Acta Scientiarum
http://www.uem.br/acta
ISSN printed: 1679-9275
ISSN on-line: 1807-8621
Doi: 10.4025/actasciagron.v39i2.32554

Prediction of genetic gains by selection indexes and REML/BLUP methodology in a population of sour passion fruit under recurrent selection

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ABSTRACT. Breeding programmes must be improved to accelerate the development of new cultivars due to the commercial importance of passion fruit. This study compared four selection indexes and the REML/BLUP methodology in an assessment of predicted genetic gains in the traits of interest. A total of 81 full-sib progenies derived from the third cycle of recurrent selection were assessed for one harvest in one environment. The experiment was arranged in a randomized complete block design with five plants per plot. The following traits were assessed: number of fruits, total yield, fruit mass, fruit longitudinal diameter, fruit transverse diameter, fruit pulp percentage, shell thickness and content of soluble solids. The Mulamba & Mock index produced the best results for the selection of progenies. The REML/BLUP method was the most efficient and selected progenies with predicted genetic gains better than the selection indexes tested.

Keywords: mixed models, *Passiflora edulis* Sims, predicted genotypic values, simultaneous selection.

Predição de ganhos genéticos por índices de seleção e metodologia REML/BLUP em uma população de maracujá-azedo sob seleção recorrente

RESUMO. Tendo em vista a importância do cultivo do maracujazeiro, é de grande relevância o aprimoramento dos trabalhos de melhoramento genético a fim de possibilitar com maior rapidez o desenvolvimento de novas cultivares. O objetivo do presente trabalho foi comparar quatro índices de seleção e o método REML/BLUP na avaliação de ganhos genéticos preditos das características de interesse. Foram avaliadas 81 progênies de irmãos-completos, oriundas do terceiro ciclo de seleção recorrente, em uma safra, em um ambiente. O delineamento experimental utilizado foi o de blocos ao acaso com parcelas constituídas por cinco plantas. As características avaliadas foram: número de frutos, produção total, massa do fruto, diâmetro longitudinal do fruto, diâmetro transversal do fruto, porcentagem de polpa do fruto, espessura da casca e teor de sólidos solúveis totais. O índice de seleção de Mulamba & Mock proporcionou os melhores resultados para a seleção das progênies. O método REML/BLUP mostrou-se mais eficiente, tendo selecionado progênies com ganhos genéticos preditos melhores que os dos índices de seleção testados.

Palavras-chave: modelos mistos, *Passiflora edulis* Sims, valores genotípicos preditos, seleção simultânea.

Introduction

Passion fruit belongs to the Passifloraceae family, and *Passiflora edulis* Sims is the main cultivated species (sour passion fruit) (Bernacci, Soares-Scott, Junqueira, Passos, & Meletti, 2008), accounting for approximately 90% of Brazilian orchards, mainly due to its quality, productivity, vigour and juice yield.

According to the (Instituto Brasileiro de Geografia e Estatística [IBGE], 2014) records, Brazil is the largest producer of sour passion fruit, with an estimated production of 780 thousand tons. Due to the importance of this culture, breeding programmes must be improved to accelerate the development of new cultivars (Silva et al., 2014).

The literature offers little information on *Passiflora* breeding programmes that use recurrent selection. Therefore, this effort represents a pioneering research proposal that allows the generation of a large amount of knowledge on the genetic characteristics of this fruit as well as agreement on breeding methods that can be applied to passion fruit (Silva et al., 2014).

Use of the recurrent selection breeding method is expected to increase the frequency of favourable alleles, thus improving the phenotypic expression of the trait under selection and preserving genetic variability to allow genetic gains in the following cycles (Hallauer, Miranda Filho, & Carena, 2010).

The use of selection indexes is an additional character established by the optimal combination of several analysed characteristics that allows efficient and simultaneous selection for many characters and thus the correct classification of genotypes (Cruz, Regazzi, & Carneiro, 2004). The adoption of selection indexes has often been applied in sour passion fruit breeding with the aim of progeny selection (Gonçalves, Viana, Bezerra Neto, Pereira, & Pereira, 2007; Neves, Bruckner, Cruz, Viana, & Barelli, 2011; Freitas, Oliveira, Jesus, Cruz Neto, & Santos, 2012).

