Estimates of Genetic Parameters and Selection Strategies in F1 Progenies Obtained from Endogamic Lines of Sour Passion Fruit

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Authors' contributions

This work was carried out in collaboration between all authors. All authors read and approved the final manuscript.

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ABSTRACT

Aims: This experiment was to obtain the genetic parameters and to define the best selection strategy in F1 progenies of sour passion fruit from the crossing between inbred lineages and heterozygous genotypes.
Study Design: Experimental design was completely randomized blocks with nine progenies and five replicates with four plants per plot.
Place and Duration of Study: Experimental Farm of Araponga operated by the Universidade Federal de Viçosa in Araponga county, Minas Gerais, Brazil from August 2015 to February 2017.
Methodology: Fruit characteristics of the progenies were evaluated in the first year of production. Data were analyzed using ANOVA, and the genetic parameters were estimated. The selection strategies were indices of Mulamba and Mock and Smith and Hazel, Selection Among and Within Families, and Combined.
Results: Estimates of genetic parameters for fruit mass, pulp mass, bark mass, and bark thickness showed high genetic variability. The heritability coefficients for these characteristics were 0.95; 0.34;

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1.00 and 1.00, respectively. Total soluble solids, titratable total acidity, pulp yield, and total soluble solids/total titratable acidity ratio values showed heritability coefficients equal to zero. Combined selection had the highest gains, followed by selection among and within families.

Conclusion: Estimates of genetic parameters for the passion fruit population indicated high genetic variability. All the selection strategies indicated gains with selection, with emphasis for combined selectionin genetic improvement of sour passion fruit.

1. INTRODUCTION

Brazil is one of the world's leading producers of passion fruit. In 2014, production of sour passion fruit in Brazil was around 820,000 tons [1]. The sour passion fruit is native to Brazil and is widely distributed throughout South and Central America [2]. The species *Passiflora edulis* Sims is allogamous and autoincompatible [3] and presents high genetic variability, despite its commercial exploitation. Given these characteristics, passion fruit breeding programs have advocated obtaining hybrids and exploring heterosis, which is one of the great challenges to the selection of materials that express their phenotype in the largest possible number of agronomic characters of importance [4,5].

Heterosis has been commonly explored in programs of genetic improvement of crossbred plants through crossbreeding between selected inbred lines and by presenting complementarity through superior offspring [6]. Inbreeding lines are obtained through self-fertilization, but this strategy is made difficult due to self-incompatibility of sour passion fruit. Inbreeding in this case is often obtained through crosses between sister plants and backcrosses. Few studies currently exist in the literature regarding the genetic parameters and the gains obtained with the selection of progenies obtained from self-fertilized genotypes of passion fruit.

Studying the genetic parameters of the population and the best selection strategy to be applied is necessary to obtain the greatest gain from selection in a breeding program for any crop. Genetic parameters estimated in a population refer specifically to that population [7]. These estimates are essential to know the genetic structure of the population since they allow us to understand the origin of the present variation, which directs the breeder to the best applied selection strategy.

Several selection strategies applied to passion fruit culture have been reported in the literature [4, 8, 9, 10]. The selection indices of Mulamba and Mock [11] and Smith [12] and Hazel [13] and the selections among and within and combined selections are often applied to the genetic improvement of passion fruit. The selection indices are interesting because they allow simultaneous selection considered from different characteristics. Selection index corresponds to a value, defined by a linear function of genotypic values of several characters, which is weighted by a relative economic value attributed by the breeder based on breeding objectives [14].

The selections among and within and combined selections are different from the selection indices estimates gained for each characteristic. Prediction of gains referring to individual criteria allows the breeder to direct the selection to those desired characteristics [15]. However, the combined selection differs from the selection among and within by making an individual selection in the population. The selection among and within is initially considered the families; specifically, within the selected families of the superior individuals [16, 7, 17].

In this sense, the objective was to obtain estimates of genetic parameters and to define the best selection strategy in F1 progenies of passion fruit obtained from inbred lines for fruit characteristics.

