complete model	–1369.48		–2162.60		2724.47	

Effect	Total number of fruit		Total fruit weight	
	Deviance	LRT (χ^2)	Deviance	LRT (χ^2)
Genotype	3953.46	5.75*	9011.69	5.22*
Plot	3983.56	35.85**	9045.28	38.81**
Complete model	3947.71		9006.47	

*and **significant at 5 and 1 % of probability by Qui-square test. LRT (χ^2) = likelihood ratio test.

Table 2 – Variance component estimates and genetic parameter: (σ_g^2) genetic variance between families; (σ_{plot}^2) environmental variance between plots; (σ_e^2) residual variance; (σ_f^2) individual phenotypic variance; (C^2plot) coefficient of determination of plot effects; (h_a^2) total individual heritability; (h_{pm}^2) heritability of the progeny mean; (h_{ad}^2) additive heritability within the plot; (*Acprog*) accuracy of progeny selection, and overall mean of traits obtained by the REML procedure for 14 traits evaluated in 540 plants of 18 S_1 families of *Psidium guajava*. (Campos dos Goytacazes municipality, in the state of Rio de Janeiro, Brazil).

Variable	σ_g^2	σ_{plot}^2	σ_e^2	σ_f^2	C^2plot	h_a^2	h_{pm}^2	h_{ad}^2	*Acprog*	Mean
Fruit mass	474.78	44.67	1186.66	1706.11	0.026	0.32	0.89	0.07	0.94	177.07
Fruit length	21.38	1.65	83.49	106.54	0.01	0.23	0.86	0.04	0.93	75.51
Fruit diameter	5.95	1.38	21.73	29.07	0.04	0.24	0.83	0.04	0.91	64.84
Length/diam. ratio	0.00	0.00	0.01	0.01	0.03	0.08	0.63	0.01	0.79	1.16
Placental mass	25.25	4.13	120.09	149.48	0.02	0.19	0.82	0.03	0.90	44.33
Pulp yield	0.00	0.00	0.00	0.00	0.01	0.06	0.58	0.01	0.76	0.74
Endocarp thickness	1.99	2.10	15.87	19.97	0.10	0.11	0.61	0.02	0.78	37.02
Mesocarp thickness	0.30	0.03	4.35	4.69	0.00	0.07	0.66	0.01	0.81	10.38
Pulp mass	295.13	46.67	853.96	1195.78	0.03	0.29	0.87	0.06	0.93	132.43
Total Soluble Solids (Brix)	0.28	0.07	2.13	2.49	0.02	0.13	0.75	0.02	0.86	12.66
pH	0.00	0.01	3.64	3.66	0.00	0.00	0.02	0.00	0.14	3.55
Peel thickness	0.00	0.01	0.22	0.24	0.05	0.03	0.38	0.00	0.62	1.76
Total number of fruits	166.62	216.89	830.90	1214.42	0.17	0.16	0.62	0.03	0.79	37.41
Total weight fruit	4059786.00	5791305.24	20951618.89	30802710.14	0.18	0.15	0.60	0.03	0.77	5997.61

This, by inference, enables selection of genotypes with the highest values for these traits. Conversely, the lowest values are associated with peel thickness, total soluble solids, pH, pulp yield, length/diameter ratio, and mesocarp thickness traits with values of 0; 0.28; 0; 0; 0; 0; and 0.30, respectively.

It is possible, then, to conclude that genetic gains associated with the selection of these traits are low because the variance found for these traits is mostly environmental, leading to low magnitude heritability values. This genotypic variance estimate, as stated by Cruz et al. (2014), enables identification of the genetic variability of a population and evaluation of the efficiency of different breeding strategies to generate genetic gains and maintain an adequate genetic basis.