Genetic assessment based on REML/BLUP mixed models (maximum non-biased restricted likelihood/best linear unbiased prediction) has received special attention from researchers because of the potential for outstanding genetic progress and great accuracy in the selection process. The mixed model allows simultaneous modelling of fixed and random effects. Currently, BLUP is most widely used in the latter. The REML/BLUP methodology has been frequently applied in fruit breeding aimed at selection of progeny and/or individuals in pequi trees (Giordani, Fernandes, Titon, & Santana, 2012), peach trees (Bruna , Moreto, & Dalbo, 2012), açaí trees (Farias Neto, Resende, & Oliveira, 2011) and coconut trees (Farias Neto, Lins, Resende, & Muller, 2009).

The objective of the current study is to compare four selection indexes and the REML/BLUP methodology in an evaluation of predicted genetic gains for the traits of interest in the UENF passion fruit breeding programme.

Material and methods

Eighty-one full-sib progenies derived from the third cycle (C_{03}) of recurrent selection of passion fruit genetic breeding were evaluated in Itaocara-Ilha Barra do Pomba (21°40’ S, 42°04’ W, and altitude of 76 m) in Northwestern Rio de Janeiro State, Brazil. The progenies were planted in November 2011, and the harvest season occurred from August 2012 to April 2013. During this period, the average annual temperature was 22.5°C, and the average precipitation was 1,041 mm.

The field experiment was arranged as a randomized complete block design with two replicates and five plants per plot. A vertical trellis was chosen as the conduction system and consisted of treated eucalyptus fence posts with 2.5 m height, 4 m spacing and one number 12 wire located 1.80 m above ground, with spacing of 3.5 m between the planting lines.

All plants received the treatments recommended for crop cultivation, such as plant conduction and control of weeds, pests and diseases. Daily drip irrigation was used during the dry season. Seedlings were fertilized monthly with 22.5 g urea and 45 g potassium chloride per plant. In addition, 100 g of limestone and 200 g of simple superphosphate were applied to each plant at planting.

The following traits were assessed: number of fruits (NF) (obtained from a count of the total number of fruits in the plot produced by the first flowering season), yield (obtained from weekly harvest. At the end of the evaluation period, the masses of the fruits per plot were summed and converted into tons per hectare), fruit mass in grams (MF) (given as the arithmetic mean mass of ten fruits sampled per plot with the aid of a digital scale), longitudinal fruit diameter in mm (DLF) (obtained from longitudinal measurements of the fruits with a digital calliper and sampling of ten fruits per plot), transverse diameter of the fruit in mm (DTF) (obtained by measuring the transverse dimension of the fruits with a digital calliper and sampling of ten fruits per plot), percentage of fruit pulp (PP) (obtained by the ratio between the pulp mass and the total fruit mass and sampling of ten fruits per plot), shell thickness in mm (EC) (determined by the arithmetic mean of the measurements of four points of the outer shell in the middle portion of the fruits, cross-sectioned in the direction of the wider diameter, with a digital calliper using samples of ten fruits per plot), soluble solids content in °Brix (SST) (obtained from refractometry using a portable ATAGO N1 digital refractometer with readings in the range of 0 to 32° Brix. The readings were performed on aliquots of juice from the pulp in samples of ten fruits).

The Smith (1936), Hazel (1943), Williams (1962) Pesek and Baker (1969) and Mulamba & Mock (1978) selection indexes were tested for selection of the best 25 progenies. In the computational analysis, economic weights were assigned by trials for each analysed characteristic according to relevance. The selection of superior progenies using selection indexes was performed with the aid of the Genes software system (Cruz, 2013).