2. MATERIALS AND METHODS

2.1 Plant Material

Nine progenies of full-sibs of passion fruit (*Passiflora edulis* Sims) were evaluated for fruit characteristics. The progenies were obtained from crosses among strains with low requirement in photoperiod (2nd generation of self-pollination [18]) and genotypes with some degree of resistance to Fusarium (*Fusarium* sp.). All strains were selected by the Genetic Improvement Program in Passion Fruit of the Universidade Federal de Viçosa, as described in Table 1.

Table 1. Identification (ID) and ancestry of the sour passion fruit progenies evaluated. Araponga county, Minas Gerais, Brazil in 2016

ID	Parentage	
	Female genitor (♀)	**Male genitor (♂)**
H42	Mutant genotype with low requirement in photoperiod and temperature (UFV-M7. 1)	Mix resistant mutant genotype of 13 isolates of *F. oxysporum* f sp. *Passiflorae* (UFV54)
H43	Genótipo mutante resistente ao mix de 13 isolados de *F. oxysporum* f sp. *Passiflorae* (UFV54)	Mutant genotype with low requirement in photoperiod and temperature (UFV-M7.1)
H44	BRS Sol do Cerrado resistant to the Mix of 13 isolates of *F. solani* (Sol35)	Mutant genotype with low requirement in photoperiod and temperature (UFV-M7.1)
H45	Mutant genotype with low requirement in photoperiod and temperature (UFV-M7.1)	BRS Sol do Cerrado resistant to *F.solani* isolate 19 (Sol23)
H46	BRS Sol do Cerrado resistant to *F.solani* isolate 19 (Sol23)	Mutant genotype with low requirement in photoperiod and temperature (UFV-M7.1)
H47	Mutant genotype with low requirement in photoperiod and temperature (UFV-M7.2)	BRS Sol do Cerrado resistant to *F.solani* isolate 19 (Sol23)
H48	BRS Sol do Cerrado resistant to *F.solani* isolate 19 (Sol23)	Mutant genotype with low requirement in photoperiod and temperature (UFV-M7.2)
H49	Mix resistant mutant genotype of 13 isolates of *F. oxysporum* f sp. *Passiflorae* (Sol35)	Mutant genotype with low requirement in photoperiod and temperature (UFV-M7.2)
H50	Mix resistant mutant genotype of 13 isolates of *F. oxysporum* f sp. *Passiflorae* (UFV54)	Mutant genotype with low requirement in photoperiod and temperature (UFV-M7.2)

2.2 Local Characterization

The experiment was conducted at the Experimental Farm of Araponga operated by the Universidade Federal de Viçosa in Araponga county, Minas Gerais, Brazil from August 2015 to February 2017. The positions of the site were described at 20° 40' 00" south latitude and 42° 31' 00" west longitude with an altitude 885 m relative to sea level.

2.3 Experimental Design and Conducting the Experiment

Experimental design was completely randomized blocks with nine progenies and five replicates with four plants per plot. Controlled crosses in plants kept in greenhouse conditions were carried out to obtain the progenies during the month of December 2014. The fruits were harvested fully ripe at about 65 days after pollination. Seedling production was carried in the month of March 2015 and the planting was carried after five months. Spacing used was of 4 × 3 m, and the plants was conducted in a system of "espaldeira" with a wire of wire height of 1.80 m.

During the experiment, the cultural practices recommended for cultivation, such as plant management, pruning, fertilization [19], irrigation, weed control, and pest and disease control, were accomplished.

2.4 Characteristics Evaluated

In the first year of production of the F1 population of passion fruit, the following analyzes were carried out to characterize the fruits: FM: fruit mass (g); FL: fruit length (mm); FD: fruit diameter (mm); PM: pulp mass (g); BT: bark thickness (mm); BM: bark mass (g); TSS: soluble solids content (ºBrix); YP: yield of pulp (%); TTA: titratable total acidity (% citric acid); TSS/TTA: total soluble solids/titratable total acidity ratio.

