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Intrapopulation recurrent selection by mixed models in papaya of the Formosa group

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Abstract – Few cultivars of papaya from the Formosa group are available to producers, and the development of new genotypes is indispensable. Thus, the use of effective selection strategies to obtain more productive cultivars and better quality fruits is also necessary. The aim of this study was to select of half-sib families (HSF) of papaya using the methodology of mixed models. Nineteen HSFs from the Incaper's papaya breeding program were evaluated in a randomized block design with five replicates and nine plants per plot. The selection was made based on fruit mass (FM), pulp thickness (PT), soluble solids content in pulp (SS) and number of fruits (NF). The genetic parameters and genotypic values were estimated by the REML/BLUP procedure. The selected HSFs increased FM by 26.1%; the PT in 10.5%; the SS in 7.5% and; the NF in 13.0%. The additive heritability within the progenies and the individual variation coefficient obtained indicate that the selection between and within the HSFs can provide greater genetic gains. The selection based on the REML/BLUP methodology was efficient to obtain simultaneous genetic gains for all variables under study despite the negative correlation between them.

Index terms: *Carica papaya* L., REML/BLUP, genetic gain, genotypic values.

Seleção recorrente intrapopulacional via modelos mistos em mamoeiro do grupo Formosa

Resumo – Poucas cultivares de mamoeiro do grupo Formosa estão disponíveis aos produtores, sendo imprescindível o desenvolvimento de novos genótipos. Assim, o emprego de estratégias eficazes de seleção para a obtenção de cultivares mais produtivas e de frutos de melhor qualidade se faz necessário. O objetivo deste estudo foi selecionar famílias de meios-irmãos (HSF) de mamoeiros utilizando a metodologia de modelos mistos. Foram avaliadas 19 FMIs oriundas do programa de melhoramento do mamoeiro do Incaper, em delineamento de blocos ao acaso, com cinco repetições e nove plantas por parcela. A seleção foi realizada com base na massa do fruto (FM), na espessura da polpa (PT), no teor de sólidos solúveis na polpa (SS) e no número de frutos (NF). Os parâmetros genéticos e os valores genotípicos foram estimados pelo procedimento REML/Blup. As HSF selecionadas incrementaram a FM em 26,1%; a PT em 10,5%; o SS em 7,5%, e o NF em 13,0%. A herdabilidade aditiva dentro das progênies e o coeficiente de variação individual obtidos indicam que a seleção entre e dentro das HSF podem proporcionar maiores ganhos genéticos. A seleção baseada na metodologia REML/Blup foi eficiente para obtenção de ganhos genéticos simultâneos para todas as variáveis em estudo, a despeito da correlação negativa existente entre elas.

Termos para indexação: *Carica papaya* L., REML/Blup, ganho genético, valores genotípicos.

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Introduction

Brazil is the second largest producer and exporter of papaya (*Carica papaya* L.) with cultivated area of approximately 32 thousand hectares, production of about 1.6 million tons year $^{-1}$ and productivity around 50 t ha^{-1} (FAOSTAT, 2017). For the papaya tree there are two heterotic groups - Solo and Formosa - that differ mainly in relation to fruit size and commercial uses. The fruits of papaya from the Formosa group weigh more than 1 kg and are more used by the industry and hotel chain.

Despite the large area of production and consumption, few cultivars of papaya from the Formosa group are available to producers, which can cause the genetic vulnerability of the crop, limiting its genetic progress. Therefore, the development of new cultivars can contribute to reduce this risk, besides increasing productivity and improving the quality of papaya fruits. This study will be facilitated by the use of efficient methods of genetic parameters estimation and the selection of genotypes of interest (PINTO et al., 2013).

Efficient selection of higher genotypes, which will be used as parents in subsequent generations, is even more important in perennial or semi-perennial species (FERREIRA et al., 2016). As the life cycle of these species is long, inadequate selection can harm the work done over the years. A safe way to identify genetic material with characteristics of interest is the evaluation based on genotypic values, which has additive nature and greater accuracy (RAMOS et al., 2014). These estimates can be obtained using mixed linear models of the restricted maximum likelihood / best linear unbiased prediction (REML/BLUP).