The mixed models were assessed by the Selegen-REML/BLUP software system (Resende, 2007a) for the model that considered the randomized block design in one location and one harvest, according to the model below:

$$Y = Xr + Zg + Wp + \varepsilon,$$

where Y is the vector of phenotypic values, r is the vector of repetition effects (assumed to be fixed) added to the overall average, g is the vector of individual genotypic values (assumed to be random), p is the vector of plot effects (assumed to be random), and ε is the error vector or residue-vector (random). The capital letters refer to the incidence matrices for these purposes. The distributions and structures of the variance associated with the terms of the model are described by the following:

$$y|b,V \sim N(Xb,\ V)$$
$$g\ |I\sigma_g^2\ \sim N(0, I\sigma_g^2\ )$$
$$p|\sigma_p^2 \sim N(0, I\sigma_p^2)$$
$$\varepsilon|\sigma_\varepsilon^2 \sim N(0, I\sigma_\varepsilon^2)$$
$$V = Z\ \sigma_g^2 Z\ ' + WI\sigma_p^2 W' + I\sigma_e^2$$

The breeding values of each progeny were obtained by adding each genotypic effect (g) to the overall mean of the experiment (μ). The genetic gain is equivalent to the average of the vectors of the predicted genetic effects for the progenies selected. The overall mean added to the genetic gain results in an improved population average.

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

σ^2_g: Genotypic variance among full-sib progenies, equivalent to half the additive genetic variance plus one quarter of the genetic variance of dominance and disregarding epistasis;

σ^2_f: Phenotypic variance;

h^2_{mp}: Heritability of average progeny, assuming complete survival;

Acprog: Accuracy of progeny selection, assuming complete survival;

The index of coincidence was obtained using the ratio between twice the number of progenies in which both selection indexes coincide and the sum of the total number of progenies containing the selection index A plus the total number of progenies containing the selection index B (Pedrozo, Benites, Barbosa, Resende, & Silva, 2009).

Results and discussion

The Pesek and Baker (1969) index resulted in undesirable gains for the traits NF, MF and DLF, with values of -0.26, -1.89 and -1.17%, respectively (Table 1).

Table 1. Estimates of the percentage gains based on the selection differential for simultaneous selection in eight traits in the third cycle of intrapopulation recurrent selection in full-sib progenies of passion fruit.

Trait[1]	Selection indexes				REML/ BLUP
	Pesek and Baker	Smith and Hazel	Mulamba and Mock	Williams	
NF	- 0.26	28.00	22.35	28.02	77.98
Yield	1.72	10.54	10.15	13.02	19.26
MF	- 1.89	1.69	0.69	1.94	25.22
DLF	- 1.17	- 0.48	0.18	0.27	23.85
DTF	0.79	1.44	0.54	1.43	20.65
PP	0.69	- 0.47	3.11	- 0.86	19.40
EC	- 1.80	0.55	- 4.08	0.29	0.00
SST	0.52	- 0.24	0.84	0.43	19.71

[1] NF, (1) NF, number of fruits; yield, in t ha^{-1}; MF, fruit mass in grams; DLF, longitudinal diameter of the fruit in mm; DTF, transverse diameter of the fruit in mm; PP, percentage of pulp; EC, shell thickness in mm; SST total soluble solids in °Brix.

Gonçalves et al. (2007) assessed six productive traits of a population of yellow passion fruit structured in Design I in two locations (Viçosa, Minas Gersis State and Miracema, Rio de Janeiro State) and observed that the Pesek and Baker (1969) index showed the highest gain for the trait of number of fruits per plant, unlike the results observed in this study.

The objective of passion fruit breeding programmes is development of plants with a greater number of fruits, which should also be larger and have greater masses, to meet the demands of the market. However, the work of Pesek and Baker (1969) stands out based on the desired gain in the trait EC because fruits with a thinner peel tend to have a larger amount of pulp.