2.5 Statistical Analyzes

Statistical analyzes were performed using the Genes Software [20]. The fruit characteristics were analyzed using ANOVA and by applying a randomized block design with information within the plots in order to obtain the genetic parameter estimates and to identify the best selection strategy, according to the model described below.

$$Y_{ijk} = \mu + G_i + B_i + \varepsilon_{ij} + \delta_{ijk}$$

Y_{ijk} = k-[th] plant observation, in the i-[th] family, of the j-[th] block; μ= general mean of the population; G_i = effect of the i-[th] family $i = 1, 2, ..., g$, $G_i \sim$NID $(0, \sigma_g^2)$; B_i = effect of the j-[th] block; ε_{ij}= random environmental effect among plots $\varepsilon_{ij} \sim$NID $(0, \sigma_e^2)$; δ_{ijk} = random effect among plants within the plot $k = 1, 2, ..., n$ e $\delta_{ijk} \sim NID(0, \sigma_d^2)$.

Estimation of the genetic parameters of the studied population was composed of families of full-sibs ($\sigma_g^2 = \frac{1}{2}\sigma_A^2 + \frac{3}{4}\sigma_D^2$), with: $\sigma_A^2 =$ genetic variance and $\sigma_D^2 =$ variance attributed to dominance deviations). The estimated genetic variance component among family means$\widehat{(\sigma}_{gm}^2)$; genetic variance within families ($\widehat{\sigma}_{gd}^2$); heritability at the mean level of full-sib families (h_m^2) ; heritability at the family level for selection among plants within families (h_d^2); coefficient of genetic variation among families (CV_{ge}), in %; and the coefficient of experimental variation (CV_{ex}), in %.

Afterwards, the selection gains were estimated by applying the selection strategies: Mulamba and Mock index [11] (MMI); Smith and Hazel index [12] [13] (SHI); selection among and within families (SBW); and combined selection (CS). For the use of the indices of MMI, SHI in the selection, the original population averages were adopted as economic weights and with the selection of 50% of progenies evaluated. Characteristics were evaluated in the character addition, except for bark thickness and bark weight, which were evaluated based on the direction of decrease.

3. RESULTS

3.1 Estimates of Genetic Parameters

The results obtained indicated significant differences at the 1% probability level by the F test for most of the characteristics evaluated, except for TSS, TTA, and TSS/TTA (Table 2).In the studied population, no genetic variance estimates were observed among family means for the TTA variable. For the FM the genetic variance estimate was 512.92. The genetic variance within families presented values around 0.03 for TTA and 452.12 for FM. In relation to the coefficients of heritability among and within families, values higher than 0.90 were observed for FM, BT, and BM. Values equal to zero were observed for FL, TSS, PY, TTA, and TSS/TTA.

The characteristics of FM, PM, BT, and BM presented the highest coefficients of genetic variation, varying between 12.34% and 14.56%. The other characteristics presented coefficients of genetic variation of 2.59, 3.26, 1.03, 4.78, 1.48, and 2.53%, respectively, for FL, FD, TSS, PY, TTA, and TSS/TTA. For the coefficient of environmental variation, the observed values were between 3.60 and 11.21%. The highest

values were for FM (9.68%), PM (10.29%), BT (8.63%), and BM (11.21%).

For the TSS/TTA among genetic coefficient of variation and coefficient of environmental variation, the FM, FD, PM, BT, and BM presented values between 0.90 and 1.30. The FL, TSS, TTA, and TSS/TTA presented a ratio of coefficients ranging from 0.25 for total titratable acidity to 0.66 for length of fruit (Table 2).

3.2 Selection Indices

The total gains with the MMI and SHI indices were 35.29 and 31.62%, respectively (Table 3). The values predicted with the application of the indices were lower than those obtained with the SBW and with the CS. For the MMI, the characteristics of FM, PM, BT, and BM provided the greatest gains with selection with values of 8.79; 7.71; 5.79 and 9.72%, respectively.

The characteristics of PY and TSS/TTA presented losses with selection for the two indices applied. The highest losses were observed for SHI, which also showed loss in selection for TSS. For BT, the greatest difference of selection gain among the indices applied was verified. The observed selection gains were 5.34% for the MMI and 3.85% for the SHI. The selection gains for SHI ranged from -1.10% for TSS/TTA and 8.77% for FM.

