

Genotypic selection of multispecific hybrids obtained through crosses between commercial *Passiflora edulis* and wild passiflora species

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Abstract - The interspecific introgression of resistance genes to diseases in commercial varieties through interspecific crosses has been adopted as a strategy in breeding programs of sour passion fruit. This work aimed to evaluate 11 progenies of multispecific hybrids obtained from crosses involving seven *Passiflora* species, in addition to four commercial cultivars, using the REML/BLUP method. The experiment was carried out as a randomized block design with six repetitions and three plants per plot. Ten fruit traits were evaluated. The additive, multiplicative, and sum of ranks indexes were applied to determine the most appropriate selective strategy in the simultaneous increase of fruit weight, number of fruits, and yield. Plants from the 325 x VAO progeny showed a lower bacterial defoliation index and better means predicted for the traits number of fruits and productivity. The progenies 325 x LD4, PL3 x LD4, and the controls CSB-Marília and BRS-Gigante Amarelo showed plants with better-predicted means for traits related to fruit quality. The genetic gains demonstrated good prospects for the use of wild species in sour passion fruit genetic breeding.

Index terms: Passion fruit, genetic breeding, genetic gain, plant selection.

Seleção genotípica de híbridos multiespecíficos obtidos por meio de cruzamentos entre *Passiflora edulis* “flavicarpa” comercial e espécies de passifloras silvestres

Resumo – A introgressão de genes de resistência a doenças em variedades comerciais, por meio de cruzamentos interespecíficos, tem sido adotada como estratégia nos programas de melhoramento de maracujá-azedo. Este trabalho objetivou avaliar 11 progênes de híbridos multiespecíficos obtidas através de cruzamentos envolvendo sete espécies de *Passiflora*, além de quatro cultivares comerciais, utilizando o método REML/BLUP. O experimento foi conduzido em blocos casualizados, com seis repetições e três plantas por parcela. Dez caracteres foram avaliados. Os índices aditivo, multiplicativo e de soma de ranks foram utilizados para determinar a estratégia de seleção mais adequada no melhoramento simultâneo de peso de fruto, no número de frutos e na produtividade. Plantas da progênie 325 x VAO apresentaram menor índice de desfolhamento por bacteriose e melhores médias preditas para os caracteres número de frutos e para produtividade. As progênes 325 x LD4, PL3 x LD4 e testemunhas CSB-Marília e BRS-Gigante amarelo apresentaram plantas com melhores médias preditas para caracteres relacionados à qualidade de fruto. Os ganhos genéticos obtidos demonstraram boas perspectivas para o uso de espécies silvestres no melhoramento genético do maracujá.

Termos para indexação: Maracujá, melhoramento genético, ganho genético, seleção de plantas.

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Introduction

Brazil is the world's largest producer and consumer of passion fruit (*Passiflora edulis* Sims). In 2019, the mean Brazilian passion fruit yield was 14.27 ton ha⁻¹ (IBGE 2020). However, the crop's potential may exceed 40 tons ha⁻¹ year⁻¹ (FONSECA, 2017). The Brazilian low mean yield is related to phytosanitary issues; inadequate crop management; non-utilization of improved cultivars; and non-utilization of cultivars adapted to the edaphoclimatic conditions of each region of the country (FALEIRO et al., 2019b). Therefore, passion fruit breeding programs aim to develop new cultivars that are more productive and, mainly, resistant to pests and pathogens.

Bacterial spot, caused by *Xanthomonas axonopodis* pv. *passiflorae*, stands out as one of the major diseases affecting the passion fruit crop (JUNQUEIRA et al., 2016). This disease affects the aerial part of the plant, which can lead to intense defoliation, plant drought, and, consequently, the premature death of plants (PERUCH et al., 2011). Some *Passiflora* species are resistant to the main diseases affecting the aerial part of the plant (passion fruit woodiness disease, bacterial spot, and anthracnose), under field conditions, in the Federal District (JUNQUEIRA et al., 2005).

The introgression of resistance genes from wild species and commercial varieties into the sour passion fruit, through interspecific crosses, has been adopted as a strategy by the passion fruit breeding program of Embrapa and its partners (FALEIRO et al., 2011). However, most wild species have some undesirable agronomic traits. As a result, progenies obtained from interspecific crosses must go through pre-breeding strategies and a selection process between and within progenies to recover the agronomic traits of the recurrent genome, maintaining the genes of resistance to pests and diseases (FALEIRO et al., 2011). Thus, it is important to select plants that produce fruits with physical-chemical characteristics capable of meeting the requirements of the market to which it is destined (BRUCKNER, 2011). For the processing industries, the fruits must have high values of juice yield, total soluble solids, and total titratable acidity (MELLETTI et al., 2002; ABREU et al., 2009). For *in natura* consumption, it is interesting to be able to acquire attractive fruits, of larger size, high concentration of total soluble solids and low total titratable acidity, in order to guarantee its flavor (BRUCKNER, 2011). In this way, breeding programs aim to obtain fruits with double aptitude, focusing on the highest pulp yield while preserving the qualities required by the fresh fruit market, with the largest fruit size.

The high genetic variability observed in progenies from interspecific crosses contributes to the increase of the selection efficiency. Genetic assessment based on REML/BLUP mixed models has great potential for increasing the genetic progress and accuracy in the selection process (FREITAS et al., 2013). Additionally, this method uses the pedigree information, thus considering kinship and inbreeding (RESENDE, 2016). Due to its advantages, the use of REML/BLUP has significantly increased in the estimation of genetic parameters and genotype selection in fruit species, such as papaya (OLIVEIRA et al., 2012), guava (QUINTAL et al., 2017), peach (BRUNA et al., 2012), coconut (FARIAS NETO et al., 2009), passion fruit (SILVA et al. 2016; FERREIRA et al., 2016; FREITAS et al., 2016; SILVA et al., 2017), among other crops.

