

# Novel selection strategy for half-sib families of sour passion fruit *Passiflora edulis* (Passifloraceae) under recurrent selection

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**ABSTRACT.** Several strategies have been employed in the breeding of passion fruit with a view to the generation of superior progeny. In an effort to develop more precise methods in breeding, we compared the efficiency of the Post-Hoc Blocking Row-Col technique, which is an a posteriori technique that consists of the overlapping of a block structure on the original-field design, with a randomized-block design and compared different selection strategies within and among half-sib families, using the REML/BLUP mixed-model methodology. Twenty-three half-sib families from the third cycle of recurrent selection of the breeding program of Universidade Estadual do Norte Fluminense Darcy Ribeiro - UENF were evaluated. The trial took place in the experimental unit of UENF, in Itaocara - RJ, Brazil. Plants were trained on vertical stakes, with four replicates and three plants per plot. They were assessed individually for the traits number of fruits per plant, fruit mass per plant, fruit length, fruit diameter, peel thickness, total soluble solids, pH, pulp percentage, and production per plant. No significant difference was found in the test of efficiency of the designs for any of the evaluated traits. Within-family heritability ( $h^2_{ad}$ ) had a similar magnitude to individual heritability ( $h^2_a$ ), indicating that even in the 4th cycle of recurrent

selection, genetic variability still exists within the evaluated progeny. Selection within half-sib families provided superior gains when compared with selection among families for the traits number of fruits; production; fruit mass, length, and diameter; total soluble solids; pH; and pulp percentage. The best selection strategy was within families, as it generated higher selection-gain estimates than those obtained with selection between families and the direct-selection and index-selection approach.

**Key words:** *Passiflora edulis*; Breeding; Heritability; Post-hoc Blocking Row-col

## INTRODUCTION

The genus *Passiflora* originated in Tropical America, with 150 species native to Brazil. The most commercially relevant species is passion fruit (*Passiflora edulis*), which constitutes 95% of the *Passiflora* orchards in the country. It is also the most widely cultivated species of the genus in the world (Bernacci et al., 2008; Meletti, 2011).

Ever since the 70s, Brazil has stood out as the largest producer of passion fruit worldwide, which is the result of a growing expansion of cultivated area. However, its yield is still considered low relative to the production potential that can reach 30,000 kg.ha<sup>-1</sup>.yr<sup>-1</sup> (Hafle et al., 2009). In 2016, the Brazilian harvest was 703,489 t from an area of approximately 50,000 ha, with an average yield of 14,101 kg.ha<sup>-1</sup>. Of this total, the state of Rio de Janeiro generated 5956 t, with an average yield of 15,510 kg.ha<sup>-1</sup> (IBGE, 2016). Nevertheless, the crop faces restricting factors such as the low yield caused by phytosanitary problems and lack of genotypes adapted to its growing regions, among other issues. In this scenario, breeding is an essential step to address those needs (Silva et al., 2009).

In 1999, the Universidade Estadual do Norte Fluminense Darcy Ribeiro (UENF) started the passion fruit breeding program via intrapopulation recurrent selection by collecting various genotypes from three producing regions in Rio de Janeiro State (Viana et al., 2004). The program aims at the release of higher-yielding cultivars adapted to the climatic conditions of the northern region of the state, and others Brazilian fruits crops area (Ribeiro et al., 2019).

In general, experiments with passion fruit, including the trials conducted at UENF, adopt the randomized-block design (Viana et al., 2003; Gonçalves et al., 2009; Silva et al., 2009). However, the efficiency of this design may be compromised as the number of treatments increases. Heterogeneity may influence the evaluation of genotype performance as well as the estimates of variance components (Ramalho et al., 2005).

An alternative to overcome this problem is the use of the 'Post-Hoc Blocking Row-Col' method for the evaluation of various traits. It is an *a posteriori* technique that consists of the overlapping of a block structure on the original-field design (Gezan et al., 2006), with the addition of rows and columns. In this way, in addition to the block and treatment effects, the effects of rows and columns are also present in the commonly used linear model. This procedure allows for greater accuracy in the treatment of phenotyped traits in the population (Silva et al., 2016).