For environmental variance between plots (σ^2_{plot}), the highest values were observed in the total number of fruits (5791305.24), total fruit weight (216.89), pulp mass (46.67), and fruit mass traits (44.67). The highest residual variance (σ^2_e) was found in total fruit weight, fruit mass, pulp mass, and total number of fruit traits (20,951,618.89; 1,186.66; 853.96; and 830.90, respectively). For all traits, the contribution of the residual variation of the entire experiment was higher than the environmental variance between plots. Thus, it is important to emphasize the environmental variation has a reference value with a certain level of precision with which the experiment was carried out. Attributes managed by various gene complexes exposed to significant levels of influence by environmental conditions of cultivation and great magnitudes of environmental variance were confirmed by higher values compared to other variance components, with emphasis on the genotypic variance between families (Table 2). This gave rise to selection difficulties which demand more accurate statistical methods for better execution (Viana and Resende, 2014). Environmental variance, however, depends on a number of factors, and most of them can be managed by breeders. Amongst these factors are the best distribution of seeds, fertilizers, fertilization, and proper irrigation control and best management practices should improve experimental accuracy and efficiency in the selection process.

With respect to the estimated phenotypic variance (σ^2_f), the highest values were for total number of fruits, fruit mass, total fruit weight, mass of pulp, placental mass, and fruit length traits (30,802,710.14; 1,706.11; 1,214.42; 1,195.78; 149.48, and 106.54, respectively). High values for phenotypic variance are predicted in populations for which the evaluated traits are of quantitative heritability. The expression of these traits is influenced by several genes and greatly affected by environmental factors, which leads to high phenotypic variance values. The lowest values for this estimate are in the pulp yield (0.00), length/diameter ratio (0.01), and peel thickness (0.24) traits. This finding for phenotypic variance may or may not suggest a low environmental effect on these traits. Herein, it depends, on both

heritability and selective accuracy, which they also showed low values, primarily because of the lack of variation in genotype.

The coefficient of determination of plot effects (*C²plot*) was of low magnitude, with the exception of the total number of fruits and total fruit weight traits (17 and 18 %) (Table 2). The *C²plot* quantifies the plot variability within the blocks, in which estimates up to 10 % do not affect the genetic parameter estimate. In accordance with Resende (2002), high values of C² show high variability between plots within blocks and positive environmental correlation between observations within plots. As such, high results for C² demonstrated that the experiment can be improved by the use of smaller plots. The other variables with lower values indicated that low environmental variation continued within the plots, suggesting low environmental variability between plots within the block and that the experimental design applied was efficient in its response to the proposed goals of the analyses.

Heritability coefficients varied from 0.02 to 0.89 on the basis of the family mean (h^2_{pm}). Fruit mass (0.89), pulp mass (0.87), fruit length (0.86), fruit diameter (0.83), placental mass (0.82), and total soluble solids (0.75) displayed the highest values for this estimate. By analyzing the additive heritability coefficients within the plot (h^2_{ad}) and total individual heritability (h^2_a), these coefficients were found to be much lower than heritability according to the family means. Resende (2002) states that, generally, individual heritabilities of low magnitude are common for quantitative traits and, as a general rule, lead to moderate magnitudes of heritabilities at the level of progeny means. It is worth mentioning that high values for progeny mean that heritability implies high genetic progress given the selection uses progeny information, indicating a strong possibility of gain for the *Psidium guajava* breeding program. As expected, progress by selection depends directly on heritability. Thus, selection based on family means may be more efficient than within the families themselves.

Selection between and within families, however, can be conducted so as to use all variability existing in the population, thereby maximizing the genetic gains. Heritability has its predictive role in trait genetic research, demonstrating the reliability with which the phenotypic value represents the genetic value (Silva et al., 2013). Its value can be increased both by the introduction of greater genetic variation in the population, and by the improvement in experimental conditions which reduce the contribution of environmental variation to total phenotypic variation.

