

# Genotype selection by REML/BLUP methodology in a segregating population from an interspecific *Passiflora* spp. crossing

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Received: 30 June 2014 / Accepted: 18 January 2015 / Published online: 7 February 2015  
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**Abstract** The restricted maximum likelihood/best linear unbiased prediction (REML/BLUP) method involves, simultaneously, the estimation of variance components and the prediction of the genetic values, considering the optimum procedure to make inferences in genetic and non-phenotypic levels. By using the mixed models methodology, this study aimed to estimate genetics parameters and genotypic values in a segregating population comprising 118 individuals from *Passiflora* interspecific crossing. The experiment was arranged in randomized block design with two repetitions. The traits number of fruits, level of soluble solids and pulp mass presented large genetic variability, a fact that contributed to high heritability estimations and selective accuracy, and revealed excellent possibilities to the selection and breeding of *Passiflora* segregating populations. By comparing

the average of the 30 selected genotypes with the general average of the population, it was possible to observe higher gain estimations for the number of fruits (319.15 %) and pulp mass (73.12 %), lower gains for fruit mass (21.50), soluble solids level (13.43), longitudinal fruit diameter (6.32) and transverse fruit diameter (4.99) as well as low reductions in shell thickness (−0.0036) and length of the androgynophore (0.0056), in relation to the first ordinated individuals. The assessed population presenting genetic variability and the superior individuals for each trait were identified, thus enabling the continuity of the selective process. The analyses by the REML/BLUP methodology and by the presented model proved adequate for gain prediction, with good genetic breeding perspectives.

**Keywords** Mixed models · Genetic breeding · Genetic parameters · Interspecific hybrids

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## Introduction

Brazil stands out in the global scenario as the biggest passion fruit producer. Mean productivity in 2013 was 15 t ha<sup>-1</sup> (IBGE 2014). Such an estimation highlights passion fruit production potential and indicates the importance of this crop to the Brazilian economy. Northeastern Brazil has been leading the national production and accounts for more than half of the national production, being followed by the

southwestern, northern, midwestern and southern regions (IBGE 2014). However, the national mean productivity is considered low, due to phytosanitary issues, inadequate cultivation techniques and a reduced number of genetically improved populations adapted to the edaphoclimatic conditions of the plantation region (Pimentel et al. 2008).

Genetic breeding programs aim to achieve more productive cultivars which are also resistant to plagues and pathogens, including the Cowpea aphid-borne mosaic virus (CABMV), which hardens the fruits on the trees and is regarded as one of the most harmful issues to the economy. The disease leads to production losses and low quality fruits, and reduces the longevity of the orchards (Nascimento et al. 2006).

There are no reports of the existence of *Passiflora edulis* genotypes proven to be resistant to CABMV (Junqueira et al. 2005; Maciel et al. 2009). Thus, the introgression of resistant genes from wild species into a commercial species via interspecific hybridization is one of the strategies adopted to control the disease, since there is no effective chemical control.

Interspecific hybridization is a technique often used for transferring genes from a resistant to a susceptible genotype. Successful hybridization requires the progenitor species to be genetically similar and to present some chromosomal homology, so as to minimize the problems of incongruity or incompatibility in the cross, thus enabling the use of the hybrid (Soares-Scott et al. 2003). Among the wild species indicated as potential sources of resistance to diseases that affect passion fruit, *Plumularia setacea* DC deserves special attention because it is resistant to CABMV (Maciel et al. 2009; Oliveira et al. 2013). Interspecific crosses between *P. edulis* and *P. setacea* aimed at developing CABMV-resistant genotypes have been recorded in the literature and are considered valuable for exploitation in breeding programs (Junqueira et al. 2005).

Segregating populations from interspecific crossing present high genetic variability, which increases selection efficiency within these generations. Successful selection depends not only on the variability of the experimental material but also on the accuracy of the selection methods employed. Thus, it is important to use methods that estimate the variance components and enable the prediction of individual genetic values from future genotypes to the selection. The inference of genotypes, within any stage of the breeding

program, must be based on genetic rather than phenotypic averages, since genotypic averages are the future averages of the selected individuals (Borges et al. 2010).

Mixed model methodologies are used as an optimum selection procedure and involve the estimation of variance components by means of the restricted maximum likelihood model (REML) and the prediction of genotypic values by the best linear unbiased prediction (BLUP), which results in a more accurate selection process (Resende 2002; Alves and Resende 2008).

According to Resende (2002), the use of genetic assessment techniques, based on mixed models such as REML/BLUP, tend to maximize the obtained genetic gains, since they are an estimation procedure specifically used to analyze unbalanced data, such as in the current study, predicting genetic values from individuals in progeny tests.