BLUP is a selection procedure that allows the optimization of genetic additives effects, of dominance or genotypic. Thus, the BLUP maximizes the selective accuracy and allows the simultaneous use of several sources of information, such as those of experiments installed in one or several places, the degree of kinship of the individuals under selection and the coincidence between the selection and recombination unit. For the application of BLUP it is necessary to estimate some components of variance and genetic parameters. The REML is the optimal procedure to obtain these components, surpassing the analysis of variance for unbalanced data or non-orthogonal treatments (RESENDE, 2016).

The selection based on genotypic values obtained through REML/BLUP has deserved special attention from the researchers and are used for annual species (VITTORAZZI et al., 2017), forest (HARDNER et al., 2016) and fruit species, such as for yellow passion fruit (FERREIRA, et al., 2016; SILVA, et al., 2017) and for guava (QUINTAL et al., 2017). For the papaya from the group Solo, Pinto et al. (2013) and Ramos et al. (2014) concluded that the genotypic values predicted by the mixed models are more efficient than the phenotypic values in the selection of individuals of interest. However, for the papaya of the Formosa group, the selection studies are scarce using the methodology of the mixed models.

In view of the above, the objective was to use the mixed model methodology to select half-sib families (HSF) of papaya from the Formosa group, based on production and fruit quality characters.

Material and methods

The experiment was installed in the municipality of Sooretama (19º03' S; 40º08' W), north of the State of Espírito Santo, one of the main producing regions of papaya in the state. The climate of the region is classified as tropical with dry season (classification of Köppen: Aw). During the execution of the experiment, between November 2015 and December 2016, the average air temperature was 31°C, the average temperature range was 15.8°C and the accumulated rainfall was 771.8 mm, considered a time of great water deficit in the region (INCAPER, 2017).

The 19 half-sib families (HSF) previously selected from a population of the cultivar Rubi Incaper 511 (MELO et al., 2015) were evaluated. The Instituto Capixaba de Pesquisa, Assistência Técnica e Extensão Rural (Incaper) launched in 2010, the 'Rubi Incaper 511', being the first open pollinating cultivar of the Formosa group (CATTANEO et al., 2010). From this cultivar, a new phase of the Incaper breeding program began to be developed in 2013, seeking to improve productivity, increase soluble solids content, and reduce the incidence of diseases. For the formation of the HSF studied, 150 plants were selected based on the objectives of the breeding program. The seeds of the selected plants, in which the female parental was known and the male parental was the pollen mixture of the population, formed the HSFs. These HSFs, in turn, were selected by Melo et al. (2015). Given this, the HSFs evaluated corresponded to a second selection cycle.

The seedlings were produced on Bioplant Plus® commercial substrate. Transplanting was carried out in November 2015 in a randomized block design, with five blocks and nine plants per plot, of which five were considered useful. As a border, it was used the 'Rubi Incaper 511'. Three seedlings were planted per hole and, after the emergence of the flower buds, thinning was done keeping only one hermaphrodite plant per hole. The spacing used was 3.5 m x 2 m, keeping the lines clean. The irrigation system used was drip irrigation and cultural treatments were performed according to Martins and Costa (2003).

For the purpose of selection, four variables were used: fruit number (FN), fruit mass (FM), pulp thickness (PT) and soluble solids content (SS). The number of fruits was obtained by counting the commercial fruits harvested at 180 and 240 days. For the FM (in grams), the PT (in cm) and the SS (in °Brix) it was calculated the means of the evaluations realized in three fruits per useful plant, in stage 2 of maturation (15% of the surface of the yellow peel).

The genetic parameters were estimated using the methodology of mixed models via REML/BLUP, considering the statistical model $y = Xr + Za + e$, where: y is the vector of phenotypic values; r is the vector of the repetition effects (assumed as fixed) added to the general mean; a is the vector of individual additive genetic effects (assumed to be random); e is the vector of errors or residues (random). Capital letters represent the incidence matrices for these effects (RESENDE, 2000). The following genetic parameters were estimated: general mean of the experiment; σ^2_a: additive genetic variance; h^2_{mp}: heritability of the average progeny; h^2_{ad}: additive heritability within progeny; Ac_{prog}: accuracy of progeny selection; CV_{gi}: coefficient of individual additive genetic variation (%); CV_{gp}: coefficient of genetic variation between progenies (%); CV_e: coefficient of residual variation (%); CV_r = coefficient of relative variation; PEV: variance of prediction error of genotypic values; and σ_g: standard deviation of the predicted genotypic value. The equations of mixed models and the iterative estimators of the variance components by REML via EM (*Expectation-Maximization*) can be obtained in Resende (2000) and in Ferreira et al. (2016).