The quality of genotypic evaluation should preferably be deduced based on accuracy. According to Resende (2002), the values of selective accuracy (Acprog) varied from very high to low in magnitude, between 0.91 and 0.14. The highest estimates were seen in fruit mass (0.94), fruit length (0.93), pulp mass

(0.93), fruit diameter (0.91), and placenta mass (0.90) traits, and the lowest estimates were for pH (0.14) and peel thickness (0.62) traits. For the other traits, such as total fruit weight, total number of fruits, total soluble solids, pulp yield, and length/diameter ratio, the accuracy values were above 0.70.

Resende (2002) states accuracy above 90 % is only possible for traits with high heritability, and that accuracy values greater than 0.70 are sufficient to provide a more accurate inference about the genetic value of progenies. As a measurement related to precision in selection, accuracy is the main element of genetic progress which may be modified by a person aiming at maximizing genetic gain. Similarly, in an experiment using 17 families of full siblings of segregating guava, Quintal et al. (2017a, b) reported high accuracy for traits, such as fruit mass (0.82), pulp yield (0.84), total fruit weight (0.75), soluble solid content (0.86), and vitamin C (0.89).

Best individual selection by individual BLUPs

For purposes of selection, the 30 best individuals were considered for all the traits analyzed separately. Genetic gains were predicted, and the new estimated means were either higher or lower, according to the type of gain sought when selecting the individuals with respect to the overall mean of the traits.

With regard to the selection of genotypes for the agronomic traits under evaluation, relevant gains could be achieved in the selection of some traits by individual BLUP estimates. When comparing the mean of these 30 individuals with the overall population mean, the best mean estimates of genetic gain were found for total fruit weight (62 %), total number of fruits (48 %), pulp mass (26 %), fruit mass (26 %), and placental mass (26 %). Thus, when selecting on the basis of these traits, successful selection may be achieved, as these traits are related to yield. For this reason, it is interesting to note that the ones with the highest predicted genetic gains have the highest coefficients of genotypic variation and high values of heritability estimates and selective accuracy, which may explain the highest genetic gains.

The other traits displayed gains of low magnitude, especially the diameter/length ratio, pulp yield, mesocarp thickness, endocarp thickness, soluble solid content (Brix), pH, and peel thickness traits. Such occurrence is the result of low genetic variability within families, which can be visualized by estimating individual heritability. This low variability is due to the first generation of self-fertilization performed, in which homozygosity increases and heterozygosity decreases in the progeny, resulting in more homogeneous fruits and consequent allele fixation (Falconer and Mackay, 1996).

Families 1, 12, 4, 6, and 8 contributed to most of the genotypes selected for the traits under evaluation indicating great potential for these families to generate productive genotypes. As such, the best selection method in terms of breeding is the one that predicts satisfactory gains in the evaluated traits. When predicting the genetic gain, the selection criteria provide effective guidance for breeding programs and decide which selective scheme can be successfully adopted (Cruz et al., 2014), as it becomes possible to verify which are the best families and the best individuals within these families.

Considering the amplitude of phenotypic means for the evaluated traits, mainly those related to yield, the mean ranged from 35.60 to 4.173 kg per plant, with genetic gains of high magnitude (52 to 46 %), for the total fruit weight of the 30 selected individuals. With respect to the total number of fruits, mean values from 177 to 45 fruits per plant and those with satisfactory genetic gains (51 to 47 %) were noted. For the fruit mass, a genetic gain by selection from 27 % to 25 % was verified, presenting a mean from 321 g to 153 g per fruit. After analyzing the pulp mass, gains from 27 % to 25 % were observed, with a mean from 222 g to 90 g. In this scenario, a number of available cultivars have been used by rural producers, including 'Paluma', 'Rica', 'Sassaoka', 'Pedro Sato', 'Cortibel', and 'Século XXI' cultivars (Santos et al., 2011). As such, a comparison of the yield potential of the selected genotypes with the commercial cultivars 'Paluma' and 'Pedro Sato' is justified.