The use of the REML/BLUP methodology has been increasingly used in plant breeding procedures, especially in perennial plants. It has been applied to enhance forest species such as the rubber tree (Kalil et al. 2000) and eucalyptus (Rocha et al. 2006), species that produce stimulating food, such as coffee (Petek et al. 2008), and fruitful species, including West Indian cherry (Paiva et al. 2002), cupuaçu fruit (Alves and Resende 2008), papaya (Oliveira et al. 2012) and acai berry (Teixeira et al. 2012).

The selection of the best individuals to be used as parents of the next generation is essential for the genetic breeding of any crop. This work aims to contribute to future activities of the passion fruit breeding program conducted by the Universidade Estadual Norte Fluminense Darcy Ribeiro (UENF). In this study, superior individuals, selected for the main traits of agronomic interest, may be backcrossed with passion fruit in more advanced stages of the breeding program.

Therefore, the current work aimed to: (1) estimate the genetic parameters and obtain the genetic value of the assessed traits by means of the REML/BLUP mixed models methodology; and (2) perform the selection of plants within progenies, in order to identify superior genotypes from the interspecific crossing between *P. edulis* and *P. setacea* to achieve generation enhancement in the passion fruit genetic breeding program which has been developed at UENF.

## Materials and methods

### Genetic material

A total of 118 interspecific hybrids obtained by *P. edulis* × *P. setacea* crossing from the passion fruit breeding program of the UENF were assessed. Hybridizations were performed using *P. edulis* as the female and male parents in order to obtain the progenies (Table 1).

The two genotypes of *P. setacea* and the six of *P. edulis* used in the crossing were obtained from the Active Germplasm Bank of the Universidade Estadual de Santa Cruz (BAG—Passifloras), located in Ilheus County, Bahia, and from the intra-population recurrent selection program of the Universidade Estadual Norte Fluminense Darcy Ribeiro, respectively. The parents *P. setacea* and *P. edulis*, used in interspecific crosses, showed resistance and susceptibility to CABMV, respectively, when assessed by severity of symptoms and serological tests as PTA-ELISA (plate-trapped antigen–enzyme-linked immunosorbent assay) (Santos 2013).

### Interspecific hybridizations

Interspecific hybridizations were performed between July 14 and August 8, 2010, at UESC within a greenhouse by using *P. edulis* as female and male genitor, in order to obtain the progenies. The temperature inside the greenhouse ranged from 28 down to 22 °C, and relative humidity was between 60 and 98 %. Artificial crossings were performed at different times, from 1330 to 1430 hours for *P. edulis* genotypes, and

from 1900 to 1930 hours for the *P. setacea* genotypes. Flower buds from the genitors were protected with paper bags in the morning. Anthers from the donor species were collected, deposited in Petri dishes with silica gel and stored in a refrigerator (10 °C) until the stage of receptor flower anthesis (1230 hours anthesis in *P. edulis* plants and from 1800 to 1900 hours in *P. setacea* plants). During pollination, anthers from donor species were carefully rubbed on the stigma of the receptor species with tweezers. After the artificial hybridization, crossings were identified and flowers were protected again for 24 h. Fruits resulting from the successful hybridizations were protected with a nylon mesh until full ripening.

### Cultivation conditions

The genotypes were planted in November, 2011, within the experimental area of Antônio Sarlo Agricultural School, Northern Rio de Janeiro State (21°45'S, 41°20'W; 11 m altitude). The vertical cordon conduction system was used, with 2.5-m-high and 4-m-long fence posts, and a #12 wire thread was set 1.80 m from the ground. Crop treatments were carried out according to specific recommendations for this crop. The experiment was arranged in an unbalanced randomized block design for plants within the progenies, with two repetitions.

The first fructification occurred in March, 2012. The harvest and the fruit assessment took place between March and September 2012. Fruit development in hybrid plants occurred through natural pollination. A total of 118 genotypes were evaluated in this study, producing at least one fruit per plant.

**Table 1** Genotypes of *P. edulis* (*Pe*) and *P. setacea* (*Ps*) used in interspecific crossing to obtain full-sibling progenies of *Passiflora* spp.

Genitors/crossings	Progenies	Genotypes
<i>Pe</i> 139 (40) × <i>Ps</i> 367	UENFH-1	1, 2, 3, 4, 7, 8, 9, 10, 11, 12, 14, 16, 19, 20, 22
<i>Pe</i> 139 (38) × <i>Ps</i> 367	UENFH-2	2, 3, 4, 7, 10, 11, 12, 13, 14, 15, 16, 17, 18, 20, 23
<i>Pe</i> 139(29) × <i>Ps</i> 367	UENFH-3	2, 4, 6, 7, 8, 9, 10, 11, 13
<i>Pe</i> 89(11) × <i>Ps</i> (365)	UENFH-4	2, 3, 5, 9, 13, 17, 21
<i>Ps</i> 367 × <i>Pe</i> 139(40)	UENFH-5	1, 2, 3, 4, 5, 7, 8, 9, 10, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23
<i>Ps</i> 367 × <i>Pe</i> 139(36)	UENFH-6	6, 27
<i>Ps</i> 367 × <i>Pe</i> 89(11)	UENFH-7	1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14
<i>Ps</i> 365 × <i>Pe</i> 139(36)	UENFH-8	3, 8, 13, 16, 28, 45, 47, 48, 55, 58, 61, 62, 63, 68, 74
<i>Ps</i> 365 × <i>Pe</i> 89(7)	UENFH-9	1, 3, 5, 9, 11, 12, 16, 21, 29, 36, 37, 38, 40, 47, 52, 53, 54, 55, 56, 57

All plants that produced fruits were evaluated. Ten samples were taken from each plant which had produced up to ten fruits.