The Smith (1936) and Hazel (1943) indexes delivered genetic gains for the traits NF and yield, with values of 28.00 and 10.54%, respectively (Table 1). A positive gain was noted for MF, but the value was low (1.69%). However, undesirable gains were observed for the traits DLF (-0.48%), PP (-0.47%), EC (0.55%) and SST (-0.24%). Thus, this method is not indicated for selection of progenies in that population because undesirable gains were observed for most traits of economic interest. Gonçalves et al. (2007) observed results similar to those obtained in this study. The authors found that the Smith (1936) and Hazel (1943) indexes showed the lowest predicted gain in several alternatives, which resulted in unsatisfactory gains compared with the other indexes assessed.

The genetic gains predicted by the Mulamba and Mock (1978) index were satisfactory for all traits (Table 1) assessed. Genetic gains of 22.35, 10.15, 3.11 and -4.08% were observed for NF, yield, PP and EC, respectively. Gonçalves et al. (2007) analysed various selection indexes in a sour passion fruit population structured in Design I and indicated the Mulamba and Mock (1978) selection index because it produced greater predicted genotypic gain and is considered promising for selection of superior progenies. In a cycle of recurrent selection that preceded the population evaluated in this study, Silva, Viana, Gonçalves, Amaral Junior, and Pereira (2009) observed that when using the Mulamba and Mock (1978) index, the predicted genetic gains were 1.03% for number of fruits, 3.18% for fruit mass, 0.47% for fruit length, 1.36% for fruit width, and 0.65% for shell thickness. In the cycles of recurrent selection that preceded this study, the results obtained by the authors mentioned above led to the conclusion that an increase in gains occurred with the advance of recurrent selection for the main traits of sour passion fruit, which indicates that the chosen selection method is satisfactory. Freitas et al. (2012) used the Mulamba and Mock index (1978) in sour passion fruit and observed satisfactory simultaneous gains in productivity, fruit mass, pulp yield and content of total soluble solids as well as reduced disease severity.

The Williams (1962) index allowed satisfactory genetic gains for the traits NF, yield and MF, with values of 28.02, 13.02 and 1.94%, respectively (Table 1). These gains were greater than those obtained by the Mulamba and Mock (1978) index. Positive but low gains were observed for DLF (0.27%), DTF (1.43%) and SST (0.43%). Simultaneous selection was not satisfactory for PP and EC because they presented gains of -0.86 and 0.29%, respectively. These results demonstrate that the Williams (1962) index is suitable for selection of progenies in the current population, but undesirable gains were observed for the traits of interest PP and EC. Neves et al. (2011) analysed the feasibility of using the Williams index (1962) in sour passion fruit and concluded that the index created the selection of 35 families with gains in productivity and pulp weight.

In mixed models, estimators and predictors are obtained using iterative processes. To begin the iterative process, the initial value adopted for h^2 was equal to 0.10, as recommended by Resende (2007a). The process produced results for the components of genotypic (σ^2_g) and individual phenotypic (σ^2_f) variance, heritability (h_{mp}^2), and accuracy of selection of progenies (Acprog), as included in Table 2.

Table 2. Estimates of genetic and phenotypic parameters of full-sib progenies of sour passion fruit for the traits of number of fruits (NF), yield and fruit mass (MF) in Itaocara, Rio de Janeiro State.

Estimate	NF	Yield	MF
σ^2_g	5253.48	17.21	200.82
σ^2_f	38792.86	187.65	949.82
h^2_{mp}	0.23	0.18	0.34
A_{cprog}	0.48	0.36	0.59
Average	305.13	15.9	167.46

(1)NF, (1) NF, number of fruits; Yield, in t ha^{-1}; MF, fruit mass in grams.

The main evaluated traits of NF, yield and MF presented estimated values for the genotypic variance of 5253.48, 17.21, and 200.82, respectively (Table 2). These values indicate that the population studied presents high genetic variability for these characters, which demonstrates that it is possible to select progenies with increased yield and increased fruit mass. Knowledge of the genotypic variance is highly important for breeding programmes because it indicates the range of genetic variation of a character that breeders intend to improve.

