

ARTICLE

Plant selection in F_2 segregating populations of papaya from commercial hybrids

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Abstract - The objective of this paper was to estimate the genetic parameters and additive genetic values in segregating populations of papaya using the mixed model methodology. Two F_2 populations from Tainung and Calimosa hybrids were evaluated. The experimental design was an augmented block with four replicates, and Golden and Calimosa cultivars were the common treatment. Estimates of individual heritability were high for fruit length (FL) and weight (FW), moderate for fruit diameter (FD), and low for total soluble solids (TSS) and fruit firmness (FF). Considering FF and TSS as main traits for selection, genotypes of Calimosa- F_2 population showed better performance to FF, but worse concerning TSS. It was selected 18.3% and 24.6% of plants from Tainung- F_2 and Calimosa- F_2 populations, respectively. Negative correlation between TSS and FF was not able to reduce the genetic gains. The segregating populations from Calimosa hybrid are more promising for the selection of papaya lines.

Key words: heritability, breeding, genetic parameters.

INTRODUCTION

Currently, the most commercially grown papaya varieties (*Carica papaya* L.) belong to Solo and Formosa groups, which are basically represented by varieties and hybrids, respectively. Nevertheless, the low number of genotypes recorded for marketing has restricted the development of papaya crop and its genetic variability (Oliveira et al. 2010a).

Among the hybrids, Tainung no.1 and Calimosa are the most commercially grown (Oliveira et al. 2007). As an alternative to reduce the production cost, producers have used the seeds of F_1 hybrids in F_2 , F_3 , F_4 and further generations, in order to cultivate new production areas which has led to the loss of the main characteristics of the original hybrid, producing fruits with lower quality and completely lacking marketing standards (Costa and Pacova 2003). However, from the genetic improvement point of view, the genetic variability available in the segregating populations can be exploited to produce new hybrid combinations through the selection of new papaya lines.

The success of the breeding methods that exploit the selfing of individuals is in the amount of genetic variability and uniformity of the trait (Borém and Miranda 2009). In the case of papaya, wide variability has been observed from F_2 to F_4 populations (Karunakaran et al. 2010), which maximizes the potential for selection in these generations. On the other hand, early selection of plants in the breeding program presents low efficiency when compared with the following stages of selection, given the low values of heritability for important agronomic traits in accordance with some species (Skinner et al. 1987, Backes et al. 2002). However, high heritability values for some of these traits can be found in papaya, such as plant height and plant height at first fruiting, time to produce the first fruits, stem diameter, fruit weight and length, pulp thickness, fruit cavity index and soluble solids content (Silva et al. 2008, Karunakaran et al. 2010). According to Matsuoka et al. (2005), an interesting strategy at this stage is the selection of the best plants carried out with higher selection intensity for traits with high heritability, without forgetting the secondary characteristics to prevent the disposal of valuable genotypes.

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Considering that the success of the selection depends not only on the variability of the experimental material, but also on the accuracy of the selection methods used, it is important to use methods that estimate the variance components and allow the prediction of genetic values of individuals that are candidates for selection (Resende 2007). A standard procedure for estimating variance components is the REML procedure (Restricted Maximum Likelihood) and the optimal method for prediction of genetic values is the BLUP (Best Linear Unbiased Prediction), at individual level (Resende 2002). The REML/BLUP procedure is called mixed model methodology.

The main advantages of BLUP are: a) the estimation and prediction in a non-biased single procedure; b) the possibility of taking into account selection and inbreeding effects over the generations, whereas that degree of relationship between individuals is known; c) the maximization of the correlation between true breeding and predicted values; d) the prediction of the genetic value from individuals not observed in the sample; e) the ability for prediction in unbalanced experimental designs; f) the fact that, among all linear predictors, BLUP presents the lowest mean square error (Resende 2002).

The objectives of this paper were to estimate variance components and heritability; predict genotypic values and genotypic gains for the evaluated traits, and also to select the best individuals in F₂ segregating populations of papaya, based on agronomic traits of major importance in papaya crop using mixed model methodology.