#### Assessed traits

- Number of fruits per plant (NF): weekly harvests were performed and, by the end of the assessment period (about 6 months), the total number of fruits per plant was summed;
- Mean mass of the fruits (FM): the fruits were weighed by means of a semi-analytic digital scale expressed in g; all the collected ripe fruits throughout the productive cycle;
- Transversal diameter of the fruit (TD): set on the equatorial region of the fruits. It was measured by a caliper expressed in mm;
- Longitudinal diameter of the fruits (LD): set on the longitudinal region of the fruits and measured by a caliper expressed in mm;
- Shell thickness (ST): set by the arithmetic average of the measurements of four spots on the external bark, in the mid portion of the fruits (transversally cut towards the larger diameter), and measured by a digital caliper expressed in mm;
- Mean mass of the pulp (PM): obtained by weighing the pulp (seeds with aryl), by means of a semi-analytic scale expressed in g;
- Level of soluble solids (LSS): obtained by refractometry, using an ATAGO N1 portable digital refractometer reading within a line from 0 to 32 °brix. Readings were performed in aliquots of juice from the pulp;
- Length of the androgynophore (LA): set throughout the extension that supports the sexual organs measured by a digital caliper expressed in mm.

#### Mixed model for assessment and selection of plants and estimation of genetic parameters

Traits were assessed by means of the Selegen-REML/BLUP software system (Resende and Duarte 2007). The analysis followed the statistical model  $y = Xr + Zg + Wp + e$  in which  $y$  is the vector of data,  $r$  is the vector of the repetition effects (assumed here as fixed) added to the general average,  $g$  is the vector of individual genetic effects (assumed here as random),  $p$  is the vector of the portion effects (random)

and  $e$  is the vector of residues (random). Capital letters refer to the incidence matrixes for the aforementioned effects. The following variance components were estimated (individual REML):

$\hat{\sigma}_g^2$ : genotypic variance among complete-siblings, equivalent to  $\frac{1}{2}$  of the additive genetic variance plus  $\frac{1}{4}$  of the dominance genetic variance, disregarding the epistasis' effects;

$\hat{\sigma}_f^2$ : individual phenotypic variance;

$\hat{h}^2_a$  = individual heritability in strict sense, disregarding the fraction (1/4) of prevalence genetic variance;

$\hat{h}_{mp}^2$ : heritability of the average of the progenies, assuming complete survival;

Acprog: accuracy of progeny selection, assuming complete survival;

#### Results and discussion

##### Estimations of genetic parameters by mixed models

The higher values for genotypic variance were found for the characters NF, FM and PM (111.98; 32.25 and 17.97, respectively). This indicates that the assessed population presents high genetic variability for these features (Table 2). On the other hand, low values were found for LD, TD, LSS, LA and ST. They ranged from 7.77 to 0.0024 (Table 2). However, it is not possible to conclude that the genetic gains related to the selection for these traits are lower, since the high estimates for heritability may occur for traits with low values of genetic variance, which was observed for LSS (0.36), since the environmental effect on the trait is reduced. Knowledge of the genotypic variance is very important for breeding programs because it indicates the extension of the genetic variation of a trait, with the use of breeding technologies (Cruz and Carneiro 2006).

In turn, the higher values for phenotypic variance were found for NF and FM (444.51 and 257.11, respectively). This indicates a stronger effect of the environment on the expression of such traits. Silva and Viana (2012) applied the method of moments to assess 140 progenies of complete-siblings of passion fruit, from the second recurrent selection cycle in northern Rio de Janeiro. They obtained phenotypic variance

**Table 2** Estimations of the genotypic variance components among full-sibling progenies ( $\hat{\sigma}_g^2$ ), individual phenotypic variance ( $\hat{\sigma}_f^2$ ), individual heritability in strict sense ( $\hat{h}_a^2$ ), progeny mean heritability ( $\hat{h}_{mp}^2$ ), selection accuracy of the progenies (Acprog), additive heritability within the part ( $\hat{h}_{ad}^2$ )

