EMPLOYMENT OF DIGITAL PHENOTYPING IN THE SELECTION OF FULLSIBLING FAMILIES OF PASSION FRUIT THROUGH REML/BLUP

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Abstract: Digital phenotyping has been used to measure seed morphological traits, which are applied efficiently in the quantification of genetic diversity. The objective of this work was to estimate the genetic parameters to predict the genetic gain via indexes of selection of the REML/BLUP methodology using morphophysiological traits of seeds of sour passion fruit. Seeds from 98 full sibling families (FSF) were evaluated in a randomized block design with three replications and three plants per plot. Thirteen morphophysiological traits of the seeds were evaluated, and the morphological traits were measured through digital image analysis. The genetic parameters were estimated using the REML/BLUP methodology and the classic, multiplicative and Mulamba and Mock selection indexes were used to rank all individuals, where the 30 best FSFs per index were selected. Genetic variability was observed for the morphophysiological traits of the seeds of complete sibling families of passion fruit, with narrow-sense heritability of high magnitude for the traits of greatest morphophysiological interest tested. All selection indexes provided genetic gains, and the classic index had the greatest gains for the main traits of morphophysiological interest of the seed.

Keywords: Image analysis; *Passiflora edulis* Sims, seeds.

Introduction

Fruit growing is one of the sectors of agribusiness that has expanded the most, which is evidenced by the growth in demand for fruit in the foreign market and the increase in the per capita consumption of fruit in the world (FAO, 2017). Within the Brazilian fruit culture, the sour passion fruit (*Passiflora edulis* Sims) is one of the fruits that stands out for its high nutritional value and appreciation of its fruits. It is adapted to the edaphoclimatic conditions of almost all Brazilian states. Also, the domestic production of passion fruit has increased year after year, nevertheless, the average productivity is low, especially in *Cerrado*, a region where passion fruit has the greatest economic potential (Silva et al., 2014).

Among the factors responsible for the low productivity, the lack of production Technologies and cultivars adapted to the regions and phytosanitary problems stand out. Hence, improvement programs for sour passion fruit have contributed to improving plant morphological, physiological and agronomic traits so that they promote the raise in greater productivity and improvement in fruit quality (Cavalcante et al., 2017; Silva et al., 2017). However, there are still few reports involving the improvement of seed quality in these programs, since the seed is one of the main factors for the success in the establishment and production of passion fruit crops (Ocampo et al., 2016; Yang and Wen, 2016).

Much information is known about the quality of the seeds, however, there are several factors that affect this quality, especially the genotype, the climatic conditions during seed development, the occurrence of harmful insects and microorganisms, the nutrition of the mother-plant, harvest period and management, the occurrence of mechanical injuries, the adequacy of drying and processing operations, the conditions and period of storage and the chemical treatment (Marcos Filho, 2013). It is also observed that some species present dormancy in their seeds, which may delay germination for a period from ten days to three months. However, commercial production is facilitated when cultural practices can be continuously and uniformly applied. So, there is a need for uniformity in plant development, which begins with seed germination and later with seedling emergence (Zaidan and Barbedo, 2004; Welter et al., 2011).

The use of digital seed phenotyping has already been successfully used to obtain physical traits of the seeds. This is achieved through the capture and analysis of images that enable the quantification of their physical traits, allowing the production of spreadsheets and graphics on the material studied (Ferreira et al., 2018; Torres et al., 2019). In Brazil, with the purpose of capturing images, histograms and graphs that facilitate the analysis of seeds and seedlings, the company Tbit developed the Groundeye® System Mini equipment in 2011 that allows to obtain results regarding traits such as color, geometry and texture of seeds (Andrade et al., 2016; Ferreira et al., 2018).