Superior genotypes should be selected considering multiple traits simultaneously since cultivars of economic importance combine traits of interest to the farmer and consumer (RODRIGUES et al., 2011). Simultaneous selection can be performed by different methods, and the selection indexes are often used in fruit trees (TEIXEIRA et al., 2012; SILVA and VIANA, 2012; ATROCH et al., 2010). These indexes are obtained as linear combinations of measures of several traits. Selection indexes can be efficient since they allow the evaluation of all available information, attribute different weights to the studied traits, and value attributes considered of greater importance by the researcher (FALCONER, 1996). Such indexes are generally constructed from estimates of genetic parameters and phenotypic means obtained by the analysis of variance method (PEDROZO et al., 2009). However, the construction of indexes through components of variance estimated by REML and genetic values predicted by BLUP may result in a more accurate selection process (RESENDE, 2016). The selection index via mixed models can be obtained using three approaches: the additive or classic index (SMITH, 1936; HAZEL, 1943), the multiplicative index (SUBANDI et al., 1973), and the sum of ranks index (MULAMBA; MOCK, 1978).

Both the classic index and the multiplicative index recommend the attribution of economic weights in their construction. According to Resende (2002), better-earning predictions can be obtained by selection indexes with economic weights that consider the correlation structures between the selected characters. Correlations can circumvent difficulties in improving traits that have measurement problems due to the pronounced effect of the environment or low heritability by allowing the selection of correlated traits that do not present these problems (FALCONER; MACKAY, 1996). It is up to the breeder to check which traits should participate in the selection index to predict better gains for the traits under evaluation and associate the direct and indirect selections for increasing the gains of the character of greatest interest. Teixeira et al. (2012) aimed to determine

the most appropriate simultaneous selective strategy for incrementing fruit production components in acai palm. According to the authors, an economic weight that considers the correlation structure among the traits selected by the index discriminates the most productive acai palm progenies better.

The objective of this work was to estimate genetic parameters and obtain genotypic values predicted for seven quantitative fruit traits, number of fruits, yield, and defoliation index caused by the bacterial spot disease. This study also aimed to identify and compare the efficiency of three selection indexes in the simultaneous increase of production components in a sample composed of 11 progenies of sour passion fruit multispecific hybrids, involving wild species and commercial cultivars, and four commercial cultivars used as reference materials.

Material and Methods

A total of 11 full-sib progenies were obtained from interspecific crosses involving six wild species (*P. alata* Curtis silvestre, *P. aff. amethystina* “macrocarpa”, *P. caerulea* L., *P. hatschbachii* Cervi, *P. incarnata* L., *P. quadrifaria* Vanderpl.) and commercial matrices of *P. edulis* Sims (GA e LD4), which were used as recurrent parents (Table 1). The genotypes GA and LD4 are used as parents to obtain the cultivars BRS Gigante Amarelo and BRS Sol do Cerrado, respectively. The wild accesses used in the crossings belong to the germplasm bank “Flor da Paixão”, located at Embrapa Cerrados, in Planaltina, DF. As parents, the genotypes 325, M Rubi, Vermelhão, ML1, T3R3P1, PL3, and PL4 were also used. They are described below:

Table 1. Cultivars, multispecific hybrids, and their respective genetic origins.

Pi Genotype	Genetic origin/number of plants evaluated
1 BRS Gigante Amarelo	<i>P. edulis</i> / 12
2 BRS Sol do Cerrado	<i>P. edulis</i> / 10
3 SCS 437 Catarina	<i>P. edulis</i> / 12
4 PL3 x GA (T4R4P1) x LD4	[(<i>P. hatschbachii</i> x <i>P. quadrifaria</i>) x <i>P. incarnata</i>] x <i>P. edulis</i> (BC4) / 10
5 ML1 x LD4	(<i>P. edulis</i> x <i>P. cf. amethystina</i>) x <i>P. edulis</i> (BC6) / 10
6 LD4 x ML 1	<i>P. edulis</i> x (<i>P. edulis</i> x <i>P. cf. amethystina</i>) (BC6) / 11
7 ML 1 x Vermelhão (T3R3P1)	[(<i>P. edulis</i> x <i>P. cf. amethystina</i>) x <i>P. edulis</i> (BC5)] x (<i>P. caerulea</i> x <i>P. edulis</i>) (BC5) / 9
8 Vermelhão (T3R3P1) x ML 1	(<i>P. caerulea</i> x <i>P. edulis</i>) (BC5) x [(<i>P. edulis</i> x <i>P. cf. amethystina</i>) x <i>P. edulis</i> (BC5)] / 9
9 Vermelhão (T3R3P1) x 325	(<i>P. caerulea</i> x <i>P. edulis</i>) (BC6) x (<i>P. caerulea</i> x <i>P. edulis</i>) (BC5) / 12
10 325 x Vermelhão (T3R3P1)	(<i>P. caerulea</i> x <i>P. edulis</i>) (BC5) x (<i>P. caerulea</i> x <i>P. edulis</i>) (BC6) / 10
11 PL4 x LD4	[(<i>P. edulis</i> x <i>P. incarnata</i>) x <i>P. edulis</i> (BC3)] x [(<i>P. edulis</i> x <i>P. cf. amethystina</i>) x <i>P. edulis</i> (BC5)] / 11
12 PL3 x LD4	[(<i>P. hatschbachii</i> x <i>P. quadrifaria</i>) x <i>P. incarnata</i>] x <i>P. edulis</i> (BC2) / 12
13 M Rubi x ML 1	[(<i>P. alata</i> x <i>P. edulis</i> “roxo”) x <i>P. edulis</i>] x [(<i>P. edulis</i> x <i>P. cf. amethystina</i>) x <i>P. edulis</i> (BC5)] / 10
14 MSC-Marília	<i>P. edulis</i> / 9
15 325 x LD4	<i>P. caerulea</i> x <i>P. edulis</i> (BC6) / 10

Pi: progeny to which the individual belongs; BC: backcrossing

325: it was selected by Fuhrmann et al. (2014) for standing out among progenies of interspecific hybrids, as the most resistant genotype to the bacterial spot disease, with higher means of fruit weight, pulp weight with seed, and desirable total soluble solids.

M Rubi: it is a genotype used to obtain the cultivar BRS Rubi do Cerrado that has genes from *P. alata* and *P. edulis* “roxo” (typical wild form), with a good resistance degree to the main diseases when cultivated in the Planalto Central, but susceptible in other regions.

Vermelhão: it is a plant selected from the progeny obtained by crossing 325 x LD4 (BC₃) for presenting good productivity. This progeny results from crosses involving the species *P. caerulea* and *P. edulis* (bispecific hybrid). *P. caerulea* is considered a promising source of resistance to *Xanthomonas axonopodis* pv. *passiflorae*.