	NF	FM (g)	TD (mm)	LD (mm)	ST (mm)	PM (g)	LSS (°Brix)	LA (mm)
$\hat{\sigma}_g^2$	111.98	32.25	2.93	7.77	0.0024	17.97	0.36	0.12
$\hat{\sigma}_f^2$	444.51	257.11	25.46	59.46	0.55	58.92	1.17	1.71
$\hat{h}_a^2$	0.50 ± 0.26	0.25 ± 0.18	0.23 ± 0.17	0.26 ± 0.18	0.0089 ± 0.034	0.61 ± 0.28	0.62 ± 0.29	0.14 ± 0.13
$\hat{h}_{mp}^2$	0.87	0.47	0.61	0.64	0.043	0.79	0.89	0.62
Acprog	0.93	0.68	0.78	0.80	0.20	0.90	0.95	0.78

NF number of fruits, FM fruit mass, TD transversal diameter of the fruit, LD longitudinal diameter of the fruit, ST shell thickness, PM pulp mass, LSS level of soluble solids, LA length of the androgynophore

estimations of 1789.00 and 328.25 for NF and FM, respectively. However, the current study found lower values, which indicated a lower environmental effect on the expression of these traits. On the other hand, the lowest estimated phenotypic variation for ST (0.55) does not indicate a lower environmental effect, since this trait presented lower heritability and selective accuracy (Table 2).

Regarding heritability estimations, the estimated values for  $\hat{h}_a^2$  ranged from 0.62 to 0.0089. The high values of individual heritability obtained for LSS, PM and NF (0.62, 0.61 and 0.50, respectively) indicate that individual selection can be successful. However, when the heritability related to the average of families is considered ( $\hat{h}_{mp}^2$ ), significantly superior magnitudes are observed, often showing values three times higher than the individual heritability for LSS, NF and PM (0.89, 0.87 and 0.79, respectively). High  $\hat{h}_a^2$  and  $\hat{h}_{mp}^2$  estimations for LSS, NF and PM indicate that it is possible to succeed in both cases: between and within the progenies, respectively. However, high individual heritability related to the additive inheritable effects show that individual selection might be effective in the selection of superior segregating genotypes. Heritability magnitude shows the importance of performing a selection of genotypes based on their predicted genotypic value instead of the observed phenotype.

On the other hand, lower  $\hat{h}_a^2$  and  $\hat{h}_{mp}^2$  estimations, observed for FM and ST, might be due to the low value for genetic variance associated with high phenotypic variance. The use of more elaborated selection

obtained by means of the REML procedure for eight assessed traits in 118 interspecific hybrid genotypes obtained from the crossing between *P. setacea* and *P. edulis*. A Universidade Estadual do Norte Fluminense Darcy Ribeiro, Campos dos Goytacazes, RJ, 2013

methods is indicated for such variables. The use of mixed models for selection procedures is justifiable because, even with low heritability traits, the favorable genetic gains are predicted and the genotypes have the potential to be selected.

Oliveira et al. (2012) applied mixed models (REML/BLUP) to assess papaya F<sub>2</sub> segregating populations and verified high individual heritability values for length and diameter of the fruit and low LSS values, differently from the outcomes found by the current study.

Viana et al. (2004), aiming to start a breeding program for growing areas in Brazil, have estimated heritability coefficients in a passion fruit population and found high broad sense heritability for the trait number of fruits (92.10 %). For this, a joint analysis was conducted on the data from two environments. de Moraes et al. (2005) also found high  $\hat{h}_{mp}^2$  values for NF (82.20 %), whereas Silva and Viana (2012) found a value of 39.19 for the same trait. However, it is worth pointing out that such estimations were obtained by the method of moments or by variance analysis and the values were different from those estimated via mixed models. Besides the estimation method, it is important to consider that heritability estimations can change, among other factors, according to the genetic structure of the assessed populations. Although it is one of the most important pieces of information of population genetics, heritability is not an immutable estimation, due to the transient action of the effects of the alleles involved with the expression of the traits under analysis.

According to Falconer (1987), heritability is a property that holds more than one trait as well as the population and the environmental circumstances to which individuals are subjected. So, its values can be affected by any change in any of the components of the genetic and phenotypic variances. Such parameters may change according to the assessed trait, estimation method, population diversity, experimental unity under consideration, size of the assessed sample, endogamy level of the population, number and types of environments under consideration, and accuracy in the conduct of the experiment and data collection (Hallauer and Miranda Filho 1988). Thus, such estimations must not be extrapolated to other populations.

In the current study, accuracy values from 0.20 to 0.95 were achieved and were considered from low to very high in magnitude (Table 2). The higher values were obtained for LSS, NF and PM (0.95, 0.93 and 0.90, respectively), whereas low magnitude estimations were observed for ST (0.20) (Table 2). The quality of the genotypic assessment must be mainly inferred according to its accuracy. Resende and Duarte (2007) state that an accuracy above 90 % can only be achieved for variables with high heritability values. This corroborates the results found by the current study for the traits LSS and NF. The variables presenting higher accuracy values show good genetic control in the expression of characters and indicate good precision for the obtained results. Accuracy values higher than 0.70 are good enough to indicate precise inferences about the genetic value of the progenies. On the other hand, low accuracy estimations are usually related to low heritability estimations, as observed for ST. Once it is a measurement associated with selection preciseness, accuracy is the main element in genetic breeding that might be changed by man in order to maximize genetic gain (Resende 2002).