Under this assumption, Cardoso et al. (2011) asserted that the first crop of guava tree 'Paluma', from approximately 12 to 14 months after field planting, can reach up to 15 kg of fruit per plant in irrigated areas of the northeast. Fruits are large (above 200 g) and have a high content of soluble solid ($\pm$ 10° Brix), which gives the fruit an excellent taste. On average, it produces 188 fruits per plant. The Pedro Sato cultivar, in turn, had vigorous plants with relatively high yields, slightly oval fruit, with a mean weight from 155 g to 282 g, without thinning, and with a soluble solid content that ranged from 6.3° to 9.7°. As such, by comparing the phenotypic means of the evaluated agronomic traits of the S_1 families with the means of the 'Paluma' and 'Pedro Sato' commercial cultivars, it should be pointed out they were either equal or higher, proving the potential of these families to form a new cultivar in lines after successive generations of self-fertilization, in case there were no inbreeding depression, or for use as parents in future crosses, so as to obtain superior genotypes.

With regard to the fruit shape, it can be seen that the evaluated fruits are within the required standards, and the mean length/diameter ratio of the fruit varied from 1.21 to 1.20 between the selected genotypes, with low gains in the selection (5 to 4 %). The fruit shape prediction is determined by the ratio between the length and diameter of the fruit, which is an estimator of industrial quality; in other words, the closer to 1, the rounder the fruit is (Campos et al., 2013).

The pulp yield showed a mean from 0.87 to 0.71 and genetic gains from 3 to 2 %. As Lima et al.

(2002) stated, fruit selection should be made using values above 70 %, which confirms the potential of the population under study, a population that, in general, presented a mean above this index.

Given that the total soluble solids (Brix) trait does not obtain genetic gains in great magnitude (6 to 5 %), genotypes are not a problem in this population, as the data observed for the variable are within the range of values that is appropriate for both the fresh fruit market and the juice and candy industry (14.99 to 12.93). Findings from this variable were higher than those reported by the authors Kadam et al. (2012), who found between 7.55° and 8.33° Brix for guava of the 'Paluma' variety.

Based on the results shown, it should be stressed that the phenotypic mean of the genotypes selected for quality and production traits tended to be equal to or higher than the materials already launched in the market, confirming that the selection strategy via mixed models and with the use of inbred families, is efficient in generating gains in the selection.

Simultaneous selection of traits via additive selection index, multiplicative selection index, and mean rank adapted from Mulamba

Selection indexes are generally used to choose superior materials on the basis of a complex of variables that gather attributes of interest for the breeder, so as to provide better simultaneous gains (Cruz et al., 2014). As regards the genetic gain estimate, there were genetic gains for all indexes (Table 3). Out of the three selection indexes used, the one which produced the highest gains by selection was the multiplicative index, with a mean of 74 %, followed by the mean rank adapted from Mulamba (19 %) and the additive index (2 %).

The multiplicative index also showed closer coincidence of the presence of individuals from selected families using estimates of individual BLUPs for the fruit mass, total number of fruits, total fruit weight, pulp mass, and placental mass traits. The majority of the 30 genotypes selected by BLUPs for these traits belong to families 1 (249 %), 6 (214 %), 4 (156 %), 12 (127 %), and 8 (104 %), also selected by the multiplicative index, with their corresponding expected genetic gains. Pedrozo et al. (2009), who compared the efficiency of three selection indexes from estimated variance components and genotypic values predicted by the REML/BLUP methodology in three populations (A, B, and C) of the first clonal generation of sugarcane, found that the multiplicative index was the one that showed the highest selection efficiency, as it showed the highest coefficient of coincidence of selected genotypes with the selection strategy for the tons of soluble solids per hectare (TBH) trait, the highest direct selection gains, and the highest indirect gains for TBH.