According to Resende and Dias (2000), besides genetic variability, success in a breeding program depends almost entirely on the adoption of precise selection methods. Various strategies have been employed in the breeding of passion fruit aiming at the generation of superior genotypes. The use of direct selection within and among families, combined selection, and mixed models (REML/BLUP) has been reported in the literature (Gonçalves et al., 2007; Oliveira et al., 2008; Santos et al., 2008; Assunção et al., 2015).

In the previous cycles of UENF's passion fruit breeding program via intrapopulation recurrent selection, the typically used method was selection of the best families, wherein the families are recombined in the half-sib structure. For the continuity of recurrent-selection cycles, half-sib families are obtained and later evaluated. In this stage, pollen is collected indiscriminately within the experimental plots to obtain the families.

Considering that this process occurs is at family level, the present study was developed to check the existence of genetic variability within families by evaluating plants individually; and to determine whether there is an increase in genetic gain with the use of the best plants within each half-sib families for the generation of full-sib families. Additionally, we compared the efficiency of the Post-Hoc Blocking Row-Col technique and the randomized-block design.

## MATERIAL AND METHODS

### Experimental conditions

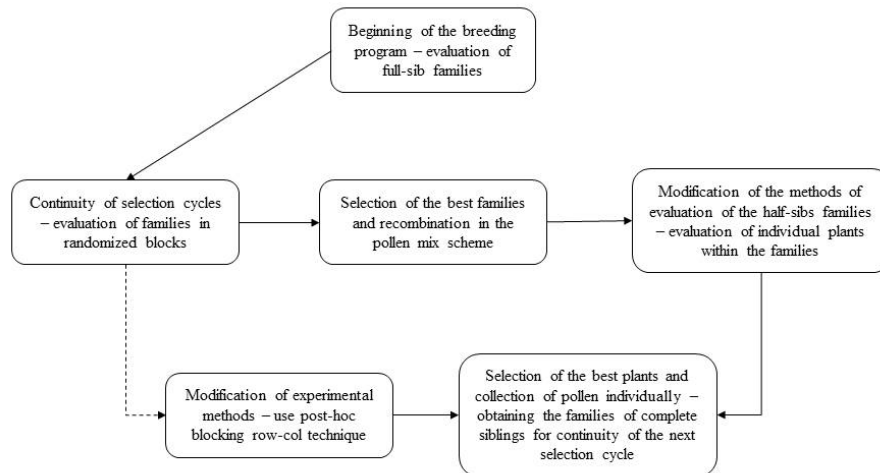
The experiment was conducted between January 2016 and January 2017 at the Experimental Unit of UENF in Itaocara - RJ, Brazil (21°40' S, 42°04' W, and 76 m asl in relation to sea level) following the methodology adopted by Cavalcante et al. (2017). The soil in the experimental area is classified as a Red-Yellow Argisol (Embrapa, 2006).

Twenty-three half-sib families obtained from the breeding program of UENF via recurrent selection by manual pollination were evaluated. The experiment was set up as a randomized-block design (RBD) with four replicates and three plants per plot, with each plant assessed individually. To evaluate the Post-Hoc Blocking Row-Column technique, an arrangement with 27 rows and 12 columns was implemented on the experimental design in a RBD.

Plants were trained in the vertical-stake system using treated 2.5-m-high Eucalyptus fence posts spaced 4 m apart and 12-gauge wire at 1.80 m from the soil. The distance between planting rows was 3.5 m, so as to allow for the passage of equipment within the experiment, and 3 m between furrows. Liming, time-of-planting fertilization, and topdressing were applied based on the soil analysis, following recommendations of Incaper (2008). All cultivation treatments such as pruning and pest, disease, and weed control were performed whenever necessary, according to recommendations for the passion fruit crop.

When deemed necessary, plants were irrigated using the drip system with a flow of four liters per hour during dry periods. For fruit production, natural pollination was performed by bees of the genus *Xylocopa*.

To optimize the selection gains in the generation phase of families, we modified the evaluation process, doing the phenotyping in individual plants within each family. In order to select the best plant within each family, these plants will be crossed in pairs to form the families that give continuity to the recurrent selection program (Figure 1).



**Figure 1.** Scheme of the UENF sour passion fruit breeding program. Proposed amendment to the methodology for evaluating families and collecting pollen on individual plants within the best families.