#### Genotype selection and estimations of genetic gain by BLUP

The 30 best individuals were selected for all the analyzed variables, out of the 118 assessed, accounting for 25.42 % of the genotypes. The genetic gains were predicted and the new estimated averages were higher than the general average of all the analyzed variables (Table 3).

The genetic values predicted by BLUP regard the values observed without the environment effects. Therefore, in opposition to what happens with vegetative propagation species, in which all the genotypic value is capitalized, in the case of outcrossing species, or those of crossed pollination, in which progeny tests are conducted, only the additive effects are transmitted to the descendants, which should be used as genitors in the next generations (Alves and Resende 2008). The genetic gain estimated by BLUP is equivalent to the average of predicted genetic values for the selected genotypes, and the new average refers to the general average added to the gain. This results in the improvement of the population average for the assessed traits.

By comparing the average of the 30 selected genotypes with the general average of the population, higher gain estimations were observed for the traits NF (319.15 %) and PM (73.12 %), lower gains for FM (21.50 %), LSS (13.43 %), LD (6.32 %) and TD (4.99 %), and small reductions in ST (−0.0036 %) and LA (0.0056 %), in comparison to the individuals first in the order.

The present work aimed to identify promising genotypes for NF, in other words more productive genotypes. Thus, the individual with the best score was individual number 1, within progeny 5. The gain predicted according to the selection of this individual was 319.15 %, which allowed on average an addition of 50.65 fruits. The individual in the 30th position was individual 9, within progeny 4, with a gain of 129.80 (Table 3).

Many hybrids, sexual or somatic, are completely sterile, which prevents their use in genetic breeding programs. In the population assessed, female sterility was discarded, since the hybrid fruit were produced by natural pollination. Soares-Scott et al. (2003) evaluated the meiotic behavior of hybrids *P. edulis* × *P. setacea* and found that the hybrids studied showed regular meiosis and pollen viability, which may suggest that the hybrids assessed in this study can be male-fertile.

The high estimations for heritability and selective accuracy favored a high genetic gain percentage for NF (319.15 %). Divergent crossings, similar to those assessed in the current study, originate populations with high genetic variability, a fact that may help in obtaining high heritability estimations, which, in their turn, favor the achievement of higher genetic gain. Besides heritability, the selection differential may,

**Table 3** Genetic gain and new predicted averages estimated via REML/BLUP in 118 interspecific hybrids obtained from crossings between *Passiflora edulis* and *Passiflora setacea* for nine morphoagronomic traits (Universidade Estadual do Norte Fluminense Darcy Ribeiro, Campos dos Goytacazes, RJ, 2013)