ML1: it is a bispecific hybrid, with genes from *P. edulis* and *P. amethystina*, and has good tolerance to virosis, moderate resistance to bacterial spot and anthracnose, and good fruit production.

T3R3P1: it is a plant selected from the progeny obtained by crossing 325 x LD4 (BC₃) for presenting good results for fruit weight, number of fruits per plant, and low defoliation index and injured area in the main branch due to anthracnose.

PL3 and PL4: they are plants selected from the cross between *P. hatschbachii* x *P. quadrifaria*. In the initial stage, an F₁ plant was crossed with *P. incarnata*, from which a plant registered as cultivar BRS Rosa Púrpura was selected due to its flower color and for presenting a high resistance degree to leaf diseases. Subsequently, BRS Rosa Púrpura was crossed with the genotype GA (*P. edulis*). As a result of this crossing, PL3 and PL4 were selected as plants with good degrees of resistance to diseases.

These multispecific hybrids (hybrids obtained from crossing two or more species) were selected over the years in the passion fruit breeding program of Embrapa and partners, as they showed good resistance to diseases, satisfactory yield, and/or quality of fruits (FURHMMAN, 2011; BELLON, 2014). Four commercial cultivars were evaluated as control plants: 'BRS Gigante Amarelo', 'BRS Sol do Cerrado', 'SCS 437 Catarina', and 'CSB-Marília' (Table 1).

The experiment was installed in a clayey typical Red Dystrophic Latosol at the beginning of October 2017, in the experimental area of Embrapa Cerrados, located in Planaltina, DF, Brazil (15°36'19''S, 47°42'40''W, 1,007 m a.s.l). The area is inserted in the Cerrado morphoclimatic domain, and it is characterized by a seasonal tropical climate (Aw). The crop was managed using a 1.8 m-high vertical trellis system comprised of 5 m-distant wooden stakes and two pieces of smooth wire, at 1.4 and 1.8 m from the ground. The "mudão" type seedlings (SOUZA et al., 2014) were field transplanted at a spacing of 2 m (between-plants) and 3 m (between-rows), as indicated by Junqueira et al. (2006). The experiment was arranged as a randomized block design with six repetitions and three useful plants per plot.

Harvesting and fruit evaluations were performed from March to April 2018 (first flowering period). Five fruits per plant were evaluated for the following traits: fruit weight (FW), in grams; fruit transversal diameter (TD), in centimeters; fruit longitudinal diameter (LD), in centimeters; peel thickness (PT), in centimeters; pulp yield (PY), in percentage; seedless pulp weight (SPW), in

grams; total soluble solids (TSS), in °Brix. The following traits were also recorded: number of fruits per plant (NF) in the off-season period; estimated yield in the off-season (EY), in ton ha⁻¹; and defoliation index caused by the bacterial spot disease (DEF), in percentage.

Data were analyzed using the software Selegen-REML/BLUP (RESENDE, 2016). The analysis was based on the statistical model $y = Xr + Za + Wp + e$, in which: y is the vector of phenotypic values; r is the vector of repetition effects (assumed to be fixed), added to the overall mean; a is the vector of individual additive genetic effects (assumed to be random); p is the plot effect vector (random); and e is the error vector (random).

The following components of variance were estimated (individual REML):

σ_a^2 : additive genetic variance

h_a^2 : individual narrow-sense heritability, that is, heritability of the additive effects ($h_a^2 = \sigma_a^2 / \sigma_f^2$), in which σ_f^2 is the phenotypic variance

h_{mp}^2 : heritability of the mean of the progenies $\rightarrow h_{mp}^2 = (0.50 \sigma_a^2) / [0.50 \sigma_a^2 + \sigma_p^2 / b + (0.50 \sigma_a^2 + \sigma_e^2) / nb]$; in which b is the number of blocks; n is the number of plants per plots; σ_a^2 is the additive genetic variance; σ_p^2 is the variance among plots; σ_e^2 is the environmental variation.

Acprog: accuracy of progeny selection, assuming complete survival ($Acprog = \sqrt{h_{mp}^2}$)

Mean: overall experimental mean

The traits FW, NF, and EY were used to construct the additive index (AI), the multiplicative index (MI), and the sum of ranks index (SRI), which were obtained from the REML/BLUP method, as follows (VIANA and RESENDE, 2014):

$$AI = ((p_1 \times NF) \times (GV \times NF)) + ((p_2 \times FW) \times (GV \times FW)) + ((p_3 \times EY) \times (GV \times EY))$$

$$MI = (GV \times NF) \times (GV \times FW) \times (GV \times EY)$$

$$SRI = (r \times GV \times NF) + (r \times GV \times FW) + (r \times GV \times EY)$$

In which: p_x : economic weight established for the trait; GV: predicted genotypic value; r : genotype rank.

Concerning the additive index, the economic weights used comprised the ratio between the genetic correlation of the trait under selection and fruit yield. The sum of all genetic correlations among the traits that compose the index and fruit yield were used as the economic weight, according to Resende (2002).

Estimates of predicted genetic gains by selection indexes were obtained based on the mean of the predicted individual genotypic values. The three best-ranked progenies were selected.

Results and Discussion

Estimates of genetic parameters and genotype correlations by the mixed model method

Components of variance management, characterization, and evaluation occurred in an unbalanced experiment. Estimates of individual trait heritability (h^2_a) varied from 0.007 to 0.503 (Table 2). It was low to high (null to 0.25) for all traits, except for PT. The highest values were verified for LD, PT, and NF traits, reaching 0.24, 0.5, and 0.24, respectively (Table 3). Different

studies evaluating sour passion fruit progenies had also recorded low h^2_a for FW (ROCHA, 2014; FREITAS, 2014; SANTOS et al., 2015; SILVA et al., 2017); TSS (ROCHA, 2014; FREITAS, 2014); NF (ROCHA, 2014; FREITAS, 2014; SILVA et al., 2017); EY (FREITAS, 2014; SILVA et al., 2016; SILVA et al., 2017); and TD, LD, and PT (ROCHA, 2014; SANTOS et al., 2015). The low h^2_a values here recorded indicate the need to use elaborated selection methods, as the progeny test. The low heritability magnitude demonstrates the importance of selecting genotypes based on their predicted genetic values and not on the observed phenotypic values (OLIVEIRA, 2012).