## Evaluated Traits

Mature fruits were collected on the ground per plant for phenotyping using the following traits: number of fruits per plant (NF); fruit mass per plant, in grams (FM); pulp percentage (PP); peel thickness, in millimeters (PT); total soluble solids, in Brix degrees (TSS); potential of hydrogen (pH); and plant production in kilograms (PROD).

The number of fruits per plant was determined from harvests throughout the experiment. Fruit mass was calculated by dividing the total production per plant by the total number of fruits. Pulp percentage was determined by weighing the pulp of five fruits per plant (weight of seed with aril), dividing this number by the total weight of the five fruits, and multiplying the result by 100.

Fruit length and diameter were measured on a composite sample of five fruits per plant in their longitudinal and transverse directions, using a digital caliper. Peel thickness was determined using a digital caliper, by measuring the middle part of the five fruits, which were cut transversely in the largest diameter.

Total soluble solids were determined by refractometry, by placing drops of fruit juice individually on an RTD-45 digital refractometer, with reading in the Brix range of 0 to 95°. The pH was measured by immersing the sensor of a W3B digital pH meter (potentiometer with glass electrode) in the juice extracted from the fruits. Plant production was calculated as the amount harvested in kilograms throughout the experiment.

## Statistical Models

To compare the randomized-block model (RBD) with Post-Hoc Blocking Row-Col method, an analysis was performed in R software via the ASReml package (Gilmour et al., 2009). The equations are shown below — first, using a RBD model, and then the row-column model.

$$Y_{ijk} = \mu + \text{block}_i + \text{fam}_j + \varepsilon_{ij} \quad (\text{Eq. 1})$$

$$Y_{ijkl} = \mu + \text{block}_i + \text{fam}_j + \text{row}_k + \text{col}_l + \varepsilon_{ijkl} \quad (\text{Eq. 2})$$

where  $Y_{ijk}$  is the value of the respective trait in block  $i$  ( $i = 1-4$ ), in individual  $j$  ( $j = 1-263$ ), in row  $k$  ( $k = 1-27$ ), and in column  $l$  ( $l = 1-12$ );  $\mu$  is the overall mean;  $\text{Block}_i$  corresponds to the fixed effect of blocks;  $\text{Fam}_j$  corresponds to the random effects of individual  $\sim$  NIID ( $0, A\sigma_a^2$ ),  $\text{row}_k$  corresponds to the random effects of rows  $\sim$  NIID ( $0, I\sigma_{\text{row}}^2$ ),  $\text{col}_l$  corresponds to the random effect of columns  $\sim$  NIID ( $0, I\sigma_{\text{col}}^2$ ); and  $\varepsilon_{ijkl}$  is the random residual effect for block  $i$  in individual  $j$ , line  $k$ , and column  $l \sim$  NIID ( $0, I\sigma_e^2$ ).  $I$  is the identity matrix, and  $A$  is the kinship matrix derived from the pedigree information.

Chi-squared statistics ( $\chi^2$ ) was used to compare the models through the likelihood ratio test (LRT). This comparison is aimed at evaluating the significance of the Post-Hoc Blocking Row-Col technique in the analysis of observations. Based on LRT, we chose the best model to predict the BLUP of the additive genetic values and estimate the variance components via REML.

According to the model described in Viana and Resende (2014), deviance ( $D$ ) was analyzed as follows:

$$D = -2\ln(L) \quad (\text{Eq. 3})$$

$$\ln(L) = -1/2\ln|X'V^{-1}X| - 1/2\ln|V| - 1/2(y-Xm)'V^{-1}(y-Xm) \quad (\text{Eq. 4})$$

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

The LRT was used to test the significance of effects, as shown next:

$$\text{LRT} = -2\ln(L_{\text{se}}) + 2\ln(L_{\text{fm}}) \quad (\text{Eq. 5})$$

where  $L_{\text{se}}$  is the maximum point of the maximum likelihood function for the reduced model (without the effects) and  $L_{\text{fm}}$  is the maximum point of the maximum likelihood function for the full model.