The indices classified the progenies differently with agreement only in the order of the progenies H46 and H50, which were positioned 6th and 8th, respectively. For the MMI, the first four ordered progenies were H45, H47, H49, and H44 whereas for the SHI they were H44, H49, H48 and H45 (Table 4).

The MMI placed the progenies with the highest values of FM, FL, and FD at the top of the positioning. The values verified for the first positions varied among 205.71 g for H45 (1st) and 185.93 g for H44 (4th). The H49 progeny, which presented a FM of 194.95 g, was classified into the 5th position due to its low average PY and the high average of BT and BM. On the other hand, the classification attributed by the SHI did not preferentially order progenies with greater FM. In the higher positions were progenies, H44 (1st), H49 (2nd), H48 (3rd), and H45 (4th). The values of BT and BM for these progenies ranged between 5.06 and 5.98 mm, and 88.51 and 107.86 g, respectively.

Table 2. Summary of variance analysis and estimates of genetic and environmental parameters of fruit characteristics evaluated in progenies of full-sibs in a sour passion fruit population from the experiment conducted in Araponga County, Minas Gerais, Brazil in 2016

SV	DF	Mean square									
		FM	FL	FD	PM	BT	BM	TSS	YP	TTA	TSS/TTA
Blocks	4	1395.50	81,43	67,19	254.62	1.49	744.23	2.87	58.12	0.26	6.48
Progenies	8	10822.50**	150.44**	141.65**	2654.5**	8.00**	3562.80**	1.36 ns	127.4**	0.06 ns	1.56 ns
Among	32	1137.99	46.51	27.73	324.15	0.71	378.01	0.98	18.76	0.04	0.90
Within	127	595.72	25.03	14.05	284.97	0.39	178.91	0.95	27.22	0.04	0.82
Mean		179.24	90.48	75.36	90.07	5.04	89.24	13.77	50.22	1.891	7.38
$\hat{\sigma}_{gm}$		512.92	5.50	6.03	123.42	0.39	168.68	0.02	5.76	0.00	0.03
$\hat{\sigma}_{gd}$		452.12	19.35	10.43	274.59	0.31	126.18	0.94	29.46	0.03	0.80
h_m^2		0.95	0.00	0.51	0.34	1.00	1.00	0.00	0.00	0.00	0.00
h_d^2		0.90	0.00	0.27	0.17	1.00	1.00	0.00	0.00	0.00	0.00
CV_{ge}		12.64	2.59	3.26	12.33	12.34	14.55	1.03	4.78	1.48	2.53
$CV_{ex}(\%)$		9.68	3.88	3.60	10.29	8.63	11.21	3.71	4.44	5.74	6.60
CV_{ge}/CV_{ex}		1.30	0.67	0.90	1.20	1.43	1.30	0.28	1.08	0.26	0.38

**: Significant at 1% probability by F test; ns: Non-significant by the F-1 test and 5% probability; FM: fruit mass (g); FL: fruit length (mm); FD: fruit diameter (mm); PM: pulp mass (g); BT: bark thickness (mm); BM: bark mass (g); TSS: soluble solids content (◦Brix); YP: yield of pulp (%); TTA: titratable total acidity (% citric acid); TSS/TTA: total soluble solids/titratable total acidity ratio;$\hat{\sigma}_{gm}$: estimation of variance among mean families; $\hat{\sigma}_{gd}$: estimation of variances within families; h_m^2: coefficient of heritability among family averages; h_d^2: coefficient of heritability within families; CV_{ge}:

coefficient of genetic variation among families; $CV_{ex}(\%)$: experimental coefficient of variation $CV_{ex}(\%) = (\frac{100\sqrt{QME/n}}{\mu})$.