Table 2. Estimates of the components of variance among full-sib progenies of sour passion fruit, individual genotypic variance (σ^2_a), individual phenotypic variance (σ^2_p), individual narrow-sense heritability (h^2_a), heritability of the mean of the progenies (h^2_{mp}), accuracy of progeny selection (A_{cprog}), and the overall mean of the population obtained by the REML method, for ten traits evaluated in 11 progenies of multispecific hybrids of sour passion fruit and four commercial cultivars. Embrapa Cerrados, Planaltina-DF, Brazil, 2018.

Components of variance	FW (g)	TD (cm)	LD (cm)	PT (cm)	PY (%)	SPW (g)	TSS (°Brix)	NF	EY (ton ha ⁻¹)	DEF (%)
σ^2_a	112.62	0.06	0.14	0.0084	0.0001	28.95	0.021	16.12	2.146	0.006
σ^2_f	2929.38	2.24	1.18	0.0336	0.0224	373.34	5.77	131.43	22.64	0.063
h^2_a	0.077	0.0549	0.245	0.503	0.015	0.155	0.007	0.245	0.189	0.205
h^2_{mp}	0.355	0.325	0.676	0.848	0.121	0.496	0.049	0.689	0.605	0.538
A_{cprog}	0.59	0.57	0.82	0.92	0.35	0.70	0.22	0.83	0.78	0.73
Mean	202.53	7.88	9.68	0.63	0.42	58.55	9.18	16.29	5.75	0.31

FW: fruit weight; TD: fruit transverse diameter; LD: fruit longitudinal diameter; PT: peel thickness; PY: pulp yield; SPW: seedless pulp weight; TSS: soluble solids content; NF: number of fruits; EY: estimated yield; DEF: defoliation index.

Table 3. Genotypic correlation estimates among nine traits evaluated in 11 progenies of multispecific hybrids of sour passion fruit and four cultivars. Embrapa Cerrados, Planaltina, DF, Brazil.

Traits	Correlations								
	TSS	TD	LD	PT	SPW	NF	EY	DEF	PY
FW	0.30	0.78**	0.36	0.64*	0.61	0.12	0.36	-0.17	-0.49*
TSS		0.25	0.46	-0.07	0.68**	-0.3*	-0.23	-0.13	0.12
TD			0.1	0.57**	0.48	0.29	0.47*	-0.03	-0.34**
LD				0.19	0.24	-0.23**	-0.14*	0.36	-0.04
PT					-0.13	0.18	0.34	0.38	-0.88**
SPW						-0.16	-0.01	-0.53*	0.15
NF							0.96**	-0.37	-0.03
EY								-0.39	-0.15
DEF									-0.33*

** , * : significant at 1 and 5% probability by the Student's T-test, respectively. FW: fruit weight; TD: fruit transversal diameter; LD: fruit longitudinal diameter; PT: peel thickness; PY: pulp yield; SPW: seedless pulp weight; TSS: total soluble solids; NF: number of fruits; EY: estimated yield; DEF: defoliation index.

The estimated h^2_a (0.503) was considered high for PT only. Silva et al. (2012) recorded similar results (0.5) for this trait in sour passion fruit progenies. Thus, selection for PT based on phenotypic values and simple strategies, such as mass selection, may be successful. Peel thickness is determinant for the industry and the fresh fruit market because of its negative correlation with pulp and juice yields in sour passion fruit (VIANA et al., 2004; NEGREIROS et al., 2007).

As expected, the values for h^2_{mp} were higher than those obtained for h^2_a . Estimates of h^2_{mp} ranged from 0.049 to 0.85, and the highest values were registered for LD, PT, and NF (0.67, 0.85, and 0.69, respectively) (Table 2). In these situations, selection may be more effective using progeny information. Viana et al. (2004), Moraes et al. (2005), and Santos et al. (2015) found high h^2_{mp} values for NF (0.87, 0.92, and 0.82, respectively) in populations of sour passion fruit. The trait NF is very important for breeding since it is directly related to yield. Peel thickness and LD are also relevant traits to be considered in the selection process, as they presented negative correlations with PY and NF, respectively (PT and PY: $r = -0.88$; LD and NF: $r = -0.23$) (Table 3). The indirect selection for PY based on PT values is an interesting strategy for selecting superior progenies for PY as a low heritability value was observed for this trait.

The lowest h^2_{mp} values were estimated for TSS (0.049) and PY (0.121) (Table 2). Low estimates of heritability occur due to the environmental effect on the trait. Ferreira et al. (2016) pointed out that the BLUP method is recommended for low heritability traits since it estimates considerable values of genetic gain in the selection of individuals. Heritability is not only a property of a trait but also of the population and environmental conditions to which individuals are exposed. Additionally, this parameter may vary according to the trait evaluated; estimation method; population diversity; the experimental design and experimental unit considered; the size of the sample evaluated; inbreeding level of the population; number and types of environments considered; and the precision in conducting the experiment and in data collection (HALLAUER and MIRANDA FILHO, 1988; BORÉM, 2005). Therefore, these estimates must not be extrapolated to other populations (SANTOS et al., 2015).

Accuracy values ranged from 0.22 to 0.92 and were considered of low to very high magnitude (Table 2). According to Resende and Duarte (2007), accuracy refers to the correlation between the true genotypic value of the genetic treatment and the estimated or predicted value obtained from the experiment information. This statistic varies from 0 to 1, and can be classified as very high ($\check{r}gg \geq 0,90$), high ($0,70 \leq \check{r}gg < 0,90$), moderate ($0,50 \leq \check{r}gg < 0,70$), and low ($\check{r}gg < 0,50$). The quality of the genotypic evaluation should be preferably inferred based on accuracy. The accuracy value of 0.92 for PT

was very high (Table 2). Values considered as high were obtained for LD (0.82), NF (0.83), yield (0.78), and DEF (0.73), while low and moderate magnitude estimates were obtained for FW (0.59), TD (0.57), PY (0.35), and TSS (0.22) (Table 2). Accuracy values above 0.90 are only possible for traits of high heritability (RESENDE and DUARTE, 2007). Accuracy values higher than 0.70 are sufficient for a precise inference about the genetic value of progenies (SANTOS et al., 2015).