Analyses for the prediction of genetic gains and estimate of variance components via REML/BLUP were undertaken in Selegen statistical genetics software, using the model that enables the evaluation of individuals in half-sib families (Resende, 2016). The model below was used:

$$y = X_r + Z_a + W_p + e \quad (\text{Eq. 6})$$

where  $y$  is the vector of data;  $r$  is the vector of replicate effects (assumed fixed) added to the overall mean;  $a$  is the vector of individual additive genetic effects (assumed random);  $p$  is the vector of plot effects; and  $e$  is the vector of errors or residuals (random).  $X$ ,  $Z$ , and  $W$  represent the incidence matrices for the said effects.

The solutions for the mixed-model equations were obtained by iterative methods of resolution of linear-equation systems. Iterative estimators of the variance components via EM (Expectation-Maximization) algorithms.

$$\sqrt{\text{individual narrow-sense heritability in the block; } h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_e^2}}$$

- ✓ Phenotypic variance;  $\sigma_f^2 = \sigma_a^2 + \sigma_e^2$   
 ✓ additive genetic variance;  $\sigma_a^2 = \left[ \hat{a}' A^{-1} \hat{a} + \sigma_e^2 \text{tr} \left( A^{-1} C^{22} \right) \right] / q$   
 , where:  
 tr: trace matrix operator;  
 $C^{22}$  originates 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: matrix of coefficients of the mixed-model equations.  
 ✓ prediction accuracy of genetic values;  
 $r_{aa}^2 = [1 - \text{PEV} / \sigma_a^2]^{1/2}$

Three selection strategies were employed to check whether there were increases in genetic gain. Selection within family consists of selecting the two best plants of the 23 half-sib families, totaling 46 plants. Another method is selection among families using the 18 best families. For both strategies, gains from selection were provided by analyses performed in Selegen statistical genetics software, and percentage gains were estimated by the equation  $SG\% = (\text{gain} \times 100) / \text{overall mean}$ , where *gain* is the predicted genetic gain; and *overall mean* is the mean of the evaluated trait. The third method is the selection strategy obtained by Silva et al. (2009) using the direct-selection and index-selection methodology.

## RESULTS AND DISCUSSION

### Performance of the models and deviance analysis

According to the likelihood ratio test, the model proposed by Post-Hoc Blocking Row-Col method had similar results to the randomized-block model, with no significant differences for any of the evaluated traits (Table 1).

**Table 1.** Likelihood ratio test, comparing the proposed models for the randomized complete block design (RCB) and post-hoc blocking (Row-Col), in characteristics of sour passion fruit cultivated in Campos dos Goytacazes-RJ, Brazil, 2019.

Traits	RCB	Row-Col	$d = 2[\log L_2 - \log L_1]$	$\chi^2$ P-value
Number of fruits	-965.05	-965.05	0.00035	0.99
Production	-2281.53	-2281.53	-1.31E-05	1
Fruit mass	-1049.66	-1049.56	0.200	0.90
Fruit length	-617.38	-616.72	1.314	0.51
Fruit diameter	-1335.28	-1334.82	0.914	0.63
Peel thickness	-163.23	-162.83	0.802	0.66
Pulp percentage	-595.43	-595.26	0.339	0.84
Total soluble solids	-305.93	-305.91	0.043	0.97
pH	389.86	391.80	3.870	0.14

Silva et al. (2016) found a different result in an investigation of 81 full-sib progeny of passion fruit. They observed that the Post-Hoc Blocking Row-Col model had better or equal performance when compared with the randomized-block model, for all evaluated traits. For the traits number of fruits and fruit production, those authors detected significant

differences ( $P < 0.01$ ) between the evaluated models. Based on the favorable results obtained, the proposed Blocking Row-Col model was chosen for all subsequent analyses. Kempton et al. (1994) found that this technique was superior to the randomized-block approach in trials with cereals, with more efficient gains obtained with the former method.

One of the possible explanations for the lack of significant differences between the two tested models is the lower number of families used in the present study. Thus, there were no problems related to heterogeneity in the plots within each block. The randomized-block design loses efficiency when a higher number of treatments is evaluated, because the number of blocks increases proportionally to the number of treatments and it becomes difficult to maintain the homogeneity of plots within large blocks, which complicates comparisons between treatments. In this way, when using the randomized-block design, the experimental error is expected to increase with the number of treatments (Gomez and Gomez, 1984).