Digital seed image analysis has been used for the identification of cultivars, determination of seeds of different colors, mechanical damage and classification of different seed sizes (Kara et al., 2013; Pinto et al., 2015; Andrade et al., 2016). Also, it has been used to explore the diversity between genotypes in breeding programs for guava (Krause et al., 2017) and passion fruit (Fachi et al., 2019). In addition, the method of digital analysis of seed images is fast, requiring less than one minute for digitization and measurement. In addition, it is easily repeatable, reliable and non-destructive (Santos et al., 2015; Krause et al., 2017). This method reduces the error in trait measurements, which combined with accurate selection methods increases the efficiency of the breeding program. One of these selection methods is through the REML/BLUP methodology (maximum restricted likelihood/best unbiased linear prediction) that provides more precise and accurate data, increasing the efficiency of breeding programs (Resende, 2002). Another important point in the selection is the use of selection indexes, which are used in plant improvement for the selection of multiple traits, which enables the achievement of more

productive and adapted genotypes, as they gather several favorable attributes (Cruz et al., 2012).

Thus, the objective of this study was to estimate the genetic parameters and to project the genetic gain by different indexes of selection via REML/BLUP methodology using physiological and morphological traits of sour passion fruit seeds obtained through the use of digital phenotyping.

Material and Methods

The seeds of the evaluated 98 full siblings families (FSF) came from the experiment conducted in the experimental area of the Mato Grosso State University (Unemat), municipality of Tangará da Serra, Mato Grosso State (MT) (14º 39' south latitude and 57º 25' west longitude and altitude 321 m). The experimental design was the randomized blocks, with three replications and three plants per plot. It was used a spacing of 3 m between plants and 3 m conducted under a vertical trellis. The fruits of each FSF were harvested in June and July 2016, when the fruits reached their physiological maturity (70% yellow). The seeds were removed, washed, dried and stored in a cold chamber at 7° C until use (Silva et al., 2015; Oliveira et al., 2017).

The traits analyzed were mass of a thousand seeds (MTS), which was determined by the randomly counting of eight samples of 100 seeds per FSF, which were weighed, where the values of the mass of a thousand seeds were expressed in grams, with one decimal place according to Brazil (2009). The water content (WC) was determined using the oven method at 105º C (± 3), for 24 hours, as prescribed in the Rules for Seed Analysis (Brazil, 2009). Four 100-seed samples were used, which were weighed before and after being placed in the oven.

For the germination test, four replicates of 25 seeds per FSF were used. The Germitest paper in the form of a roll, moistened with distilled water equivalent to 2.5 times the dry weight of the paper was used as substrate. The rolls were taken to a BOD-type germination chamber, at a temperature change of 20-30º C, and a photoperiod of 12 hours (the 12 hours of light

was provided during the exposure of the seeds to a temperature of 30º C) for 30 days (Brazil, 2009). At the end of the experiment, the seed germination percentage (SGP) was calculated. The germination speed index (GSI) was performed from the germination test, being daily evaluated over the 30 days, where it was considered as germinated only those seeds that broke the tegument emitting radicle with the minimum of 2 mm in length (Hadas, 1976). With these data, the germination speed index was calculated according to Maguire (1962).

The seedling emergence percentage (SEP) was carried out in wooden boxes with dimensions of 400.0 x 100.0 x 10.0 cm, using washed and sterilized sand as substrate, initially moistened until reaching 60% of its water holding capacity and moistened whenever necessary. Four repetitions of 25 seeds were used for each FSF, where the planting of the seeds was carried out at 3 mm depth and lines spaced by 5 cm. The boxes were kept in a greenhouse at room temperature. The seeds were evaluated daily for a period of 45 days (Brazil, 2009). At the end of the experiment, the total number of emerged seedlings was counted and the percentage of emerged seedlings was calculated. The emergence speed index (ESI) was measured based on the seedling emergence test, the number of emerged seedlings was evaluated daily, and seedlings with totally free cotyledons were considered for that purpose. Using these data, the emergency speed index was calculated according to Maguire (1962). In the evaluation of the dry mass of the seedlings (DMS), they were packed in paper bags and taken to the air-circulation oven at 70º C for 72 hours. Weighing was done before and after drying to calculate the average dry mass weight, expressed in mg/seedling. Normal radicle length (NRL) was measured using normal seedlings from the emergency test. The evaluation was made at the end of the experiment, measuring normal seedlings with a digital caliper. The result was expressed in cm of radicle/seedling.