Significant and positive correlations were verified between FW and TD (0.78); FW and PT (0.64); EY and NF (0.96); EY and TD (0.47); and PT and TD (0.57). Strong and significant negative correlations were observed between PY and FW (-0.49); PY and PT (-0.88); DEF and SPW (-0.53); and DEF and TD (-0.53) (Table 3). The correlation results show that fruits of higher weight have a greater transversal diameter, higher peel thickness, and lower pulp yield. Similar results were registered by Oliveira et al. (2008) and Freitas et al. (2012) in the analysis of sour passion fruit progenies, showing that these relationships are stable, regardless of the genetic origin of the material. Therefore, selecting larger and heavier fruits could result in a problem, especially when fruits are destined to the industry due to the highly and negatively correlated response for PY.

Individual genotypic selection and progeny selection via BLUP

The 30 best-ranked individuals, out of a total of 145, were identified for all traits evaluated according to the predicted genetic gains and new estimates of the means (Table 4). The predicted genetic value refers to the genetic value observed with no environmental effect (Oliveira, 2012). The estimated genetic gain is equivalent to the genetic value predicted for the selected genotype, and the new mean refers to the overall mean added to the genetic gain (SANTOS et al., 2015).

Table 4. Estimates of percentage genetic gain and new predicted means estimated by REML/BLUP, obtained by the 30 best-ranked sour passion fruit genotypes selected for nine morphoagronomic traits. Embrapa Cerrados, Planaltina-DF, Brazil, 2018.

R	FW		TD		LD		PT		PY		SPW		TSS		NF		EY		DEF	
	Gain (%)	New Mean/Pi																		
1	10.55	223.90/15	10.56	8.71/15	9.94	10.65/14*	1.77	0.64/12	5.79	44.59/12	18.64	69.47/15	0.67	9.24/1*	85.22	30.17/10	74.88	10.06/10	0.10	0.31/10
2	9.63	222.03/15	7.56	8.48/15	9.33	10.59/14*	2.03	0.64/12	4.10	43.89/12	18.46	69.37/15	0.64	9.24/1*	80.09	29.33/10	74.86	10.06/10	0.19	0.31/4
3	9.19	221.15/15	6.49	8.39/15	9.01	10.56/14*	2.30	0.65/12	3.51	43.64/12	17.65	68.89/15	0.62	9.23/1*	77.33	28.88/10	73.10	9.95/10	0.42	0.31/15
4	8.9-7	220.69/15	5.91	8.35/15	8.74	10.53/14*	2.54	0.65/5	3.11	43.47/12	17.14	68.59/15	0.61	9.23/5	74.59	28.44/10	71.44	9.86/10	0.65	0.31/6
5	8.76	220.28/15	5.53	8.32/15	8.54	10.51/14*	2.77	0.65/12	2.87	43.37/12	16.80	68.39/2*	0.59	9.23/1*	71.57	27.95/10	70.02	9.78/10	0.90	0.31/1*
6	8.62	220.00/15	5.26	8.30/15	8.39	10.50/13	3.00	0.65/4	2.70	43.30/12	16.11	67.99/15	0.58	9.23/1*	69.42	27.59/10	67.55	9.64/10	1.13	0.31/4
7	8.52	219.78/15	5.07	8.28/15	8.20	10.48/12	3.22	0.65/12	2.54	43.23/12	15.61	67.70/15	0.57	9.23/5	67.82	27.33/12	65.11	9.50/12	1.35	0.31/15
8	8.42	219.58/15	4.91	8.27/15	8.02	10.46/14*	3.44	0.65/1*	2.40	43.17/6	15.20	67.46/6	0.55	9.23/13	65.88	27.02/10	62.79	9.36/10	1.58	0.31/7
9	8.27	219.27/14*	4.79	8.26/15	7.86	10.45/14*	3.66	0.65/4	2.28	43.12/6	14.84	67.25/6	0.54	9.23/13	63.99	26.71/8	60.95	9.26/7	1.81	0.31/15
10	8.14	219.01/15	4.70	8.25/15	7.73	10.43/7	3.88	0.66/4	2.18	43.08/6	14.53	67.07/15	0.52	9.23/1*	61.53	26.31/10	59.06	9.15/10	2.03	0.32/10
11	8.01	218.75/15	4.58	8.24/15	7.57	10.42/13	4.09	0.66/6	2.09	43.04/6	14.26	66.91/15	0.51	9.22/1*	59.42	25.97/10	57.49	9.06/15	2.26	0.32/10
12	7.88	218.48/15	4.43	8.23/15	7.40	10.40/7	4.29	0.66/5	2.02	43.01/7	14.03	66.77/15	0.50	9.22/13	57.61	25.67/7	55.58	8.95/10	2.48	0.32/12
13	7.75	218.22/15	4.22	8.21/8	7.26	10.39/14*	4.52	0.66/3*	1.95	42.98/8	13.82	66.65/15	0.49	9.22/5	55.96	25.40/10	53.88	8.85/10	2.71	0.32/1*
14	7.63	217.98/14*	4.02	8.20/8	7.13	10.37/7	4.74	0.66/11	1.87	42.95/6	13.62	66.53/15	0.48	9.22/1*	54.53	25.17/12	52.42	8.77/10	2.94	0.32/12

continue..