Therefore, because it showed greater ease of data analysis, the randomized-block model was chosen for the estimate of variance components and prediction of genetic values in the present study.

Table 2 contains the deviance values, whose results demonstrate the occurrence of significant differences by the chi-squared test at the 5% probability level for the traits number of fruits, fruit mass, fruit length, fruit diameter, and pulp percentage. This indicates the existence of genetic variability across the evaluated genotypes, which allows for a successful selection of superior genotypes.

**Table 2.** Deviance analysis for productive traits (number of fruits per plant, production per plant and fruit mass per plant) and fruit quality (fruit length, fruit diameter, peel thickness, total soluble solids, pH and pulp percentage) characteristics in half-sibs families of sour passion fruit cultivated in Campos dos Goytacazes-RJ, Brazil. 2019.

	Number of fruits		Production		Fruit mass	
Effect	Deviance	LRT ( $\chi^2$ )	Deviance	LRT ( $\chi^2$ )	Deviance	LRT ( $\chi^2$ )
Genotypes	1935.14	5.87**	4562.52	1.74ns	2102.79	4.11**
Full model	1929.27		4560.78		2098.68	
	Fruit length		Fruit diameter		Peel thickness	
Effect	Deviance	LRT ( $\chi^2$ )	Deviance	LRT ( $\chi^2$ )	Deviance	LRT ( $\chi^2$ )
Genotypes	1240.49	5.72**	1054.94	6.12**	325.79	2.05ns
Full model	1234.77		1048.82		323.74	
	Total soluble solids		pH		Pulp percentage	
Effect	Deviance	LRT ( $\chi^2$ )	Deviance	LRT ( $\chi^2$ )	Deviance	LRT ( $\chi^2$ )
Genotypes	404.98	0.57ns	-779.38	1.76ns	1194.56	3.77**
Full model	404.41		-781.14		1190.79	

\*\* significant at 5% probability by chi-square test. LRT ( $\chi^2$ ): likelihood ratio test.

The highest additive variance values were observed for the traits production per plant and fruit mass (3,463 and 385.94), indicating high genetic variability for these traits in the investigated population (Table 3). Ramalho et al. (1993) considered additive variance the most important for the breeder, and it is also responsible for the positive effect of selection.

**Table 3.** Estimates of genetic parameters via REML procedure, for production (number of fruits per plant - NF, production per plant - PROD and fruit mass per plant - FM) and fruit quality (fruit length - FL, fruit diameter - FD, peel thickness - PT, total soluble solids - TSS, pH and pulp percentage - PP) characteristics of passion fruit population in Campos dos Goytacazes-RJ. Brazil. 2019.

Genetic parameters	Characteristics								
	NF	PROD	FM	FL	FD	PT	TSS	pH	PP
$\sigma_a^2$	259.46	3,463.9	385.94	13.75	7.33	0.31	0.22	0.003	10.60
$\sigma_p^2$	622.59	15,829	1,179.85	41.69	20.41	1.25	1.71	0.01	35.10
$h_a^2$	0.41	0.21	0.32	0.33	0.35	0.24	0.13	0.21	0.30
$h_{ap}^2$	0.55	0.36	0.48	0.51	0.53	0.38	0.23	0.36	0.48
$h_{ad}^2$	0.37	0.19	0.28	0.27	0.29	0.22	0.12	0.18	0.25
$c_{plot}^2$	0.05	0.10	0.05	0.004	0.005	0.11	0.16	0.08	0.01
$Ac_{prog}$	0.74	0.60	0.69	0.71	0.73	0.62	0.47	0.60	0.69
Average overall	47.32	7.77	168.13	87.26	77.27	6.59	11.5	2.68	46.24

Additive genotypic variance among passion fruit progenies ( $\sigma_a^2$ ). Individual phenotypic variance ( $\sigma_p^2$ ). Heritability in the narrow sense ( $h_a^2$ ). Heritability based on the average progenies ( $h_{ap}^2$ ). Additive inheritance within the family ( $h_{ad}^2$ ). Coefficient of determination of plot effects ( $c_{plot}^2$ ). Accuracy of progeny selection ( $Ac_{prog}$ ).