Estimates of phenotypic variance were 38792.86, 187.65 and 949.82 for NF, yield and MF, respectively (Table 2). In a cycle of recurrent selection preceding that of the population assessed in the current work, Silva,Viana, Amaral Junior, Gonçalves, and Reis (2012) observed estimates of phenotypic variance of 1789.00, 14.96, and 328.28 in the progenies of full-sibs for the traits NF, yield and MF, respectively. The higher values of phenotypic variance observed in this study indicate a stronger influence of the environment compared with the previous cycle. This result is probable because Itaocara was more heavily affected by the environment than the municipality of Campos dos Goytacazes, where the previous cycles were conducted.

The h^2_{mp} estimates were 0.23, 0.18, and 0.34 for NF, yield and MF, respectively (Table 2), which classifies their magnitude as moderate ($0.15 < h^2 < 0.50$). However, it cannot be concluded that genetic gains obtained by selection will be lower because estimates of heritability values of high magnitude might occur for characters of small genetic variance, provided that the environmental effect on the trait is of small magnitude. Thus, heritability is not an immutable characteristic and is a property not only of the trait but also of the population and environmental conditions to which the population submits.

The accuracy values of 0.48, 0.36, and 0.59 found for NF, yield and MF, respectively, are classified according to Resende and Duarte (2007) as low (Acgen ≤ 0.50) and moderate (0.50 ≤ Acgen ≤ 0.70), respectively. The accuracy value indicates the precision in the access to the actual genetic variation based on the phenotypic variation observed in each trait. Low accuracy indicates that the data for these traits are less reliable, possibly because the trait is highly affected by the environment.

The mean values of the traits NF, yield and MF were 305.13, 15.9 t ha^{-1} and 167.46 grams, respectively. In a cycle preceding that of this study, the mean values reported by Silva et al. (2009) were lower except for yield, with mean values of 141.88 for NF, 16.3 t ha^{-1} for yield and 144.53 g for MF. This result highlights the potential of this population to achieve genetic gains from the UENF sour passion fruit intrapopulation breeding programme.

Compared with the selection indexes studied, the REML/BLUP methodology allowed higher predicted gains for all traits, except for EC (Table 1). The highest predicted gains were observed for the traits NF (77.98%) and MF (25.22%), which is desirable for the breeding programme. The difference between the REML/BLUP estimates of gain compared with the selection indexes investigated might be explained by the fact that the REML/BLUP methodology uses the predicted genotypic effects, the coefficient matrices of kinship, and the selection gains for each family as a solution vector. The correction of the values for environmental effects predicts the genotypic values accurately and without bias and leads to increased genetic gain with selection (Rodrigues, Vieira, Barbosa, Souza filho, & Candido, 2013). The result observed in this study indicates the REML/BLUP methodology for recombination of superior progenies in the subsequent cycles.

Resende (2007b) reported that simultaneous analysis of various traits could be efficiently performed using the multivariate REML/BLUP approach. Selection indexes commonly use economic weights, which become arbitrary genetic gains. In passion fruit, this result is even more evident due to the negative correlation between the characteristics of economic importance, namely, shell thickness and pulp percentage. Because these traits are negatively correlated, direct selection via genotypic values of the characteristics becomes compromised. Using the REML/BLUP approach for the same group of progenies and traits evaluated in this work, Silva, Muñoz, Vicent, and Viana (2016) found the highest genetic correlation between shell thickness and pulp percentage (-0.98). This high genetic correlation was expected because fruits with more pulp tend to have thinner skin, which is an objective of the UENF passion fruit breeding programme.

Santos et al. (2015) evaluated hybrids of *Passiflora* for the main traits using the REML/BLUP method and identified superior genotypes derived from interspecific cross between *P. edulis* and *P. setacea* for generation advance in the sour passion fruit breeding programme aimed at resistance to *Cowpea aphid-borne mosaic virus* (CABMV). Oliveira, Fraife Filho, Freitas, Dantas, and Resende (2012) used the REML/BLUP methodology to rate F2 segregating populations of papaya and found high values of individual heritability for length and diameter of fruit and low values for SST.