15	7.50	217.73/ 14*	3.85	8.19/ 8	7.01	10.36/ 7	4.94	0.66/ 6	1.83	42.93/ 6	13.44	66.42/ 1*	0.48	9.22/ 6	53.28	24.97/ 10	51.06	8.69/ 15	3.13	0.32/ 15
16	7.32	217.35/ 14*	3.68	8.17/ 7	6.89	10.35/ 7	5.17	0.66/ 1*	1.78	42.91/ 6	13.27	66.32/ 2*	0.47	9.22/ 6	52.14	24.78/ 10	49.80	8.61/ 6	3.35	0.32/ 115
17	7.15	217.01/ 2*	3.53	8.16/ 7	6.75	10.34/ 14*	5.37	0.66/ 6	1.73	42.89/ 6	13.10	66.22/ 6	0.46	9.22/ 1*	51.04	24.60/ 8	48.67	8.55/ 10	3.58	0.32/ 15
18	6.96	216.63/ 10	3.40	8.15/ 9	6.62	10.32/ 13	5.58	0.67/ 5	1.68	42.87/ 9	12.91	66.11/ 2*	0.46	9.22/ 1*	49.96	24.42/ 8	47.64	8.49/ 15	3.81	0.32/ 15
19	6.78	216.26/ 14*	3.28	8.14/ 8	6.50	10.31/ 13	5.78	0.67/ 6	1.64	42.85/ 6	12.71	66.00/ 14	0.45	9.22/ 6	48.98	24.27/ 8	46.72	8.44/ 9	4.03	0.32/ 15
20	6.60	215.89/ 10	3.17	8.13/ 8	6.37	10.30/ 7	5.99	0.67/ 11	1.61	42.83/ 5	12.54	65.90/ 15	0.44	9.22/ 13	48.09	24.12/ 9	45.78	8.38/ 15	4.26	0.32/ 15
21	6.43	215.55/ 2*	3.07	8.12/ 10	6.25	10.29/ 7	6.21	0.67/ 11	1.57	42.82/ 11	12.37	65.80/ 2*	0.44	9.22/ 5	47.25	23.98/ 8	44.93	8.33/ 15	4.48	0.32/ 1*
22	6.26	215.21/ 1*	2.97	8.12/ 7	6.13	10.28/ 14*	6.40	0.67/ 6	1.52	42.80/ 11	12.21	65.71/ 14	0.43	9.22/ 15	46.41	23.85/ 8	44.05	8.28/ 8	4.71	0.32/ 1*
23	6.10	214.89/ 7	2.88	8.11/ 8	6.03	10.27/ 6	6.61	0.67/ 6	1.49	42.78/ 11	12.07	65.62/ 15	0.42	9.22/ 13	45.54	23.71/ 12	43.18	8.23/ 15	4.94	0.32/ 6
24	5.95	214.59/ 7	2.80	8.10/ 3*	5.93	10.26/ 12	6.81	0.67/ 8	1.45	42.77/ 11	11.93	65.54/ 1*	0.42	9.22/ 15	44.68	23.57/ 6	42.37	8.19/ 7	5.16	0.33/ 1*
25	5.81	214.30/ 2*	2.73	8.10/ 8	5.84	10.25/ 12	7.00	0.68/ 7	1.42	42.76/ 5	11.80	65.47/ 6	0.41	9.22/ 6	43.88	23.43/ 8	41.60	8.14/ 8	5.39	0.33/ 4
26	5.67	214.02/ 14*	2.66	8.09/ 1*	5.75	10.24/ 6	7.21	0.68/ 12	1.40	42.74/ 5	11.68	65.40/ 1*	0.41	9.21/ 1*	43.11	23.31/ 7	40.87	8.10/ 7	5.65	0.33/ 12
27	5.55	213.76/ 14	2.59	8.09/ 1*	5.65	10.23/ 13	7.42	0.68/ 9	1.35	42.73/ 5	11.55	65.32/ 6	0.40	9.21/ 6	42.35	23.19/ 8	40.19	8.06/ 15	5.84	0.33/ 6
28	5.43	213.52/ 1*	2.53	8.08/ 1*	5.54	10.22/ 7	7.62	0.68/ 6	1.33	42.72/ 11	11.42	65.24/ 14*	0.40	9.21/ 2*	41.62	23.07/ 15	39.54	8.02/ 12	6.10	0.33/ 6
29	5.31	213.29/ 10	2.47	8.08/ 8	5.44	10.21/ 6	7.81	0.68/ 15	1.30	42.71/ 5	11.29	65.17/ 5	0.39	9.21/ 15	40.89	22.95/ 7	38.94	7.99/ 15	6.32	0.33/ 10
30	5.20	213.07/ 14*	2.42	8.07/ 3	5.35	10.20/ 8	8.00	0.68/ 5	1.28	42.69/ 5	11.14	65.08/ 1*	0.39	9.21/ 6	40.20	22.84/ 9	38.37	7.96/ 12	6.55	0.33/ 10

Note. R: ranking; Pi: progeny to which the individual belongs; *: control.

Comparing the new predicted means with the overall mean of the population, it was predicted greater gain estimates for the traits NF and yield of up to 85.22% and 74.88%, respectively (Table 4). Lower but satisfactory gains were predicted for the traits FW (10.55%); TD (10.56%); LD (9.94%); PY (5.79%); SPW (18.64%); and TSS (0.67%). For the traits PT and DEF, the best individuals are those with the lowest estimated values of gain: 1.77% and -0.10%, respectively (Table 4).

Plants 95, 97, and 100 from progeny 10 (Table 1) obtained the highest predicted means for the traits of greater relevance within the breeding program: DEF (31%), NF (30.17 fruits), and EY (10.06 t ha⁻¹), respectively (Table 4). Progeny 10 was obtained from crossing the species *P. caerulea* and *P. edulis* (bispecific hybrid). The *P. caerulea* species is considered as a promising source of resistance to *Xanthomonas axonopodis* pv. *passiflorae* (OLIVEIRA AND RUGGIERO, 1998; FALEIRO et al., 2005). The female parent of progeny 10 (325) is a superior genotype selected by Fuhrmann et al. (2014) due to its higher resistance to bacterial spot compared to other progenies of interspecific hybrids. This genotype presented higher FW (210.04 g), pulp weight with seeds (93.89 g), and a desirable TSS (13.2%). The male parent of progeny 10 (Vermelho - T3R3P1) is a plant selected among progenies of interspecific hybrids due to its superior performance, being first-ranked regarding its tolerance to anthracnose,

FW, and NF (unpublished data). Thus, favorable alleles for bacterial spot resistance (DEF), NF, and EY, present in the parental genotypes, could have been possibly transferred to those individuals from progeny 10 showing superior performance.

Individuals 134, 138, and 139 from progeny 15 (Table 1) presented the highest predicted means for FW, SPW, and TD (Table 4; 223.9 g, 69.47 g, and 8.71 cm, respectively). This progeny, as well as progeny 10, was obtained from crossing the species *P. caerulea* and *P. edulis*. As previously stated, the female parent of progeny 15, genotype 325, is resistant to bacterial spot. In its turn, the male parent LD4 is a selected superior genotype characterized by a predominance of flowers with four stigmas and four carpels. It is also one of the parents of the cultivar BRS Sol do Cerrado. Esashika (2018) observed that fruits formed from 4-carpellate flowers had FW, pulp weight, and TD, 20%, 40%, and 10%, respectively, higher than the estimated means for fruits from 3-carpellate flowers. Therefore, the results recorded for the individuals 134, 138, and 139 from progeny 15 suggest that favorable alleles for FW, SPW, and TD were transferred in the backcross cycles with the LD4 recurrent parent. Although FW and TD were negatively correlated to PY (Table 3), these individuals, as well as progeny 15 itself, had PY mean values above 40%, which can be considered as satisfactory (Tables 4 and 5).