## Genetic parameters

Phenotypic variance estimates ranged from 15,829 to 0.01 (Table 3). The highest values were obtained for production per plant and fruit mass (15,829 and 1,179.85 respectively), indicating a greater influence of the environment on the expression of those traits. Silva and Viana (2012) evaluated 140 full-sib families of passion fruit from the second cycle of recurrent selection and obtained a phenotypic variance estimate of 328.25 for FM. However, a higher value was obtained in the current study, indicating greater environmental variance in the expression of this trait.

We adopted the classification of heritabilities proposed by Resende (2002), according to whom values from 0.01 to 0.15 are considered low; from 0.15 to 0.50, medium; and above 0.50, high. Individual heritability estimates ( $h_a^2$ ) ranged from 0.41 to 0.13 (Table 3). Total soluble solids was the only trait with a low heritability value, suggesting difficulty in selection for this trait. One of the possible causes of this low estimate is the fact that the population had already undergone three selection cycles, and this variable would already be stabilized with the presence of low genetic variability in the population, but with values already acceptable for the fruits. Assunção et al. (2015) evaluated individual selection of passion fruit plants for fruit quality via REML/BLUP and also observed low individual heritability estimates for TSS (0.07).

As regards the other traits, individual heritabilities ( $h_a^2$ ) were of medium magnitude. Medium- and high-magnitude heritability values indicate a favorable situation for selection (Viana et al., 2004). According to Farias Neto et al. (2007), the individual heritability of 44.6% found in the selection of açai (*Euterpe oleracea*) progeny for bunch height revealed great potential for selection within the experiment.

The highest estimates for the mean heritability of progeny ( $h_{mp}^2$ ) were found for number of fruits, fruit length, and fruit diameter (0.55, 0.51, and 0.53), classified as high-magnitude values (Table 3). Because these families are already selected, selection among rather than within families is more interesting. Oliveira et al. (2008) analyzed



the genetic gains predicted using different selection indices on six fruit-related traits in 16 half-sib families of passion fruit and observed mean heritability coefficient ( $h^2_{mp}$ ) estimates of 0.11 to 0.57, and the highest heritabilities (above 0.50) were found for fruit length, number of fruits per plant, and fruit mass.

Heritability for selection within families ( $h^2_{ad}$ ) (Table 3) showed similar magnitude to individual heritability. Even in the 4<sup>th</sup> cycle of recurrent selection, there was still a difference within the evaluated families. Ferreira et al. (2016) evaluated the second cycle of recurrent selection of passion fruit of UENF and observed high-magnitude estimates of heritability within families (0.65, 0.78, and 0.67 for NF, PT, and FM, respectively), suggesting that genetic gain was greater within than among families. In this case, selection can be performed among and within families to exploit the variability and increase genetic gains.

The coefficient of determination of plot effects ( $c^2_{plot}$ ) was of low magnitude, except for the traits peel thickness, and total soluble solids (11 and 16%) (Table 3).  $c^2_{plot}$  quantifies the variability of plots within blocks, and estimates of up to 10% are not sufficient to interfere with the estimate of genetic parameters (Resende, 2002).

Accuracy is the most important parameter in the evaluation of precision in the access to the true genetic variation. Thus, higher accuracy values mean greater reliability in the evaluation and in the predicted genetic value (Resende, 2002). Resende and Duarte (2007) classified accuracy as very high ( $\geq 0.90$ ), high (0.89 to 0.70), moderate (0.69 to 0.50), and low ( $\leq 0.49$ ). High-magnitude accuracy was observed for the traits number of fruits (0.74), fruit length, and fruit diameter (0.71 and 0.73) (Table 3). Production, fruit mass, peel thickness, pH, and pulp percentage had medium-magnitude accuracy (0.60, 0.69, 0.62, 0.60, and 0.69), although this range still provides a safe estimate of predicted and inheritable genetic gains. Total soluble solids (0.47) was the only trait with low accuracy, suggesting lower reliability of the data, possibly because this trait is greatly influenced by the environment or by the low heritability, which consequently reduces the accuracy values.