Ord.	NF	FM (g)		TD (mm)		LD (mm)		ST (mm)		PM (g)		LSS (°Brix)		LA (mm)		
		Gain (%)	New average	Gain (%)	New average	Gain (%)	New average	Gain (%)	New average	Gain (%)	New average	Gain (%)	New average	Gain (%)	New average	
1	319.15	66.52 (1/5)	21.50	78.41 (17/4)	4.99	60.32 (21/4)	6.32	75.82 (2/4)	-0.0036	5.42 (3/5)	73.12	40.46 (17/4)	13.43	14.94 (11/2)	0.0056	16.04 (3/9)
2	295.52	62.77 (57/9)	20.16	77.54 (21/4)	4.63	60.11 (8/1)	5.88	75.51 (18/2)	-0.0018	5.42 (21/5)	61.91	37.84 (21/4)	12.37	14.81 (12/2)	0.0511	16.04 (57/9)
3	259.98	57.13 (56/9)	19.61	77.19 (2/4)	4.50	60.04 (3/4)	5.62	75.33 (21/4)	0.0018	5.42 (22/5)	55.58	36.36 (2/4)	11.46	14.69 (16/2)	0.081	16.05 (29/9)
4	242.21	54.31 (14/5)	18.61	76.54 (3/4)	4.43	59.99 (2/4)	5.44	75.20 (16/2)	0.0036	5.42 (4/5)	50.96	35.28 (9/4)	10.78	14.60 (15/5)	0.110	16.05 (56/9)
5	229.93	52.36 (12/5)	17.41	75.77 (13/4)	4.33	59.94 (4/3)	5.27	75.08 (10/2)	0.0073	5.42 (9/5)	47.45	34.46 (3/4)	10.32	14.53 (7/2)	0.137	16.06 (12/9)
6	219.59	50.73 (4/5)	16.53	75.19 (16/9)	4.23	59.88 (17/4)	5.14	74.98 (20/2)	0.0092	5.42 (20/5)	44.71	33.82 (13/4)	9.94	14.49 (15/2)	0.168	16.06 (52/9)
7	211.90	49.50 (18/5)	15.69	74.66 (9/4)	4.16	59.84 (11/1)	5.03	74.91 (9/7)	0.0129	5.42 (12/5)	42.61	33.33 (5/4)	9.64	14.45 (2/2)	0.199	16.07 (11/9)
8	205.54	48.49 (22/5)	15.04	74.24 (5/4)	4.07	59.79 (10/1)	4.94	74.85 (10/1)	0.0166	5.42 (18/5)	40.94	32.94 (45/8)	9.41	14.42 (13/7)	0.230	16.07 (5/9)
9	200.37	47.67 (16/5)	14.48	73.88 (20/2)	4.00	59.75 (19/1)	4.87	74.80 (11/1)	0.0184	5.42 (8/5)	39.58	32.62 (22/2)	9.26	14.40 (18/2)	0.261	16.08 (37/9)
10	193.95	46.85 (19/5)	13.93	73.52 (4/3)	3.93	59.71 (14/1)	4.80	74.74 (4/1)	0.022	5.42 (13/5)	38.29	32.32 (16/9)	9.11	14.37 (1/7)	0.293	16.08 (1/9)
11	190.92	46.18 (20/5)	13.40	73.17 (10/3)	3.88	59.68 (13/4)	4.73	74.70 (14/7)	0.023	5.42 (16/5)	36.28	31.85 (10/3)	8.88	14.35 (8/7)	0.324	16.09 (53/9)
12	186.01	45.39 (2/5)	12.86	72.82 (18/2)	3.81	59.64 (9/1)	4.68	74.66 (19/1)	0.027	5.42 (23/5)	34.53	31.44 (20/1)	8.80	14.33 (6/7)	0.355	16.09 (54/9)
13	181.85	44.73 (15/5)	12.38	72.52 (45/8)	3.76	59.61 (20/2)	4.64	74.62 (1/1)	0.031	5.42 (7/5)	33.07	31.10 (4/3)	8.65	14.32 (9/7)	0.386	16.10 (38/9)
14	178.13	44.14 (13/5)	11.85	72.18 (19/1)	3.72	59.59 (1/1)	4.58	74.59 (14/2)	0.033	5.42 (19/5)	31.75	30.79 (12/9)	8.50	14.30 (7/7)	0.417	16.10 (16/9)
15	174.54	43.58 (17/5)	11.39	71.88 (9/7)	3.67	59.56 (3/1)	4.54	74.56 (20/2)	0.036	5.42 (5/5)	30.59	30.52 (40/9)	8.49	14.28 (3/2)	0.442	16.11 (4/7)
16	170.32	42.90 (11/9)	10.97	71.61 (55/8)	3.62	59.53 (4/1)	4.50	74.53 (2/2)	0.038	5.42 (63/8)	29.56	30.28 (1/1)	8.27	14.27 (14/2)	0.473	16.11 (47/9)
17	166.28	42.26 (21/5)	10.56	71.35 (11/2)	3.56	59.50 (12/1)	4.45	74.49 (14/1)	0.042	5.42 (10/5)	28.58	30.05 (47/8)	8.20	14.26 (2/5)	0.504	16.12 (11/7)
18	162.50	41.66 (29/9)	10.19	71.11 (2/2)	3.53	59.48 (7/1)	4.41	74.46 (9/1)	0.046	5.42 (2/5)	27.72	29.85 (11/9)	8.12	14.25 (11/7)	0.536	16.12 (3/7)
19	158.85	41.08 (3/5)	9.87	70.90 (40/9)	3.48	59.44 (20/1)	4.36	74.43 (7/1)	0.047	5.42 (15/5)	26.95	29.67 (55/8)	8.04	14.24 (17/2)	0.561	16.13 (2/7)
20	155.57	40.56 (5/5)	9.57	70.70 (13/2)	3.41	59.41 (9/7)	4.31	74.40 (11/2)	0.051	5.42 (17/5)	25.57	29.50 (8/7)	7.97	14.22 (17/5)	0.592	16.13 (14/7)
21	152.61	40.09 (23/5)	9.15	70.52 (8/1)	1.93	59.38 (10/3)	4.29	74.37 (4/3)	0.053	5.42 (1/5)	25.58	29.35 (3/1)	7.82	14.21 (3/7)	0.617	16.14 (55/9)
22	149.84	39.65 (8/5)	9.03	70.36 (21/9)	1.91	59.35 (9/3)	4.24	74.34 (8/1)	0.057	5.42 (8/8)	24.98	29.21 (54/9)	7.74	14.20 (10/5)	0.648	16.14 (40/9)
23	147.13	39.22 (7/5)	8.78	70.20 (14/7)	1.87	59.32 (9/4)	4.20	74.32 (17/4)	0.060	5.42 (14/5)	24.43	29.08 (11/2)	7.66	14.19 (20/2)	0.679	16.15 (1/7)
24	144.61	38.82 (9/5)	8.55	70.05 (3/1)	1.84	59.29 (2/3)	4.17	74.30 (13/4)	0.062	5.42 (13/8)	23.83	28.94 (57/9)	7.60	14.17 (16/5)	0.704	16.15 (10/7)
25	142.09	38.42 (16/9)	8.33	69.91 (11/1)	1.81	59.26 (8/3)	4.13	74.27 (3/1)	0.066	5.42 (27/6)	23.32	28.82 (37/9)	7.51	14.16 (5/7)	0.735	16.15 (13/7)
26	139.70	38.04 (10/5)	8.10	69.75 (3/7)	1.78	59.23 (2/1)	4.09	74.23 (2/1)	0.068	5.42 (45/8)	22.33	28.70 (29/9)	7.36	14.15 (12/7)	0.766	16.16 (36/9)
27	137.30	37.67 (21/9)	7.87	69.61 (47/8)	1.75	59.20 (14/7)	4.03	74.20 (12/7)	0.071	5.42 (55/8)	22.33	28.59 (18/2)	7.28	14.14 (5/5)	0.791	16.16 (5/7)
28	134.97	37.29 (54/9)	7.67	69.48 (37/9)	1.73	59.17 (28/8)	3.99	74.16 (12/1)	0.073	5.42 (16/8)	21.86	28.48 (2/2)	7.13	14.12 (11/3)	0.822	16.17 (8/7)