Table 5. Ranking of 11 progenies of sour passion fruit multispecific hybrids and four cultivars regarding the genetic gains and new predicted means estimated by REML/BLUP for the traits fruit transversal and longitudinal diameters (TD and LD, respectively), peel thickness (PT), and pulp yield (PY). Embrapa Cerrados, Planaltina-DF, Brazil, 2018.

Ranking	TD			LD			PT			PY			
	New Mean	Pi	Gain (%)	New Mean									
1	216.69	15	3.97	8.1945	14*	6.12	10.27	12	0	0.73	12	2.11	0.43
2	212.64	8	2.43	8.0731	13	4.68	10.13	6	1.55	0.73	6	1.56	0.43
3	210.39	7	1.76	8.0208	7	4.19	10.09	5	2.73	0.73	11	1.20	0.43
4	208.85	3*	1.42	7.9941	6	3.49	10.02	4	4.04	0.72	5	1.02	0.42
5	207.78	13	1.20	7.9762	12	3.07	9.98	11	5.57	0.72	8	0.83	0.42
6	207.00	9	1.04	7.9641	15	2.58	9.93	1*	7.2	0.71	1*	0.71	0.42
7	206.35	10	0.93	7.9554	8	2.21	9.89	3*	8.41	0.70	3*	0.61	0.42
8	205.78	1*	0.85	7.9487	5	1.91	9.86	8	9.84	0.69	4	0.52	0.42
9	205.27	2*	0.75	7.9409	3*	1.67	9.84	2*	11.2	0.68	2*	0.45	0.42
10	204.80	6	0.65	7.9333	2*	1.47	9.82	7	12.63	0.67	15	0.35	0.42
11	204.37	5	0.56	7.9259	11	1.20	9.80	9	14.17	0.66	9	0.28	0.42
12	203.97	14*	0.43	7.9157	1*	0.94	9.77	14*	15	0.65	13	0.21	0.42
13	203.50	12	0.30	7.9052	10	0.69	9.75	15	16.04	0.64	7	0.16	0.42
14	203.02	11	0.16	7.8944	9	0.33	9.71	13	16.93	0.64	14*	0.07	0.42
15	202.53	4	0.00	7.8815	4	0.00	9.68	10	17.06	0.63	10	0.00	0.42

Pi.: progenie; *control

Individuals 111 and 113 from progeny 12 (Table 1) presented the greatest estimates of PY (45%) and PT (0.64 cm), respectively (Table 4). Progeny 12 results from crosses involving four species (*P. hatschbachii*, *P. quadrifaria*, *P. incarnata*, and *P. edulis* - tetraespecific hybrid) and is currently at an initial backcrossing phase (RC2). Accessions of *P. hatschbachii*, *P. quadrifaria*, and *P. incarnata*, used as parentals in this work, present thin PT

(mean values of 0.45, 0.20, and 0.45 cm, respectively). Peel thickness is an important trait for passion fruit breeding programs since fruits developed for agroindustry purposes must present thin peel and internal cavity completely filled with pulp, resulting in higher juice yield (FALEIRO et al., 2005). PT and PY were highly and negatively correlated (-0.88), indicating that the indirect selection for PY, based on PT values, is possible (Table 6).

Table 6. Ranking of 11 progenies of sour passion fruit multispecific hybrids and four cultivars regarding the genetic gains and new predicted means estimated by REML/BLUP for the traits number of fruits (NF), fruit weight (FW), estimated off-season yield (EY), and defoliation index (DEF). Embrapa Cerrados, Planaltina-DF, Brazil, 2018.

Ranking	NF			FW			EY			DEF		
	Pi	Gain (%)	New Mean									
1	10	46.66	23.88	15	6.99	216.69	10	44.93	8.33	15	0.00	30.92
2	8	33.43	21.73	14*	4.99	212.64	15	33.22	7.66	1*	1.42	31.36
3	12	28.25	20.89	2*	3.87	210.38	12	26.48	7.27	10	2.74	31.77
4	15	23.65	20.14	10	3.11	208.84	8	22.32	7.03	12	4.19	32.21
5	7	19.97	19.54	7	2.59	207.78	7	19.30	6.86	2*	5.81	32.71
6	9	17.36	19.11	1*	2.20	207.00	9	16.65	6.70	11	7.71	33.31
7	1*	14.61	18.66	6	1.88	206.35	6	14.15	6.56	6	9.77	33.94
8	6	12.50	18.32	13	1.60	205.77	1*	11.70	6.42	4	12.32	34.74
9	5	10.16	17.94	9	1.35	205.27	2*	9.45	6.29	5	15.19	35.62
10	4	8.05	17.60	3*	1.12	204.80	5	7.37	6.17	7	17.52	36.35
11	11	6.09	17.28	8	0.90	204.36	14*	5.51	6.06	8	19.68	37.02
12	2*	4.42	17.00	5	0.71	203.97	4	3.87	5.97	14*	21.97	37.73
13	14*	2.77	16.73	12	0.47	203.49	13	2.47	5.89	9	24.74	38.59
14	13	1.32	16.50	11	0.24	203.02	3*	1.19	5.81	3*	28.61	39.78
15	3*	0.00	16.28	4	0	202.53	11	0.00	5.75	13	39.84	43.26

Pi: progenie; *control

Individuals from reference cultivars CSB-Marília and BRS-Gigante Amarelo stood out in relation to LD and TSS, respectively. Plant 124 from progeny 14, CSB-Marília (Table 1), had the highest LD mean value (10.65cm; a gain of 9.94%) (Table 4). According to Freitas et al. (2012), the fruit LD is negatively correlated to the NF (-0.61). In this study, the correlation between LD and NF was also negative and significant at 1% probability, estimated at -0.23 (Table 3). Thus, despite presenting higher LD mean values, progeny 14 obtained a low mean NF compared to most progenies (2.77), thereby being placed in the antepenultimate position (Table 6).