The morphological analyses of the seeds were performed in the GroundEye equipment of the Seed Technology Laboratory of the North

Fluminense State University (UENF) in Campos dos Goytacazes, state of Rio de Janeiro. GroundEye equipment allows to obtain a wide variety of information related to color, texture, geometry, uniformity, vigor of seedlings and seeds. GroundEye consists of a chamber for image capture and analysis software. The chamber consists of a tray with a transparent acrylic bottom, in which the object of analysis is placed, one or two high-resolution cameras and LED lamps for lighting. After obtaining the images, the software analyzes the images individually of the seeds, providing accurate and fast results. Four replications of 50 seeds per FSF were used, where the following morphological traits were evaluated: Seed area (SA); Maximum seed diameter (MAD); Minimum seed diameter (MID); Seed sphericity (ESF); Seed perimeter (SP). According to the model described in Viana and Resende (2014), a deviance analysis was performed to test the effects of the model. The deviance analysis was obtained, as follows:

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

$$ln(L) = -\frac{1}{2}ln|X'V - 1X| - \frac{1}{2}ln|V| - \frac{1}{2}(y - Xm)'V - 1(y - Xm)$$

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

The LRT statistical test (likelihood ratio test) was used to test the significance of the effects, as follows:

$$LRT = |-2\,ln(Lse) + 2\,ln(Lfm)|,$$

where Lse is the maximum point of the maximum likelihood function for the reduced model (without the effects) and Lfm is the maximum point of the maximum likelihood function for the complete model.

The traits were analyzed using the software Selegen - REML/BLUP (Resende, 2016), which was used to obtain the components of variance by means of the restricted maximum likelihood (REML) and the individual genotypic values by means of the best linear unbiased predictor (BLUP). From the predicted genotype values, the selection of the 30 best FSFs was carried out through three selection indexes, namely: classic index (CI), multiplicative index (MI) and Mulamba and Mock index (based on the sum of ranks) (ISR), the indexes were constructed according to the REML/BLUP methodology.

In the classic index, the direction "bigger" and "100" weights were attributed for the traits GSI and ESI and "50" weights for the traits SGP and SEP. Only the direction "bigger" was assigned for the other traits. For the rank sum index, the assigned direction was "higher" for all traits. The direction given to the program implies in directing the selection of progenies based on the traits of interest, aiming to increase or reduce the expression of the variable. After selecting the 30 best FSFs per index, selection gains (SG) were estimated based on the phenotypic values of the selected families and the enhanced means. Next, genotypic correlations between traits were performed using model 102 of the Selegen software - REML/BLUP and the correlation values were classified according to Resende (2007). The hypothesis that the correlation coefficient is equal to zero (H$_0$: $\rho = 0$) was evaluated by the t-statistic, given by:

$$t = \frac{r}{\sqrt{1-r^2}}\sqrt{n - 2},$$

where t is associated with $n - 2$ degrees of freedom (n is the number of data pairs used to calculate the correlation; n = number of the genotypes).

Results

Table 1 shows the deviance values for the evaluated traits, demonstrating the existence of a significant difference by the Chi-square test at 5% probability for all the evaluated traits.

Table 1. Deviance analysis for thirteen morphophysiological traits of seeds from families of complete brothers of sour passion fruit. Tangará da Serra, MT, 2018.

Traits [1/]	Effect		LRT (χ^2)
	Genotype	Full model	
SDM	-862.57	-1096.99	234.41*
NRL	2389.27	2169.28	219.98*
ESI	-615.14	-830.89	215.74*
SEP	-1067.85	-1305.21	237.36*
GSI	-15.50	-376.36	360.86*
SGP	-1095.63	-1357.38	261.74*
WC	733.18	218.38	514.80*
TSM	1124.50	614.87	509.62*
SA	-2987.67	-3512.14	524.47*
MAD	-2563.87	-3063.78	499.91*
MID	-2766.13	-3329.37	563.24*
SPH	1791.17	1399.62	391.54*
SP	-717.45	-1122.40	404.94*

[1/]Seedling dry mass (SDM), normal radicle length (NRL), emergence speed index (ESI), seedling emergence percentage (SEP), germination speed index (GSI), seed germination percentage (SGP), water content (WC), one-thousand seed mass (TSM), area (SA), maximum diameter (MAD), minimum diameter (MID), sphericity (SPH), perimeter (SP). * Significant at 5% probability by the Chi-square test. LRT (x^2): likelihood ratio test.