**Table 3** continued

Ord.	NF		FM (g)		TD (mm)		LD (mm)		ST (mm)		PM (g)		LSS (°Brix)		LA (mm)	
	Gain (%)	New average	Gain (%)	New average	Gain (%)	New average	Gain (%)	New average	Gain (%)	New average	Gain (%)	New average	Gain (%)	New average	Gain (%)	New average
29	132.38	36.88 (36/9)	7.45	69.34 (20/1)	1.69	59.14 (11/3)	3.95	74.13 (10/3)	0.077	5.42 (48/8)	21.39	28.37 (56/9)	7.06	14.11 (18/5)	0.854	16.17 (9/9)
30	129.80	36.48 (9/4)	7.25	69.21 (3/9)	1.66	59.11 (3/7)	3.89	74.10 (7/2)	0.079	5.42 (74/8)	20.96	28.27 (21/9)	6.91	14.09 (16/1)	0.885	16.18 (21/9)
General average	-	15.87	-	64.53	-	57.44	-	71.32	-	5.42	-	23.37	-	13.17	-	16.04

Sorted and selected individuals within each progeny in parentheses

Ord. order, NF number of fruits, FM fruit mass, TD transverse diameter of the fruit, LD longitudinal diameter of the fruit, ST shell thickness, PM pulp mass, LSS level of soluble solids, LA length of the androgynophore

direct or indirectly, affect the gain obtained by the selection (Vencovsky 1987). The genetic structure of the assessed population might have helped in increasing the gain in NF, because the more heterogeneous it is, the higher the possibility of gain due to the selection, since it is based on genetic differences (Vencovsky 1987).

According to Silva et al. (2009), the trait NF can be used as an indicator of the productive potential of the progenies, since total production is difficult to measure because the harvest period is too long and many assessments are needed to achieve more precise estimations. de Moraes et al. (2005) found a high and positive correlation between NF and the production of fruits, which enabled its use in the indirect selection of the fruits produced.

Regarding FM and PM, individual 17, within progeny 4, achieved the best score, which allowed an addition of 13.88 and 17.09 g on average, and gains of 21.50 and 73.13 %, respectively (Table 3). However, the predicted genetic gain for such individual did not seem reliable. Although it had presented higher energetic gain, this individual only produced one fruit and was not listed in the rank among the 30 individuals selected for NF. Therefore, the choice for individual 3, in progeny 4, was safer, since it produced 10 fruits, thus presenting a larger and more reliable sample. Progeny 4 stood out for FM and PM, since the five selected best individuals achieved the highest gain estimations for these traits. The following individuals were scored in the last collection for these traits: individual 3, within progeny 9, and individual 21, within progeny 9, with gains of 4.68 and 4.90 %, respectively (Table 3). According to Meletti et al. (2000), the selection of progenies with higher FM is interesting and may allow the highest gains for producers, since the weight usually has a direct and positive correlation with fruit size and thereby can achieve better prices in the market for fresh fruits.

Regarding TD and LD, the best scores were obtained by the following individuals: individual 21, in progeny 4, and individual 2, in progeny 4, with gains of 4.99 and 6.32 %, respectively (Table 3). Individuals with the lowest averages for the traits described above and ranked in the last position were: individual 3, in progeny 7, and individual 7, in progeny 2, with gains of 1.66 and 3.89 %, respectively (Table 3). Positive correlations between FM and LD, and FM and TD were found for the passion fruit tree,



which indicates that the progenies with higher weight for fruits tend to have larger fruits (longitudinally and transversally) (Silva et al. 2009). Thus, it is possible to infer that indirect gains for FM can be obtained for selected individuals with higher gain estimations for TD (4.98 %) and LD (6.32 %).