Heritability coefficient values negative and / or greater than the unit were considered respectively as 0.00 and 1.00

Table 3. Estimates of predicted gains (%) in in progenies of full-sibs in a sour passion fruit population for the Mulamba and Mock (MMI) and Smith and Hazel (SHI) indices in a sour passion fruit population for the experiments conducted in Araponga County, Minas Gerais, Brazil in 2016

Characteristics	Original mean	MMI[1]		SHI[1]	
		Predicted mean	SG	Predicted mean	SG
FM	178.58	196.12	8.79	196.09	8.77
FL	90.33	92.46	1.63	92.37	1.57
FD	75.26	77.40	2.29	77.11	1.98
PM	89.93	97.83	7.71	97.58	7.47
BT	5.02	5.34	5.79	5.23	3.85
BM	88.72	98.36	9.72	98.39	9.74
TSS	13.79	13.91	0.25	13.73	-0.12
YP	50.34	49.81	-0.89	49.68	-1.11
TTA	1.89	1.92	0.34	1.94	0.57
TSS/TTA	7.38	7.32	-0.34	7.19	-1.10
Total	-	-	35.29	-	31.62

FM: fruit mass (g); FL: fruit length (mm); FD: fruit diameter (mm); PM: pulp mass (g); BT: bark thickness (mm); BM: bark mass (g); TSS: total soluble solids content (◦Brix); YP: yield of pulp (%); TTA: titratable total acidity (% citric acid); TSS/TTA: total soluble solids/ titratable total acidity ratio; [1]: Economic weight: original mean

3.3 Selection among and Within and the Combined Selection

The SBW provided total selection gains among zero and 23.71% with emphasis on the characteristics of FM, BT, and BM, which presented total gains of 23.71, -21.61, and 28.83%, respectively (Table 5). The gains with the selection within families were higher than the gains among families for FM characteristics (13.39%) and BM (15.06%). In the selection among families, the characteristics of FM (10.32%), BT (-11.26%), and BM (-14.17%) showed the greatest gains with selection. The TSS, PY, TTA, and TSS/TTA did not show gains in selection among and within families.

The predicted gains in the CS were higher than the gains obtained with the other selection strategies applied to the population. The estimates of weights relative to the individual value of the plant (b_i), the family (b_f), the relative

value (b_i/b_f), and the expected gains from the combined selection are shown in Table 6.

The values of b_i for FM, BT, and BM were 0.75, 0.90, and 0.84, respectively. The FD and PM characteristics presented b_f values higher than the values of b_i. The observed b_i values were 0.33 for FD and 0.21 for PM. The variables FL, TSS, PY, TTA and TSS/TTA values presented b_i and bf values equal to 0.01. Consequently, the relation among b_i/b_f for these characteristics was equal to 1.00. These variables presented the lowest relative weights for both the individual value and the average number of families.

The CS applied to the population provided selection gains in all characteristics considered. However, characteristics FL, TSS, PY, TTA, and TSS/TTA presented selection gains between 0.13 and 0.24%. The highest gains with the CS were obtained for FM (28.16%), BT (-27.88%) and BM (-32.99%). The characteristics FD and PM presented, respectively, 3.36 and 8.66% of gains with the selection.

4. DISCUSSION

The estimates of genetic parameters obtained for the population indicated variability for the evaluated characteristics, with the exception of TSS, TTA, and the TSS/TTA. The genetic variability observed in the population indicates the possibility of gains with the selection. The evaluated population is composed of families of full-sibs obtained from hybridizations between genotypes from two generations of self-fertilization and heterozygous genotypes. The observed genetic variability may be a result of the heterosis provided by this hybridization. The amount of heterosis obtained from a crossover is determined by the difference in gene frequencies between the loci of the parents that determine the characteristic [7].

Heritability represents the proportion of the phenotypic variation present in the population that is due to genetic variation. Characteristics with heritability higher than 0.40 are considered very heritable [21, 22]. Heritability values higher than 0.90 were observed for FM, BT, and BM. These characteristics were also verified by the highest values of coefficient of genetic variation, which is an estimate directly proportional to the genetic variation of the population. The heritability values, the coefficient of genetic variation, and the ratio between the coefficients of genetic and environmental variation suggested that the greatest variation corresponds to the

present genetic variation and may be a reflection of the hybrid vigor caused by the hybrids that gave origin to the population. The hybrid vigor can be manifested in different characteristics that were productivity, cell size, and fruit size [6].