For each variable, the progenies were ordered according to the additive genetic effect and the genetic gain, and later the new predicted averages were calculated. The selection was applied considering several characteristics simultaneously, so the HSF were selected according to the criterion of being among the 10 best progenies in at least three of the four variables studied. The analyzes were carried out with the help of the Selegen program (RESENDE, 2016).

Results and discussion

In its launch, the cultivar Rubi Incaper 511 had fruits of 1,470 g, pulp thickness of 3 cm, soluble solids content of 10.2 °Brix and 62.9 fruits per plant (CATTANEO et al., 2010). In the present study, all variables evaluated had averages lower than those reported by Cattaneo et al. (2010) (Table 1). However, Barros et al. (2017) observed that in the summer 'Rubi Incaper 511' had FM of 1,185 g and PT of 2.84 cm and in winter FM was 1,456 g and PT of 3.21 cm, evidencing the environmental interference in the expression of these characteristics.

In a similar manner to the characteristics described above, the soluble solids content was lower, as it is influenced by temperature, precipitation, pest and disease incidence, light exposure and fruit maturity at harvest time (LUZ et al., 2015). Regarding the number of fruits, only two harvests were considered in this study, aiming to anticipate the selection process. Therefore, the NF of this experiment does not reflect the total number of fruits of the plant during the whole production period, justifying the average lower than that reported by Cattaneo et al. (2010).

The average progeny heritability (h^2_{mp}) varied from 0.64 (NF) to 0.87 (FM). Already the additive heritability within progenies (h^2_{ad}) was greater than h^2_{mp} for the four analyzed variables (Table 1). This indicates that if the selection is made between and within the progenies it may provide better genetic gains. However, considering that the selection between and within would provide a small increase in genetic gain (maximum of 9%); it is necessary to evaluate whether the financial and labor resources needed to perform the evaluation at the individual level would be compensatory.

For papaya from the Solo group, Pinto et al. (2013) obtained h^2_{mp} from 0.28 for FM; 0.32 for PT and 0.05 for SS, superior to those obtained by individual heritability, demonstrating family-based selection (progeny) would result in greater genetic gain. On the other hand, in sour passion fruit, Ferreira et al. (2016) obtained additive heritability within the progenies superior to the average heritability of progeny, in this case, in 65% for NF and 78% for FM, justifying, in this case, the selection between and within the progenies. Nevertheless, the estimation of heritability at different levels (family, individual, plot), as well as the additive heritability, made possible by the BLUP estimators, subsidize the choice of breeding methods that will provide better genetic gains.

The accuracy of progeny selection corresponds to the correlation between the genotypic value and the phenotypic value estimated from the experimental data. Because it is a correlation, the accuracy varies from 0 to 1, and the closer to the unit, the greater accuracy in access to real genetic variation (RESENDE; DUARTE, 2007). According to Resende and Duarte (2007), values of accuracy above 70% are considered high and should be sought by breeders, since they indicate greater precision in access to genotypic variation from the phenotypic variation observed in the field. In this experiment, the accuracy values obtained were higher than 0.80 for all characteristics evaluated (Table 1).

The coefficients of individual additive genetic variation (CV_{gi}) and the coefficient of genetic variation between progenies (CV_{gp}) indicated the incremental potential that can be obtained through selection, because the higher the coefficient of genetic variation, the greater the variability among the evaluated materials (FERREIRA et al., 2016). In this study, the CV_{gi} for all the variables under study was higher than CV_{gp}, indicating that there is greater variability among than within progenies (Table 1). Similar proportions were obtained for the sour passion fruit by Ferreira et al. (2016), which indicated that genetic variation can be masked by environmental variations, being a reliable alternative the evaluation by the coefficient of variation (CV_r).