Regarding the components of variances (Table 2), it was observed that for all traits, the contribution of variance within the plot ($\sigma2$in) was lower than the environmental variance between plots (σ^2plot). Individual heritability values in the narrow sense (h_a^2) and heritability of the progeny mean (h_{pm}^2) were shown to be of high magnitude for all evaluated traits (> 50%). Accuracy estimates (Acprog) were of high magnitude and showed little variation between the evaluated traits, ranging from 0.8175 (ESI) to 0.8766 (MID), indicating good reliability of the estimates.

Table 2. Estimates of the genetic parameters for seedling dry mass (SDM), normal radicle length (NRL), emergence speed index (ESI), seedling emergence percentage (SEP), germination speed index (GSI), seed germination percentage (SGP), water content (WC), one-thousand seed mass (TSM), area (SA), maximum diameter (MAD), minimum diameter (MID), sphericity (SPH), perimeter (SP).

Traits	σ_g^2	σ^2parc	σ^2dentro	σ_f^2	h_a^2 (%)	c^2parc	h_{mp}^2	Acprog	h_{ad}^2
SDM (g)	0.0132	0,0132	0.0117	0.0380	0.6928	0.3464	0.6795	0.8243	1.1276
NRL (mm)	55.9748	55.9748	53.8195	165.7692	0.6753	0.3377	0.6710	0.8191	1.0400
ESI	0.0241	0.0241	0.0237	0.0719	0.6700	0.3350	0.6683	0.8175	1.0150
SEP	0.0078	0.0078	0.0068	0.0224	0.6962	0.3481	0.6811	0.8253	1.1460
GSI	0.1362	0.1362	0.0647	0.3371	0.8080	0.4040	0.7306	0.8547	2.1040
SGP	0.0075	0.0075	0.0058	0.0208	0.7230	0.3615	0.6937	0.8329	1.3053
WC (%w.*b.*)	1.0324	1.0324	0.2567	2.3216	0.8894	0.4447	0.7621	0.8730	4.0220
TSM (g)	2.8240	2.8240	0.7168	6.3648	0.8874	0.4437	0.7613	0.8726	3.9396
SA (cm²)	0.0001	0.0001	0.0000	0.0002	0.8931	0.4466	0.7635	0.8738	4.1794
MAD (cm)	0.0002	0.0002	0.0001	0.0005	0.8834	0.4417	0.7599	0.8717	3.7893
MID (cm)	0.0001	0.0001	0.0000	0.0003	0.9068	0.4534	0.7684	0.8766	4.8662
SPH (mm)	14.6934	14.6934	6.0957	35.4826	0.8282	0.4141	0.7387	0.8595	2.4104
SP (cm)	0.0231	0.0231	0.0090	0.0552	0.8363	0.4182	0.7419	0.8613	2.5547

σ_g^2: genotypic variance between progenies of complete siblings, equivalent to (1/2) of the additive genetic variance plus (1/4) of the dominance genetic variance, disregarding epistasis; σ^2plot: environmental variance between plots; σ^2 within: residual variance within a plot; σ^2ph: individual phenotypic variance, h^2 2a: individual heritability in the narrow sense, obtained by disregarding the fraction (1/4) of the genetic dominance variance; c^2plot: coefficient for determining the effects of the plot; h²mp: heritability of the mean of progenies, assuming complete survival; Acprog: accuracy of progeny selection, assuming complete survival; h²ad: additive heritability within a plot, obtained by disregarding the fraction (1/4) of the genetic dominance variance and the overall mean of the experiment.