Genetic parameters in sour passion fruit populations were estimated by different authors, who presented results similar to those verified in the studied population. The characteristics of FM, PM, BM, FD, and BT presented the highest genetic variation, as evidenced by the high heritability values and coefficient of genetic variation [23, 24, 25]. The genetic parameters proved that gains were obtained with the independent selection of the strategy applied to the characteristics, which itself presented genetic variability. The applied selection indices presented smaller gains than the SBW and the CS, which were observed as negative gains of low magnitude for some characteristics. The prediction of negative gains through selection indices is related to the simultaneous selection of characters performed by the selection indices [14]. In this type of strategy, the selection of a characteristic can influence the selection gains in other characteristics and, in some cases, cause negative gains.

The MMI was higher than the SHI index, but the values observed for the two indices were close. The lower values of gains obtained with SHI compared to MMI were reported by several authors in passion fruit populations formed by families of half-brothers and full-sibs [4, 8, 25]. The differences observed between the two indices can be explained by the order of the progenies. In the case of the SHI, this makes a linear combination whereby the weighting coefficients are estimated in order to maximize the correlation between the index and the genotype coefficient. This is actually a linear combination that includes the genetic values weighted by their economic values. Opposingly, the MMI hierarchizes the genotypes initially for each characteristic by assigning absolute values to those of better performance and later the values assigned to each characteristic are summed to obtain the rank.

The greatest gains with selection were estimated for FM, BT, and BM and were related to the high genetic variability found for these characteristics in the population. In the CS and in the SBW, these characteristics presented gains with the selection greater than 20%. Both the selection gain within families obtained for SBW, as well as the individual weight of the plant in the CS,

showed greater influence in the total gain of selection obtained compared to the gain by selection among families. Larger selection gains within families than among families were due to coefficients of heritability within larger families than among families. The characteristics of FM and BM were estimated coefficients of heritability within high families and reflected the selection gains within families. In half-sibs families of *Eucalyptus grandis* [26] and families of full-sibs *Coffea Arabica* [27], has also been found some characteristics gains using selection within families were larger than among families.

The CS provided gains greater than those obtained for the other selection strategies in the progenies studied. All the evaluated characteristics presented gains with the combined selection. However, the characteristics that did not present genetic variability had gains with the selection that were close to 0.05%.

Similar results were verified for CS in a population of parental and hybrids of passion fruit for the characteristics that did not present genetic variability [25]. In the SBW, characteristics that did not indicate genetic variability did not present gains with the selection. Several works in the literature have shown the superiority of the combined selection in relation to other selection strategies, both in the genetic improvement of passion fruit and other cultivated species [7, 25, 26, 27]. The efficiency of the combined selection in relation to the other improvement methods is due to the greater number of information that is considered in the selection, since it ponders the individual performance of the plants associated to the family performance, providing the best results [26].

Estimates of genetic parameters and estimated selection gains for the passion fruit population indicated high genetic variability, which could be

Table 4. Hierarchization obtained through the Mulamba and Mock indices (MMI) and Smith and Hazel (SHI) and the means for fruit characteristics in progenies of full-sibs of a sour passion fruit population from the experiment conducted in Araponga County, Minas Gerais, Brazil in 2016

Prog.	MMI	SHI	Characteristics									
			FM	**FL**	**FD**	**PM**	**BT**	**BM**	**TSS**	**YP**	**TTA**	**TSS/TTA**
H42	7	9	153.65	88.05	71.92	81.00	4.22	73.23	14.05	52.65	1.83	7.74
H43	9	7	134.47	85.54	70.29	68.13	4.02	66.04	13.82	50.58	1.83	7.64
H44	4	1	185.93	90.27	76.00	98.01	5.06	88.51	13.93	52.70	1.89	7.45
H45	1	4	205.71	92.72	77.86	107.32	5.23	98.39	13.76	52.22	1.95	7.15
H46	6	6	179.02	89.19	74.25	94.68	4.81	84.34	13.84	52.72	1.87	7.48
H47	2	5	195.06	92.40	77.76	96.06	5.24	98.70	13.94	49.34	1.92	7.30
H48	5	3	194.95	92.06	76.58	95.06	5.98	99.88	13.21	48.81	1.99	6.77
H49	3	2	197.78	94.45	78.00	89.92	5.82	107.86	14.01	44.98	1.91	7.39
H50	8	8	160.69	88.26	74.65	79.19	4.78	81.50	13.51	49.01	1.83	7.51