The CV_r is equivalent to the variation index and refers to the magnitude of the relation between the CV_g and CV_e. According to Resende and Duarte (2007), values of CV_r equal to 1.0 are adequate to provide inferences with greater precision. In this study, were obtained values of CV_g in between 0.59 (NF) and 1.15 (MF), higher than those obtained by Pinto et al. (2013), however, lower than those published by Ramos et al. (2014). For Ferreira et al. (2016), CV_r above 0.50 may provide genetic gains, since they indicate a greater proportion of the genetic variation, thus, for all characteristics evaluated, favorable conditions for selection (Table 1).

Table 1. Estimates of genetic parameters obtained from 19 families of papaya half-sibs from the Formosa group for fruit mass (FM), pulp thickness (PT), soluble solids content (SS) and number of fruits (NF).

Variables	General average[1]	σ^2_a	h^2_{mp}	h^2_{ad}	Ac_{prog}	CV_{gi} (%)	CV_{gp} (%)	CV_e (%)	CV_r	PEV	σ_g
FM (g)	1,158.64	107,180.45	0.87	0.89	0.93	28.26	14.13	12.31	1.15	3,532.23	59.43
PT (cm)	2.76	0.08	0.77	0.82	0.88	10.31	5.16	6.32	0.82	0.00	0.07
SS (°Brix)	9.02	1.41	0.72	0.80	0.85	13.18	6.59	9.24	0.71	0.10	0.32
NF	29.53	58.90	0.64	0.69	0.80	25.98	12.99	21.95	0.59	5.35	2.31

[1] overall mean of the experiment; σ^2_a: additive genetic variance; h^2_{mp}: heritability of the average progeny; h^2_{ad}: additive heritability within progeny; Ac_{prog}: accuracy of progeny selection; CV_{gi}(%): coefficient of individual additive genetic variation; CV_{gp} (%): coefficient of genetic variation among progenies; CV_e (%): coefficient of residual variation; CV_r= coefficient of relative variation; PEV: standard deviation of predicted genotypic value; σg: variance of the prediction error of genotypic values.

According to Resende and Duarte (2007) the REML/BLUP methodology provides the ordering of the potential genotypes for selection considering each variable analyzed separately. However, the selection is more effective when performed based on several characteristics at the same time (LEITE et al., 2016). It was observed that the ordering of half-sib families (HSF) was different for all the traits studied, which makes it difficult to combine selection. Faced with this, it was chosen to select HSF that were classified among the 10 best families in at least three characteristics studied. Thus, these families were selected 113; 120; 408; 426; 438; 497; 695; and 697, which provided gains of 26.08% for FM; 10.51% for PT; 7.54% for SS and 12.97% for NF (Tables 2, 3, 4 and 5, respectively). Similar strategy was applied by Ferreira et al. (2016) in sour passion fruit that obtained approximately equal increments for number and mass of fruits.

Among the 19 half-sib families studied, twelve (63.12%) had positive additive genetic effects on the fruit mass (Table 2). The selected HSF provided a new average of 1,460.85 g, or an increase of 302.21 g on the average of the experiment. For PT, only nine families had a positive genetic effect; however, the selected HSF still provided an increase of 10.51% or 0.29 cm (Table 3). For this variable, the eight HSFs selected were among the top 10 HSF. The selection practiced for FM and PT provided that the means of these variables recovered the original values of 'Rubi Incaper 511' (CATTANEO et al., 2010). If practiced properly, only with new selection cycles, exploring the effect between and within families, it will be possible to obtain real gains for these characteristics.

For the soluble solids content, the selected families provided an increase of 0.68 °Brix (7.54%), obtaining a mean of 9.70 °Brix (Table 4). Ramos et al. (2014), testing different selection methods in papaya from the Solo group, obtained a selection gain of 5.3% for the soluble solids content, however, with a mean of 11.90 °Brix. In general, genotypes of the Formosa group have lower SS in the fruits when compared to those in the Solo group (LUZ et al., 2015, REIS et al; 2015), which explains the observed difference. Thus, obtaining gains of this magnitude in only one selection cycle indicates good possibilities for SS increment in future selection steps.