The values of the determination coefficient of the plot effects C_{plot}^2 were of high magnitude, with the highest value obtained in the MID variable (0.4534) and the lowest in the ESI variable (0.3350), indicating high environmental variation between the plots within the block. The traits ESI, SEP, GSI and SGP were considered in this work as main traits in the selection process. For these traits, all indices showed positive gains, with the classic index showing the greatest gains, 13.63% for the ESI trait, 11.92% for SEP, 16.83% for GSI and 6.92% for SGP (Table 3).

The traits SDM (21.88%) and NRL (7.32%) also had high values of selection gain. Even for the traits that showed negative gains, they were less than 1% for the classic index. According to the classification proposed by Santos (2007), it was observed that for most of the traits evaluated, the genotypic correlations were weak (<0.5), except for the traits SPH x SP (0.966), ESI x SEP (0.954), SA x MID (0.895) and GSI x SGP (0.847) that were high and significant (Table 4). When comparing the genotypic correlations between physiological traits (PDM, NRL, ESI, SEP, GSI, SGP, WC, TSM) with the morphological ones (SA, MAD, MID, SPH, SP) it was observed that they were also weak.

Discussion

The difference observed for all the evaluated traits (Table 1), indicates the existence of genetic variability between the full sibling families (FSF) of sour passion fruit, which enables the success in selecting higher FSF and achieving precision in the estimates in the variance components. The variance within the plot is lower than the environmental variance between plots for all traits, in addition, the error is greatest between rather than within the plots (Table 2). As for the coefficient of determination of the effects of plots (C²plot), it was possible to observe in the individual analysis of each variable that all values for this parameter were greater than 10%, which is inadequate for estimates of the coefficient of determination, therefore, demonstrating that there was a high environmental variation between plots and thus the environment may have caused interference in the estimates of genetic parameters (Resende, 2016). However, the environmental variance between the plots may suffer interference from some factors, most of which can be handled by breeders, among them: distribution of seeds, fertilizers, irrigation water when appropriate and obtaining the most uniform stand as possible. This better management improves experimental precision and the success with selection (Moreto et al., 2007).

Table 3. Original mean (OM) and estimates of the percentages of selection gains (SG) and the improved mean (IM) for the morphophysiological traits of seeds of full sibling families of sour passion fruit using three selection indexes.

Traits	OM	Classic		Multiplicative		Mulamba and Mock	
		SG (%)	IM	SG (%)	IM	SG (%)	IM
SDM (g)	0.390	21.88	0.476	31.98	0.516	26.67	0.495
NRL (mm)	58.077	7.32	62.330	11.57	64.795	9.10	63.359
ESI	1.095	13.63	1.244	11.98	1.226	9.35	1.197
SEP	0.649	11.92	0.727	10.38	0.717	8.38	0.704
GSI	2.208	16.83	2.579	13.88	2.514	10.92	2.449
SGP	0.841	6.92	0.899	6.06	0.892	5.38	0.886
WC (%w.b.)	10.901	-0.59	10.837	-1.42	10.747	-1.59	10.728
TSM (g)	25.188	-0.96	24.947	2.29	25.765	3.43	26.053
SA (cm²)	0.190	-0.57	0.189	1.28	0.193	4.34	0.199
MAD (cm)	0.614	-0.60	0.610	0.39	0.617	1.60	0.624
MID (cm)	0.408	0.10	0.408	0.90	0.412	2.48	0.418
SPH (mm)	18.701	2.25	19.122	8.92	20.370	1.90	19.057
SP (cm)	1.886	0.64	1.898	4.25	1.966	2.87	1.940

Traits: (SDM) − seedling dry mass; (NRL) - normal radicle length; (ESI) - emergency speed index; (SEP) - seedling emergence percentage; (GSI) - germination speed index; (SGP) - seed germination percentage; (WC) - water content; (TSM) − one-thousand seed mass; (SA) - seed area; (MAD) - maximum diameter; (MID) - minimum diameter; (SPH) - sphericity; (SP) – perimeter.