### **Modification of selection strategies**

Silva et al. (2009) evaluated a selection strategy in the stage of generation and test of passion fruit progeny and obtained genetic gains with the use of truncation selection and index selection, considering two simulations of gain: one by selecting eight superior families; and another by selecting 18 superior families. The gains observed by those authors were lower than those obtained with the two methods tested in the current study for the traits number of fruit and fruit mass. The direct gains obtained by selecting eight superior families for the respective traits were 2.97% and 7.83%, respectively; by selecting 18 superior families, the respective gains were 1.19% and 3.49%. Through index selection, when eight superior families were selected, these values were 2.47% and 3.1%, respectively; with 18 superior families selected, these values were 1.03% and 3.18%. The direct gains for each individual trait were higher than those obtained with index selection (Table 4).

**Table 4.** Estimates of predicted selection gains in three different selection methods in sour passion fruit populations cultivated in Campos dos Goytacazes-RJ. Brazil. 2019.

Traits	Selection within		Selection between		Silva et al. (2009) Direct selection		Selection index	
	Gain %	Ne	Gain %	Ne	SG% <sup>1</sup>	SG% <sup>2</sup>	SG% <sup>1</sup>	SG% <sup>2</sup>
NF	42.83	36.8	26.76	36	2.97	1.19	2.47	1.03
PROD	21.88	36.8	15.08	36	-	-	-	-
FM	14.29	36.8	8.59	36	7.83	3.49	3.1	3.18
LF	4.70	36.8	3.02	36	2.79	1.27	0.64	0.47
DF	3.70	36.8	2.35	36	3.56	1.56	2.64	1.36
ST	1.37	36.8	2.91	36	-5.85	-3.07	0.64	0.65
TSS	2.69	36.8	1.91	36	-	-	-	-
pH	2.04	36.8	1.43	36	-	-	-	-
PP	6.43	36.8	4.72	36	-	-	-	-

SG%<sup>1</sup> - Selection gain in percentage, considering the selection of 8 superior progenies. SG%<sup>2</sup> - Selection gain in percentage, considering the selection of 18 superior progenies. Ne - Effective population size.

Selection within half-sib families provided superior gains when compared with selection among families and with the gains found by Silva et al. (2009) for the traits number of fruits; production; fruit mass, length, and diameter; total soluble solids; pH; and pulp percentage (Table 4). A positive gain was obtained for peel thickness (1.37%), despite being lower than that found with selection among families (2.91), considering it is desirable to reduce the expression of this trait. Fortaleza et al. (2005) stated that passion fruits with a finer peel are preferred, since they contain more pulp.

The efficiency of simultaneous selection with selection indices using estimated genetic gains in yellow passion fruit showed that the indices contributes to higher genetic gains for all the traits evaluated in that study and the index based on the sum of ranks of Mulamba & Mock provided a balanced distribution of gains, selecting a larger number of progenies (Rosado et al., 2012).

Research points to a reduction in genetic variability after a few cycles of recurrent selection, usually due to a decline in population size (Hallauer, 1971). Genetic drift may lead to a loss of favorable alleles or a fixation of unfavorable alleles, and there may be a marked drop in genetic variability, which can compromise genetic gains (Hallauer et al., 1988). Coupled with this, in the case of passion fruit, the diversity of self-incompatibility alleles should be preserved, since crosses between related individuals via a reduction of effective number may generate pollination and fructification problems in the selected families. Therefore, the selection intensity to be applied is an important factor in as much as high intensities may cause genetic drift due to the reduced effective size of the populations generated by the recombination of the selected progeny (Reis et al., 2011).

Associated with this fact, a better balance can be established between the genetic covariance to be capitalized. The covariance between the random effect model's can be optimized in the selection within families. The pollination control, with the individual collection of the best plants, will promote a better use of the additive genetic component, capitalized in the families of half-sibs (Viana and Resende, 2014).

## CONCLUSIONS

Selection performed within half-sib families provided greater gains than selection among families. As such, the former strategy is indicated, as it promotes a lower selection intensity, thereby allowing for the generation of superior full-sib families of passion fruit.

The Post-Hoc Blocking Row-Col technique showed similar performance to the randomized-block model, with no significant differences for any of the evaluated traits. Therefore, the randomized-block design was better suited for this analysis because it is simpler to execute.

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## CONFLICTS OF INTEREST

The authors declare no conflict of interest.

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