For the number of fruits, only four families selected were among the 10 HSF best classified for the additive genetic effect, however, there was an increase of 3.83 fruits or 12.97% (Table 5). According to Oliveira et al. (2010), the number of fruits has negative correlation with FM, SS and PT. Thus, it was expected that the family ordering would be contrasting for this characteristic. Oliveira et al. (2010) also emphasized that the number of fruits is an essential production component to be considered in the selection of papaya genotypes due to their economic impact on the producer. However, due to its complex nature and negative correlations with other variables of interest, this process is difficult. Thus, selection involving this characteristic requires methodologies capable of providing genetic gains in spite of their negative interrelationship with other variables of interest. The results obtained in this study indicated the efficiency of the methodology of the mixed models by REML/BLUP in the selection of papayas genotypes with higher NF without reducing FM, SS and PT.

Table 2. Ordering by average components of 19 families of half-sibs (HSF) of papaya from the Formosa group, selected families (in bold) and increment for fruit mass (FM), considering selected HSF.

Order	HSF	Additive Genetic Effect	Genetic Gain (g)	New HSF Average (g)
1	498	525.69	525.69	1,68434
2	609	427.76	476.73	1,635.37
3	**113**	261.07	404.84	1,563.49
4	**438**	250.31	366.21	1,524.85
5	**426**	233.99	339.77	1,498.41
6	**695**	204.12	317.16	1,475.80
7	**497**	122.17	289.30	1,447.94
8	**408**	107.93	266.63	1,425.27
9	70	72.51	245.06	1,403.70
10	**697**	52.02	225.76	1,384.40
11	**120**	30.83	208.04	1,366.68
12	327	5.48	191.16	1,349.80
13	400	-121.27	167.12	1,325.77
14	591	-147.66	144.64	1,303.28
15	511	-224.76	120.01	1,278.66
16	119	-313.31	92.93	1,251.57
17	307	-379.64	65.13	1,223.77
18	179	-481.04	34.79	1,193.43
19	463	-626.20	0.00	1,158.64
HSF selected			302.21	1,460.85
Increment (%)				26.08

Table 3. Ordering by average components of 19 families of half-sibs (HSF) of papaya from the Formosa group, selected families (in bold) and increment for pulp thickness (PT) considering the selected HSF.

Order	HSF	Additive Genetic Effect	Genetic Gain (cm)	New HSF Average (cm)
1	**697**	0.36	0.36	3.12
2	**120**	0.35	0.36	3.12
3	**438**	0.29	0.33	3.09
4	609	0.28	0.32	3.08
5	**695**	0.22	0.30	3.06
6	**113**	0.17	0.28	3.04
7	**408**	0.17	0.26	3.02
8	**426**	0.07	0.24	3.00
9	511	0.00	0.21	2.97
10	**497**	-0.02	0.19	2.95
11	327	-0.03	0.17	2.93
12	591	-0.04	0.15	2.91
13	498	-0.09	0.13	2.89
14	70	-012	0.12	2.88
15	119	-0.21	0.09	2.85
16	400	-0.23	0.07	2.83
17	463	-0.33	0.05	2.81
18	307	-0.36	0.03	2.79
19	179	-0.48	0.00	2.76
HSF selected			0.29	3.05
Increment (%)				10.51

Table 4. Ordering by average components of 19 half-sibs families (HSF) of papaya from the Formosa group, selected families (in bold) and increment to soluble solids (SS) content considering the selected HSFs.

Order	HSF	Additive Genetic Effect	Genetic Gain (in ºBrix)	New HSF Average (in ºBrix)
1	463	2.31	2.31	11.33
2	179	1.80	2.05	11.07
3	119	1.42	1.84	10.86
4	70	0.67	1.55	10.57
5	**120**	0.38	1.31	10.33
6	327	0.20	1.13	10.15
7	**426**	0.18	0.99	10.01
8	**438**	0.17	0.89	9.91
9	**697**	0.02	0.79	9.81
10	**113**	-0.13	0.70	9.72
11	609	-0.19	0.62	9.64
12	307	-0.49	0.53	9.55
13	**408**	-0.57	0.44	9.46
14	511	-0.59	0.37	9.39
15	498	-0.65	0.30	9.32
16	**695**	-0.80	0.23	9.25
17	591	-0.82	0.17	9.19
18	**497**	-1.24	0.09	9.11
19	400	-1.66	0.00	9.02
HSF selected			0.68	9.70
Increment (%)				7.54

Table 5. Ordering by average components of 19 half-sibs families (HSF) of papaya from the Formosa group, selected families (in bold) and increment for number of fruits (NF) considering the selected HSF.