The index mean rank adapted from Mulamba obtained lower genetic gains, and selected the same

families as the multiplicative index, but with the ranking in a different order. Resende et al. (2014) estimated the genetic divergence between cotton accesses and classified the best ones on the basis of the selection index of mean rank adapted from Mulamba. They also indicated the MR index was the most promising for the simultaneous selection of cotton fiber traits.

The additive index was the one that produced the smallest genetic gains when compared with the other indexes, but the first families selected as superior were 12 (4 %), 1 (4 %), 8 (4%), 6 (4%), and 4 (4 %), which coincided with other indexes used. Thus, after various attempts attributing different weights, the use of the classical index made it possible to achieve favorable percentage gains.

Bearing in mind the efficiency of a selection index for implementation in breeding programs, it is important to take the gain into account by applying the index and the possibility that it has of selecting individuals based on traits of interest, without allowing for inflation or attributing too much weight to one of the traits that comprises the index. Considering this scenario, out of the indexes applied in the experiment for the selection of superior S_1 families, the multiplicative index was the most efficient, as it showed the greatest magnitude of gains and enabled the selecting of the best families in terms of quality and yield of the experiment.

Table 3 – Ranking of the 18 S_1 families of *Pisidium guajava* on the basis of the expected genetic gains, utilizing the additive index, multiplicative index, and mean rank adapted from Mulamba for 14 traits (Campos dos Goytacazes municipality, in the state of Rio de Janeiro, Brazil, 2019).

ORD.	Selection Index					
	Additive		Multiplicative		Rank*	
	S_1 Families	GS	S_1 Families	GS	S_1 Families	GS
		%		%		%
1	12	4.34	1	249.09	10	37.11
2	1	4.19	6	213.97	1	36.41
3	8	4.06	4	156.49	8	35.71
4	6	3.92	12	126.79	16	33.33
5	4	3.82	8	104.19	6	31.42
6	9	3.52	7	87.96	7	28.50
7	7	3.14	9	76.05	4	24.63
8	17	2.81	10	67.04	12	21.87
9	10	2.49	16	57.56	9	19.10
10	16	2.17	17	49.07	11	16.46
11	18	1.82	2	39.83	2	14.29
12	3	1.51	3	32.13	18	12.47
13	2	1.22	18	25.60	3	10.76
14	15	0.94	11	19.24	14	8.69
15	11	0.69	14	13.55	17	6.97
16	5	0.47	13	8.55	5	4.31
17	14	0.22	5	4.02	15	2.03
18	13	0.00	15	0.00	13	0.00
Mean (%)	2		74		19	

*Mean rank adapted from Mulamba.

Conclusions

The REML/BLUP statistical procedure was efficient in estimating the genetic parameters as well as in selecting superior genotypes.

Family genotypes 1, 12, 4, 6, and 8 were considered as superior when compared to the others because they provided the best genotypes in terms of fruit mass, pulp mass, total fruit weight, and total number of fruit traits. As such, they will have representatives selected for future self-fertilization and/or crosses.

The phenotypic means of the traits associated with the yield of genotypes selected by means of BLUPs are equal to or higher than those of commercial cultivars, proving the potential of inbred families to generate yielding genotypes.

As regards selection indexes via mixed models, the multiplicative index showed the greatest selection gain compared to the additive index and the mean rank adapted from Mulamba, proving to be effective in identifying the families with superior quality and production simultaneously.

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Authors' Contributions

Conceptualization: Ambrosio, M.; Viana, A.P.; Preisigke, S.C. **Data acquisition:** Ambrosio, M.; Viana, A.P.; Torres, G.X.; Silva, F.A.; Bezerra, C.M. **Data analysis:** Ambrosio, M.; Ribeiro, R.M.; Cavalcante, N.R.; Viana, A.P. **Design of methodology:** Ambrosio, M.; Viana, A.P.; Cavalcante, N.R.; Preisigke, S.C. **Writing and editing:** Ambrosio, M.; Preisigke, S.C.; Viana, A.P.; Cavalcante, N.R.

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