The coefficients of coincidence of 25 full-sib progenies chosen by the selection indexes and the REML/BLUP methodology are presented in Table 3. The coefficients are generally low except for the coefficients found between the indexes of Smith (1936) and Hazel (1943) and Williams (1962), with a value of 0.92, i.e., 23 coincident progenies, and between the selection index of Mulamba and Mock (1978) and the REML/BLUP methodology, which presented a value of 0.84, i.e., 21 coincident progenies (Table 3).

Table 3. Coefficients of coincidence of 25 progenies selected using a selection index and REML/BLUP methodology for the eight traits evaluated in the fruits of sour passion fruit from Itaocara, Northwestern State of Rio de Janeiro.

Selection index	Pesek and Baker	Smith and Hazel	Mulamba and Mock	Williams	REML/ BLUP
Pesek and Baker	-				
Smith and Hazel	0.48	-			
Mulamba and Mock	0.48	0.64	-		
Williams	0.48	0.92	0.64	-	
REML/BLUP	0.44	0.60	0.84	0.56	-

According to Pedrozo et al. (2009) the higher the coefficient of coincidence between two selection indexes, the greater the agreement between them will be with respect to the results of selection.

With the aim of selecting progenies of sour passion fruit, Silva and Viana (2012) evaluated the indexes based on the sum of ranks of Mulamba and Mock (1978) and the distance between the genotype and the ideotype (Cruz, 2013) and observed a coefficient of coincidence of 0.97. This result allowed simultaneous selection of superior progenies for the traits of number of fruits, total productivity, average fruit weight, fruit diameter, fruit length, fruit width and weight of fruit pulp.

Out of the 81 progenies assessed, the best 25 for the variables NF, yield and MF were selected through the REML/BLUP methodology and account for 30.86% of the progenies. Genetic gains were predicted, and the new estimated averages were higher than the overall average for all variables (Table 4).

Table 4. Estimates and ranking of the best 25 full-sib progenies, predicted genotypic values (g), genotypic values (μ + g), and new predicted average (BLUP) for the traits number of fruits, yield and fruit mass.