Order	HSF	Additive Genetic Effect	Genetic Gain	New HSF Average
1	591	11.39	11.39	40.93
2	**120**	6.80	9.09	38.63
3	463	5.51	7.90	37.44
4	**497**	4.98	7.17	36.70
5	511	4.49	6.63	36.17
6	400	4.18	6.23	35.76
7	119	3.71	5.87	35.40
8	**408**	2.04	5.39	34.92
9	327	1.19	4.92	34.46
10	**695**	0.97	4.52	34.06
11	307	0.07	4.12	33.65
12	70	-0.93	3.70	33.23
13	179	-1.88	3.27	32.80
14	498	-3.58	2.78	32.32
15	**438**	-5.14	2.25	31.79
16	609	-5.23	1.79	31.32
17	**113**	-5.44	1.36	30.90
18	**426**	-8.57	0.81	30.34
19	**697**	-14.55	0.00	29.53
HSF selected			3.83	33.36
Increment (%)				12.97

Conclusions

The REML/BLUP methodology is efficient in identifying the papaya genotypes of the Formosa group to be selected in order to obtain greater mass and number of fruits, pulp thickness and soluble solids content.

Due to the greater additive heritability within the progenies and the individual variation coefficient, the selection practiced between and within the half-sib families could provide greater genetic gains when compared to the selection based on the average of the progenies.

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Referências

BARROS, F.L.S.; KUHLCAMP, K.T.; ARANTES, S.D.; MOREIRA, S.O. Productivity and quality of papaya fruit Formosa and Solo in two harvest seasons. **Pesquisa Agropecuária Brasileira**, Brasília, v.52, n.8, p.599-606, 2017.

CATTANEO, L.F.; COSTA, A.F.S.; SERRANO, L.A.L.; COSTA, A.N.; FANTON, C.J.; BRAVIM, A.J.B. **'Rubi INCAPER 511' Primeira variedade de mamão do grupo 'Formosa' para o Espírito Santo**. Vitória: DCM/ Incaper, 2010. (Série Documentos, 187). 2010. Disponível em:<http://biblioteca.incaper.es.gov.br/digital/bitstream/item/44 /1/Folder-Mamao-Rubi.pdf> Acesso em: 10 mar. 2017.

FAOSTAT. Food and Agriculture Organization of the United Nations. **Statistical division**. Disponível em: <http://www.fao.org/faostat/en/#data/QC>. Acesso em: 21 mar. 2017.

FERREIRA, R.T.; VIANA, A.P.; SILVA, F.H.L.; SANTOS, E.A.; SANTOS, J.O. Seleção recorrente intrapopulacional em maracujazeiro-azedo via modelos mistos. **Revista Brasileira de Fruticultura**, Jaboticabal, v.38, n.1, p. 158-166, 2016.

HARDNER, M.; HEALEY, A.L.; DOWNES, G.; HERBERLING, M.; GORE, P.L. Improving prediction accuracy and selection of open-pollinated seed-lots in *Eucalyptus dunnii* Maiden using a multivariate mixed model approach. **Annals of Forest Science**, Paris, v.73, n.4, p.1035–1046, 2016.

INCAPER. Instituto Capixaba de Pesquisa, Assistência Técnica e Extensão Rural. **Balanço hídrico e armazenamento de água**. Disponível em: <https://meteorologia.incaper.es.gov.br/BH>. Acesso em: 04 nov.17

LEITE, W.S.; PAVAN, B.E.; MATOS FILHO, C.H.A.; ALCANTARA NETO, F.; OLIVEIRA, C.B.; FEITOSA, F.S. Estimativas de parâmetros genéticos, correlações e índices de seleção para seis caracteres agronômicos em linhagens F_8 de soja. **Comunicata Scientiae**, Bom Jesus, v.7, n.3, p.302-310, 2016.

LUZ, L.N.; PEREIRA, M.G.; BARROS, F.R.; BARROS, G.B.; FERREGUETTI, G.A. Novos híbridos de mamoeiro avaliados nas condições de cultivo tradicional e no semiárido brasileiro. **Revista Brasileira de Fruticultura**, Jaboticabal, v.37, n.1, p.159-171, 2015.