Table 4. Genotypic correlation coefficients between the morphophysiological traits of seeds of full sibling families of sour passion fruit. Tangará da Serra, MT, 2018

Traits	NRL (mm)	ESI	SEP	GSI	SGP	WC (%w.b.)	TSM (g)	SA (cm²)	MAD (cm)	MID (cm)	SPH (mm)	SP (cm)
SDM (g)	0.735**	0.711**	0.700**	0.311**	0.275**	-0.116ns	0.176ns	0.151ns	-0.003ns	0.247*	-0.087ns	-0.049ns
NRL (mm)		0.597**	0.524**	0.308**	0.348**	-0.255*	0.136ns	0.214*	0.061ns	0.271**	-0.013ns	0.018ns
ESI			0.954**	0.298**	0.210*	0.038ns	-0.062ns	-0.083ns	-0.183ns	0.019ns	-0.070ns	-0.106ns
SEP				0.158ns	0.102ns	0.045ns	-0.061ns	-0.080ns	-0.169ns	0.019ns	-0.095ns	-0.131ns
GSI					0.847**	-0.164ns	-0.062ns	0.089ns	-0.086ns	0.163ns	0.138ns	0.176ns
SGP						-0.114ns	-0.009ns	0.227*	-0.031ns	0.301**	0.045ns	0.102ns
WC (%w.*b.*)							0.018ns	-0.082ns	-0.134ns	-0.037ns	-0.242*	-0.275**
TSM (g)								0.318**	0.217*	0.272**	0.080ns	0.157ns
SA (cm²)									0.751**	0.895**	-0.225*	0.010ns
MAD (cm)										0.437**	0.007ns	0.199ns
MID (cm)											-0.340**	-0.13ns
SPH (mm)												0.966**

Traits: (SDM) – seedling dry mass; (NRL) - normal radicle length; (ESI) - emergency speed index; (SEP) - seedling emergence percentage; (GSI) - germination speed index; (SGP) - seed germination percentage; (WC) - water content; (TSM) – one-thousand seed mass; (SA) - seed area; (MAD) - maximum diameter; (MID) - minimum diameter; (SPH) - sphericity; (SP) - perimeter. ns Not significant. ** and * Significant at 1% and 5%, respectively, by the t test.

The narrow-sense heritability and progeny mean heritability were of high magnitude (> 50%) for all traits. High values indicate that the evaluated traits have their phenotype controlled predominantly by gene action. In this way, the physiological traits and the use of digital phenotyping of sour passion fruit seeds evaluated in this work are highly heritable, which is adequate to carry out the selection of higher genotypes in breeding programs. Accuracy is the most important parameter in assessing precision in access to true genetic variation. The higher the accuracy value, the greater the confidence in the evaluation and the predicted genetic value, thus, as the accuracy values found in this work were greater than 70%, they mean that the estimated values are reliable when compared with the real values (Biernaski et al., 2012).

The difference observed for all the traits evaluated (Table 1), indicates the existence of genetic variability between the full sibling families (FSF) of sour passion fruit, which enables success in selecting higher FSF and obtaining precision in the variance component estimates. The variance within the plot is lower than the environmental variance between plots for all traits, with the greatest error found within the plots (Table 2). As for the coefficient of determination of the effects of plots (C²plot), it was possible to observe in the individual analysis of each variable that all values for this parameter were higher than 10%, which is inadequate for estimates of the coefficient of determination, demonstrating that there was a high environmental variation between plots and thus the environment may have caused interference in the estimates of the genetic parameters (Resende, 2016). However, the environmental variance between the plots may suffer interference from some factors, most of which can be handled by breeders, among them: distribution of seeds, fertilizers, irrigation water when appropriate and obtaining the most uniform stand as possible. This better management improves experimental precision and the success with selection (Moreto et al., 2007).

The classic index was the one that provided the best distribution of gains among the traits of morphophysiological interest of the seeds (Table 3), which is considered the best index, in order to guarantee the improvement of the population genotypic value and the consequent success in the selection process. Selection gains for the traits SDM (21.88%), NRL (7.32%), ESI (13.63%), SEP (11.92%), GSI (16.83%) and SGP (6.92%) were high, providing an increase in the improved means.