Prog: progeny; FM: fruit mass (g); FL: fruit length (mm); FD: fruit diameter (mm); PM: pulp mass (g); BT: bark thickness (mm); BM: bark mass (g); TSS: total soluble solids content (◦Brix); YP: yield of pulp (%); TTA: titratable total acidity (% citric acid); TSS/TAA: total soluble solids/titratable total acidity ratio

Table 5. Estimates of selection gains (%) predicted among (SG_b), within (SG_w) and total (SG_t) in the selection percentages of 50% among and 25% within families of full-sibs of sour passion fruit. Araponga County, Minas Gerais, Brazil in 2016

Characteristics	Original mean	SG_b	SG_w	SG_t	Predicted mean
FM	178.58	10.32	13.39	23.71	220.93
FL	90.33	0.00	0.00	0.00	90.33
FD	75.26	1.51	1.30	2.81	77.37
PM	89.93	3.45	3.29	6.75	96.00
BT	5.02	-11.26	-10.34	-21.61	3.93
BM	88.72	-14.17	-11.95	-26.12	65.55
TSS	13.79	0.00	0.00	0.00	13.79
YP	50.34	0.00	0.00	0.00	50.34
TTS	1.89	0.00	0.00	0.00	1.89
TSS/TTA	7.38	0.00	0.00	0.00	7.38

FM: fruit mass (g); FL: fruit length (mm); FD: fruit diameter (mm); PM: pulp mass (g); BT: bark thickness (mm); BM: bark mass (g); TSS: total soluble solids content (◦Brix); YP: yield of pulp (%); TAA: titratable total acidity (% citric acid); TSS/TAA: total soluble solids/titratable total acidity ratio

Table 6. Estimates of weights relative to the individual value of the plant (b_i), family (b_f), relative value (b_i/b_f) and the expected gains with the combined selection for progenies of full-sibs in a passion fruit population. Araponga County, Minas Gerais, Brazil in 2016

Characteristics	Original mean	Estimates of the CS coefficients			CS	Predicted mean
		b_i	b_f	b_i/b_f	SG	
FM	178.58	0.75	0.29	2.59	28.16	228.87
FL	90.33	0.01	0.01	1.00	0.14	90.45
FD	75.26	0.23	0.33	0.70	3.36	77.78
PM	89.93	0.17	0.21	0.79	8.66	97.72
BT	5.02	0.90	0.20	4.51	-27.88	3.62
BM	88.72	0.84	0.26	3.22	-32.99	59.45
TSS	13.79	0.01	0.01	1.00	0.13	13.80
YP	50.34	0.01	0.01	1.00	0.21	50.44
TTS	1.89	0.01	0.01	1.00	0.18	1.90
TSS/TTA	7.38	0.01	0.01	1.00	0.24	7.40

FM: fruit mass (g); FL: fruit length (mm); FD: fruit diameter (mm); PM: pulp mass (g); BT: bark thickness (mm); BM: bark mass (g); TSS: total soluble solids content (°Brix); YP: yield of pulp (%); TAA: titratable total acidity (% citric acid); TSS/TAA: total soluble solids/titratable total acidity ratio

explored in the population improvement. The crosses, yielded expressive hybrid vigor, being manifested mainly in FM, FD, BT and PM. All the selection strategies indicated gains with selection, being verified the highest values for combined selection.

5. CONCLUSION

Based on the information on for genetic parameter estimates and the estimated selection a gained for the passion fruit F1 progenies, high genetic variability has been verified, which can be explored in the population improvement. Thecrosses, yielded expressive hybrid vigor, which was being manifested mainly in fruit mass, fruit diameter, bark thickness, and pulp mass. For all selection strategies, gains with selection were estimated, and the highest values for combined selection were verified. There are few studies that estimate the genetic parameters and selection gains in passion fruit populations, formed from crosses with endogamous passion fruit strains.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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