MARTINS, D. S.; COSTA, A. F. S. **A cultura do mamoeiro**: tecnologias de produção. Vitória: Incaper, 2003. 497 p. Disponível em: <http://biblioteca.incaper.es.gov.br/digital/bitstream/item/924/1/Livro-A-Cultura-do-Mamoeiro-1.pdf> Accesso em: 10 jan. 2017.

MELO, J.S.; ZANUNCIO, C.S.D.; BARROS, F.L.S.; KUHLCAMP, K.T.; ZUCOLOTO, M.; MOREIRA, S.O. Seleção simultânea de caracteres do mamoeiro utilizando índices tradicionais e valores genéticos preditos via REML/BLUP. In: ENCONTRO LATINO AMERICANO DE INICIAÇÃO CIENTÍFICA, 19., 2015, São José dos Campos. **Anais...** São José dos Campos: UNIVAP, 2015.

OLIVEIRA, E.J.; LIMA, D.S.; LUCENA, R.S.; MOTTA, T.B.N.; DANTAS, J.L.L. Correlações genéticas e análise de trilha para número de frutos comerciais por planta em mamoeiro. **Pesquisa Agropecuária Brasileira**, Brasília, v.45, n.8, p.855-862, 2010.

PINTO, F.O.; LUZ, L.N.; PEREIRA, M.G.; CARDOSO, D.L.; RAMOS, H.C.C. Metodologia dos modelos mistos para seleção combinada em progênies segregantes de mamoeiro. **Revista Brasileira de Ciências Agrárias**, Recife, v.8, n.2, p.211-217, 2013.

QUINTAL, S.S.R.; VIANA, A.P.; CAMPOS, B.M.; VIVAS, M.; AMARAL JUNIOR, A.T. Selection via mixed models in segregating guava families based on yield and quality traits. **Revista Brasileira de Fruticultura**, Jaboticabal, v.39, n.2, p.e-866, 2017.

RAMOS, H.C.C.; PEREIRA, M.G.; VIANA, A.P.; LUZ, L.N.; CARDOSO, D.L.; FERREGUETTI, G.A. Combined selection in backcross population of papaya (*Carica papaya* L.) by the mixed model methodology. **American Journal of Plant Sciences**, Irvine, v.5, n.20, p.2973-2983, 2014.

REIS, R.C.; VIANA, E.S.; JESUS, J.L.; DANTAS, J.L.L.; LUCENA, R.S. Caracterização físico-química de frutos de novos híbridos e linhagens de mamoeiro. **Pesquisa Agropecuária Brasileira**, Brasília, v.50, n.3, p.210-217, 2015.

RESENDE, M.D.V. **Análise estatística de modelos mistos via REML/BLUP na experimentação em melhoramento de plantas perenes**. Colombo: Embrapa Florestas, 2000. 101p.

RESENDE, M.D.V. Software Selegen-REML/BLUP: a useful tool for plant breeding. **Crop Breeding and Applied Biotechnology**, Viçosa, v.16, n.4, p.330 -339, 2016.

RESENDE, M.D.V.; DUARTE, J.B. Precisão e controle de qualidade em experimentos de avaliação de cultivares. **Pesquisa Agropecuária Tropical**, Goiânia, v.37, n.3, p.182-194, 2007.

SILVA, F.H.L.; VIANA, A.P.; SANTOS, E.A.; FREITAS, J.C.O.; RODRIGUES, D.L.; AMARAL JUNIOR, A.T. Prediction of genetic gains by selection indexes and REML/BLUP methodology in a population of sour passion fruit under recurrent selection. **Acta Scientiarum. Agronomy**, Maringá, v.39, n.2, p.183-190, 2017.

VITTORAZZI, C.; OLIVEIRA, G.H.F.; GERHARDT, I.F.S; DAHER, R.F.; PENA, G.F.; SILVA, F.H.L.; VIANA, A.P.; GUIMARÃES, A.G.; AMARAL JUNIOR, A.T.; PEREIRA, M.G. Indices estimated using REML/BLUP and introduction of a super-trait for the selection of progenies in popcorn. **Genetic and Molecular Research**, Ribeirão Preto, v.16, n.3, p.1-10, 2017.