Therefore, the results of the new improved mean demonstrate that the selection of the FSF by means of the classic selection index is efficient and will provide more vigorous seeds with better germination potential in the field, therefore, contributing to the improvement of the greatest concern of the producer who acquires the seed, which is the guarantee of germination and seedling emergence to establish a homogeneous stand in the field (Zaidan and Barbedo, 2004; Welter et al., 2011). Vigor is an attribute of seed quality that best expresses the performance potential of the seed in the field, where the faster the seeds and seedlings start their development and break through the soil layer, the less susceptible they will be to any environmental variation, especially in what it concerns water availability and the attack of diseases and pests (Marcos Filho, 2005).

According to Silva et al. (2017) the greater the development of the aerial part of the seedling, the greater its association with the root system, promoting the survival and development of the seedling after planting. Regarding the SDM trait, the new improved mean (0.476) shows a promising result for this trait. However, even with the gains, the NSL trait presented lower results than Castro et al. (2012) where when evaluating the formation of sour passion fruit seedlings found root length means between 6.63 cm up to 16.628 cm and a dry seedling mass of only 0.183.

The results of the new improved mean for the traits ESI (1.244), SEP (0.727), GSI (2.579), SGP (0.89) are considered satisfactory for the passion fruit crop. Similar results were found by Larré et al. (2007) when performing the germination and emergence tests on passion fruit seeds using the accelerated aging method on commercial passion fruit seeds and obtained maximum averages of ESI (0.89), SEP (0.70), GSI (3.33) and GSI (84.66). In general, the selection of the FSF by means of the classic selection index proved to be efficient and promising, therefore, helping to obtain more vigorous seeds and with better germination potential in the field and thus contributing to the improvement of the greatest concern of the producer who acquires the seed, which is the guarantee of germination and emergence of seedlings to establish a homogeneous stand in the field (Zaidan and Barbedo, 2004; Welter et al., 2011).

The negative gains for WC, TSM, SA and MAD promote a reduction in the means of these traits. However, the reductions were low and after selection, their means were 10.837% b.u, 24.947 g, 0.189 cm^2 and 0.610 cm for the traits WC, TSM, SA and MAD, respectively. According to Catunda et al. (2003), the ideal water content for storage and conservation of the germinative power of the passion fruit seed is between 8 and 10%, with water content values between 4 and 6% without compromising the quality of the seed. Araújo et al. (2009), when evaluating the physical properties of yellow passion fruit seeds (*Passiflora edulis*) during the drying process, obtained an average MMS of 27.9 g, values close to those observed in this work. In addition, traits such as SA and MAD, are linked to the point of physiological maturity, which may vary depending on the species and the environment, so it is necessary to define maturation parameters that allow the establishment of the appropriate harvesting period for fruits for extraction of the seeds. In general, a late harvesting of passion fruit may increase the amount of seed reserve material, which favors its physiological potential, mass and size. (Carvalho and Nakagawa, 2012).

For the high, significant and positive correlations (SPH x SP, ESI x SEP, SA x MID and GSI x SGP), the use of the selection to increase one of these traits, a response correlated to the others is expected, which is an advantage as the direction of the selection is the same for these characters (Paula et al., 2002). The traits that showed low and non-significant correlations, indicate that in the process of improvement of the passion fruit, the selection must be carried out for the means of the character, that is, independent of

the other characters. This fact, independence between the traits is very important for the breeder as it is possible to obtain simultaneous genetic gains on the important characters or obtain gain for a specific character without changing the others (Lúcio et al., 2013). Although the digital seed image analysis method for seed morphological traits is fast, reliable and non-destructive (Venora et al., 2009), the fact of not showing a high and significant correlation with the physiological traits, particularly with ESI, SEP, GSI and SGP, makes the measurement of these traits not useful in breeding programs of sour passion fruit.

Conclusion

Genetic variability is observed for the morphophysiological traits of the seeds of complete sibling families of sour passion fruit. Also, through mixed models, it was estimated that heritability in the restricted sense was of high magnitude for the traits of emergence speed index, seedling emergence percentage, index germination speed and seed germination percentage.

All selection indexes provided genetic gains, and the classic index had the largest gains for the main traits, emergence speed index, seedling emergence percentage, germination speed index and seed germination percentage.

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