Within progeny 1 (BRS-Gigante Amarelo) (Table 1), Plant 3 presented the highest mean TSS content (9.24 °Brix) compared to other plants of the total population evaluated. However, it is important to observe that the gain for TSS was only 0.67%, and the mean values verified among the 30 best genotypes showed a slight variation

comprised between 9.21 and 9.24. The overall mean of the population for the trait TSS (9.18 °Brix) is considered low since values above 13 °Brix are desirable for both the industry and the *in natura* fruit market (Table 2). The TSS content increases as fruit develop, and it varies according to the cultivar, region, season, orchard management, and the location of the fruit in the plant. Pathogen infection may reduce the TSS content in fruits. In 'Pera Rio' orange fruits, for example, the huanglongbing disease reduces TSS contents (SILVA et al., 2018). Fisher et al. (2010) found a negative correlation (-0.12) between the incidence of fungal diseases in peach and fruit TSS content. Santos et al. (2005) verified that the infection by powdery mildew in melon reduced the TSS content by 22.2%. Low TSS contents (8.9 to 12.9 °Brix) were also obtained by Fuhrmann (2011) when evaluating progenies of passion fruit interspecific hybrids infected by different pathogens. Hence, although the negative correlation between TSS and

DEF was not significant (Table 3), the low TSS contents observed in the population evaluated may be related to the occurrence of bacterial spot and other diseases, as no disease control was performed.

The hybrids evaluated in this study presented higher mean values for the main traits of agronomic importance than the control plants, and those hybrids ranked in first belong to progenies 10, 12, and 15 (Table 4). Individuals from progeny 325 x Vermelhão (*P. caerulea* x *P. edulis* - RC6) had an EY increase of up to 49.21 and 54.48% compared with BRS Gigante Amarelo and BRS Sol Cerrado, respectively, concerning the predicted genotypic means. These cultivars are currently the most used by passion fruit producers in several states of Brazil. Therefore, 325 and Vermelhão can be considered as the most promising matrices for obtaining new and more productive varieties.

The gains obtained by progeny selection (Tables 5 and 6) were considerably lower than those obtained by individual selection. Progeny 15 showed the highest gains for FW (6.99%) and TD (3.97%), and the lowest desirable gain for the defoliation index (0%).

Progeny 10 presented the greatest gains for NF (46.66%) and EY (44.93%) compared with other progenies. Progeny 12 obtained the highest gain for PY (2.11%), whereas progeny 14 showed the highest gain for LD (6.12%) (Tables 5 and 6).

Simultaneous selection and genetic gains via selection indexes

Estimates of the predicted simultaneous selection gains by selection indexes (AI, MI, and SRI), considering a selection intensity of 20%, are presented in Table 7. The economic weights of the traits used to obtain the AI were 11.83 (FW), 100 (NF), and 95.72 (EY). Such values are estimates of the correlation between fruit production and the traits composing the index (Table 3).

Table 7. Estimates of the new predicted means and percentage genetic gains of the best progeny, selected based on the simultaneous selection of the traits number of fruits (NF), fruit weight (FW), and estimated yield (EY), using the additive index (AI), the multiplicative index (MI), and the sum of ranks index (SRI), estimated via REML/BLUP. Embrapa Cerrados, Planaltina-DF, Brazil, 2018.

Trait	Selection Index					
	AI		MI		SRI	
	Gain %	New Mean	Gain %	New Mean	Gain %	New Mean
FW	3.68	209.69	3.68	209.69	4.24	210.82
NF	34.58	21.86	34.58	21.86	30.09	21.15
EY	33.49	7.67	33.49	7.67	32.48	7.62

Progenies 15, 10, and 8 stood out, in this order, as the best progenies for simultaneous selection when the AI and MI were used (Table 7). The selection of these three progenies resulted in gains of 3.68, 34.58, and 33.49% for FW, NF, and yield, respectively. Silva et al. (2017), Gonçalves et al. (2007), Freitas et al. (2012), and Silva et al. (2012) reported satisfactory gains for NF in progenies of sour passion fruit using the AI: Progenies 15, 10, and 7 stood out, in this order, as the best progenies for simultaneous selection when the SRI was used. This index provided gains of 4.24, 30.09, and 32.48% for FW, NF, and EY, respectively, similar to those obtained by the AI and MI (Table 7). However, lower gains were obtained for FW, NF, and EY (0.69, 22.35, and 10.15%, respectively), using the same SRI, when Silva et al. (2017) evaluated progenies of full-sib sour passion fruit in the third recurrent selection cycle. The authors observed that the selection gains increase with the advance of the recurrent selection process for the main traits and that the SRI was the most appropriate index for selecting sour

passion fruit progenies. Freitas et al. (2012), Gonçalves et al. (2007), and Silva et al. (2012) assessed different selection indexes in sour passion fruit populations and also obtained the best predicted genetic gains using the SRI. It should be emphasized that these authors considered in the index construction a higher number of traits than the used in this study. In this work, the AI and MI can be considered more appropriate because they provided more significant gains for NF and EY.

Progenies 7 and 8 gained evidence when simultaneous selection indexes were used. These progenies result from crosses involving three species: *P. amethystina*, *P. edulis*, and *P. caerulea*. The female and male parent of progenies 7 and 8, respectively (ML1) is a bispecific hybrid and present *P. edulis* and *P. amethystina* genes. ML1 has good tolerance to passion fruit woodiness disease, moderate resistance to bacterial spot and anthracnose, and good fruit production. However, this bispecific hybrid presents low pulp yield and TSS (unpublished data). As previously stated, the male and female parent of progenies

7 and 8 (Vermelhão -T3R3P1), respectively, is a plant selected among progenies of interspecific hybrids due to its higher tolerance to anthracnose, FW, and NF (unpublished data). Hence, in addition to the parents of progeny 10, the parents of progenies 15, 8, and 7 are considered as promising for obtaining new varieties.

Conclusion

The individual genotypic selection allows for high genetic gains for the traits number of fruits and yield, and satisfactory gains for all other traits evaluated.

Among the three simultaneous selection indexes assessed, the additive and multiplicative indexes were more appropriate for selecting superior full-sib progenies in the population evaluated.

Promising matrices to obtain new varieties were identified.

The knowledge generated on the nature of the genetic parameters of traits of economic importance of passion fruit by the REML/BLUP method will contribute to developing strategies for following up with the sour passion fruit breeding program from Embrapa and partners.

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