		Number of fruits					Yield (t ha^{-1})					Fruit mass (g)			
Ranking	Progeny	g	μ+g	Gain	New mean	Progeny	g	μ+g	Gain	New mean	Progeny	g	μ+g	Gain	New mean
1	26	125.82	430.95	125.82	430.96	26	0.73	16.65	0.73	16.65	69	18.70	186.17	18.70	186.17
2	56	110.96	416.09	118.40	423.53	24	0.46	16.38	0.59	16.52	5	16.08	183.55	17.39	184.86
3	24	83.86	389.00	106.89	412.02	70	0.44	16.37	0.54	16.47	3	15.65	183.12	16.81	184.28
4	70	67.45	372.58	97.03	402.16	69	0.38	16.30	0.50	16.43	8	15.44	182.91	16.47	183.94
5	1	61.19	366.33	89.86	395.00	68	0.33	16.26	0.47	16.39	68	15.27	182.74	16.23	183.70
6	68	59.11	364.25	84.74	389.87	1	0.32	16.25	0.44	16.37	42	14.14	181.61	15.88	183.35
7	19	50.38	355.52	79.83	384.97	40	0.27	16.20	0.42	16.34	47	13.91	181.38	15.60	183.07
8	69	46.47	351.61	75.66	380.80	50	0.23	16.15	0.39	16.32	72	13.78	181.25	15.37	182.84
9	47	46.09	351.22	72.38	377.51	56	0.22	16.15	0.38	16.30	75	12.75	180.22	15.08	182.55
10	34	42.18	347.31	69.36	374.49	45	0.21	16.14	0.36	16.29	51	11.32	178.79	14.71	182.17
11	45	39.31	344.44	66.62	371.76	22	0.20	16.13	0.34	16.27	78	10.45	177.92	14.32	181.79
12	38	33.84	338.97	63.89	369.03	19	0.20	16.13	0.33	16.26	2	9.72	177.18	13.94	181.40
13	16	32.80	337.93	61.50	366.64	16	0.20	16.13	0.32	16.25	41	9.57	177.04	13.60	181.07
14	10	31.89	337.02	59.39	364.52	34	0.19	16.11	0.31	16.24	6	9.11	176.58	13.28	180.75
15	22	31.89	337.02	57.55	362.69	38	0.19	16.11	0.30	16.23	33	9.05	176.52	13.00	180.47
16	23	30.58	335.71	55.87	361.00	55	0.18	16.10	0.30	16.22	7	8.06	175.53	12.69	180.16
17	40	30.32	335.45	54.36	359.50	60	0.17	16.10	0.29	16.22	53	7.69	175.16	12.39	179.86
18	55	29.28	334.41	52.97	358.11	47	0.16	16.09	0.28	16.21	73	6.40	173.87	12.06	179.53
19	50	29.02	334.15	51.71	356.85	10	0.16	16.08	0.28	16.20	1	6.33	173.80	11.76	179.23
20	60	25.89	331.02	50.42	355.55	5	0.15	16.08	0.27	16.20	24	6.05	173.52	11.47	178.94
21	17	25.37	330.50	49.23	354.36	23	0.14	16.07	0.26	16.19	52	5.19	172.66	11.18	178.64
22	11	21.98	327.11	47.99	353.12	79	0.14	16.06	0.26	16.18	44	5.17	172.64	10.90	178.37
23	54	20.81	325.94	46.81	351.94	17	0.13	16.05	0.25	16.18	29	4.82	172.29	10.64	178.11
24	5	19.38	324.51	45.66	350.80	62	0.13	16.05	0.25	16.17	59	4.81	172.28	10.40	177.86
25	9	15.08	320.21	44.44	349.58	7	0.11	16.03	0.24	16.17	48	4.26	171.73	10.15	177.62

Progeny 26 was best ranked in the identification of promising progenies for number of fruits and yield, i.e., more productive progenies. For NF, the gain predicted by the selection of this progeny was 125.82, with 431 fruits on average, and progeny 9 was ranked in the 25th position, with a gain of 44.44%, thus producing an average increase of 29.26 (Table 4). A total of 22 progenies selected for NF were also selected for yield. According to Silva et al. (2016), the high correlation observed between NF and yield (0.97) for this same group of progenies implies that it is not necessary to evaluate both characteristics in subsequent cycles, and thus the easiest or less costly trait should be measured. Considering the importance of selecting progenies with greater fruit mass (MF), the highest-ranking position was obtained by progeny 69, the expected gains of which exceeded 18.70% of the overall average. Progeny 48 was ranked at the lowest position, with an estimated gain of 4.26%.

The genotypic values predicted by BLUP refer to those observed without the environmental effect. Therefore, contrary to observations in species of vegetative propagation, in which all genotypic values are utilized, in allogamous or outcrossing species, which are subjected to progeny tests, only the additive effects are transmitted to the descendants and should be considered during the selection of genotypes that will be used as parents in the following generations (Resende, 2002).

The REML/BLUP method was more efficient than the selection indexes and allowed selection of progenies with promising predicted genetic gains for all traits assessed, primarily NF, yield and MF, which are the main traits required in the sour passion fruit breeding programme. Based on the results found in this work, the REML/BLUP methodology was indicated for the recombination of superior progenies in the subsequent selection cycles.

Conclusion

Among the four selection indexes tested, Mulamba and Mock and Williams are most suitable for selection of full-sib progenies in the sour passion fruit population under study.

The REML/BLUP method offers the best predicted genetic gains compared with those obtained by the selection indexes and is efficient in selecting progenies of sour passion fruit.

Acknowledgements

The authors thank FAPERJ and CNPq for financial support of experiments and CAPES for granting a doctoral scholarship for the first author.

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Received on July 4, 2016.
Accepted on October 10, 2016