In the case of ST, it is recommended to select any individual within progeny 5, since the first 15 genotypes obtained the lowest magnitudes in genetic gain, which is desired for this particular variable (Table 3). The skin thickness is an important trait for both the juice concentrate industry and fresh fruit market, once it is inversely proportional to juice yielding (Viana et al. 2010). Low values for genetic variability (0.0024) and  $h_a^2$  and  $h_{mp}^2$  (0.0089 and 0.043, respectively), verified for ST, led to low values of genetic gain (0.079–0.0036 %), which is a desirable result, once the decreased average is targeted. Such results indicate a low possibility of improving this variable and, consequently, only a small genetic improvement is expected.

With respect to the LSS, genotype 11, within progeny 2, obtained the best score with expected gains up to 13.43 % for the general average. Individual 16, within progeny 1, was ranked in the last position, with an estimated gain of 5.73 % (Table 3). Even presenting high estimations for  $h_a^2$  and  $h_{mp}^2$ , the genetic gain for SSL was low. This might be ascribed to small genetic differences found for this variable, once the genotypes presented similar averages. The predicted genetic gains are directly proportional to the selection differential, which means that the lower the selection differential, the lower the gain. In this case, there is an inverse situation to that obtained for NF, in which the heritability estimations were low, but the genetic differences were higher. Even with lower gain, it is possible to succeed with the selection, mainly for the first individuals in progeny 2, since they presented higher gain estimations. Oliveira et al. (2012) used the mixed models methodology in segregating populations of papaya from commercial hybrids and found low genetic gain for SSL, similarly to the current study.

Silva and Viana (2012) estimated the predicted genetic gains in a passion fruit population, by using phenotypic indexes as an alternative to the selection of superior progenies. They verified undesirable gains of 1.34,  $-0.58$  and  $-0.66$  % for the traits ST, SSL and

PM, respectively. However, the direct selections performed in the current work were carried out for genotypes and were based on predicted genotypic values by applying the BLUP method, which corrects the identified environmental effects and is more accurate than phenotypic selection.

For LA, which is expected to decrease, the individual 3, within progeny 9, was selected with a gain of low magnitude, which is desirable for the genetic breeding of this variable (Table 3). The selection for LA in the assessed segregating population is an important variable that must be measured, since it is related to fruit production and the amount of pulp. A shorter androgynophore favors pollination by smaller insects. In passion fruit, it was observed that pollination affects fruiting, since the number of seeds per fruit and pulp yield are correlated to the number of pollen grains deposited on the stigma during pollination (Akamine and Girolami 1959; Siqueira et al. 2009).

By comparing the progenies performance with the assessed traits, it was verified that, for NF and ST, progeny 5 stood out with 70 % of the selected individuals (Table 3). The cause of the low yield of some progenies may be related to the high altitude of the stigma associated with corona, provided by the long androgynophore, which hinders pollination (Junqueira et al. 2005). Regarding FM, the majority (23 %) of the selected individuals belonged to progeny 4 (Table 3). Progeny 1 was different in 43 % of the selected individuals for TD and in 40 % for LD (Table 3). Regarding PM and LA, progeny 9 stood out with 33 and 66 % of the individuals, respectively (Table 3).

The prediction of genetic values of superior genotypes is one of the main problems in the breeding of any species, since it demands real values of variance components. The use of more sophisticated models, such as REML/BLUP, enables the obtaining of the best estimations for these parameters. Such a procedure takes into account the real values of variance components which are estimated by REML. These components interact in the BLUP's mixed models equations and provide the genetic values. Thus, the REML/BLUP strategy implies a genotypic rather than phenotypic selection because it considers the treatment effects (genotype) as random (Resende and Duarte 2007).

The current study aimed to select the best individuals within segregating populations in order to have them backcrossed with passion fruits aiming to obtain more promising genotypes regarding agronomic characters in further stages of the UENF passion fruit genetic breeding program. Thus, the used strategy (REML/BLUP) was effective in identifying superior genotypes, mainly for NF and PM, main traits evaluated at the beginning of the program, which will enable more profitable gains due to their selection.

**Acknowledgments** The authors are grateful to the Graduate Program in Genetics and Plant Breeding and to the Coordination of Improvement of Higher Education Personnel (CAPES) for the scholarship provided to the first author; to the Foundation for Research Support of the State of Rio de Janeiro (FAPERJ), National Council for Scientific and Technological Development (CNPq) and Universidade Estadual do Norte Fluminense Darcy Ribeiro (UENF) for their financial support for this research; to Dr. Margarete Magalhães de Souza, for providing genotypes of *P. setacea* and the greenhouse where the crossovers were performed (Universidade Estadual de Santa Cruz, BA, Brazil).

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