MATERIAL AND METHODS

The study was carried out using two F₂ populations obtained by selfing F₁ plants from Tainung and Calimosa hybrids. The selfing of F₁ plants generated 61 and 93 F₂ plants of Tainung and Calimosa hybrids, respectively, designated as Calimosa-F₂ and Tainung-F₂ populations. The experiments were carried out at the Gregory Bondar Experimental Station (EGREB), belonging to the Executive Committee of the Plan of Cocoa Farming (CEPLAC), (lat 24° 05' S; long 39° 12' W), in Belmonte, State of Bahia. The average annual temperature is 24 °C, with relative humidity of 84.2%, annual rainfall of 1,400 mm, altitude of 105 m and the soil is classified as Dystrophic Red Yellow Latosol (Typic Haplorthox). The experiment was carried out in four augmented blocks, with 154 non-common and 2 common treatments, which are varieties of Golden and Calimosa. For data analysis, each plant was considered as a replicate of the non-common treatments, and in the case of common checks, 10 plants per block were used.

The planting was carried out at a spacing of 2.0 x 2.8 m, and a standard package of practices was followed during the period of study (Martins and Costa 2003). Aiming only hermaphrodite plants to be evaluated, the thinning of female plants was performed when they were four months old.

The main traits evaluated in the initial stages of the breeding program were the following: 1) fruit length (FL) in cm; 2) fruit diameter (FD) in cm; 3) fruit weight (FW) in grams; 4) external fruit firmness (FF), measured in pounds in three equidistant points in the fruit equator (center) region, using a penetrometer with an 8 mm tip; 5) total soluble solids (TSS) measured in Brix. The fruits were analyzed at stage 5 (100% of fruit with yellow surface), according to the standard classification by the Secretariat of Agricultural Protection (SDA) of the Brazilian Ministry of Agriculture, Livestock and Food Supply (MAPA).

The estimation of genetic parameters and prediction of genetic values were performed using a model for individuals obtained by selfing in the Selegen-REML/BLUP software (Resende 2007). The mixed linear model used is given by: $y = Xb + Za + e$, where y , b , a , are vectors of data of fixed effects (blocks, checks and segregant populations added to the general mean), of additive genetic effects (random), and of error effects (random), respectively; whereas X and Z are incidence matrices for b and a , respectively. The distribution and structure of means and variances is given by:

$$\begin{aligned} y | b, V &\sim N(Xb, V) \\ a | A, \sigma_a^2 &\sim N(0, A\sigma_a^2) \\ e | \sigma_e^2 &\sim N(0, I\sigma_e^2) \end{aligned}$$

between the random effects of the model is given by $\text{Cov}(a, e) = 0$. The variance structure of the model is given by $V = ZA\sigma_a^2Z' + I\sigma_e^2$, being A the additive genetic relationship matrix involving all individuals, in which elements are functions of identity by descent probabilities.

The mixed model equations are:

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + A^{-1}\lambda_1 \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{a} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix},$$

where: $\lambda_1 = \frac{\hat{\sigma}_e^2}{\hat{\sigma}_a^2} = \frac{1 - \hat{h}_2}{\hat{h}_2}$, $\hat{h}_2 = \frac{\hat{\sigma}_a^2}{\hat{\sigma}_a^2 + \hat{\sigma}_e^2}$ is the individual narrow sense heritability in the block; $\hat{\sigma}_a^2$ is the additive genetic variance; and $\hat{\sigma}_e^2$ is the residual variance (environmental + non additive). The iterative estimators of variance components by REML, using the EM algorithm (Expectation-Maximization), are given by: $\hat{\sigma}_e^2 = \frac{y'y - \hat{b}'X'y - \hat{a}'Z'y}{N - r(x)}$;

$\hat{\sigma}_a^2 = \frac{\hat{a}'A^{-1}\hat{a} + \hat{\sigma}_e^2 tr(A^{-1}C^2)}{q}$, whereas C^{22} refers to: , being C the coefficient matrix of mixed model equations; tr , the trace of matrix; $r(x)$: $C^{-1} = \begin{bmatrix} C_{11} & C_{12} \\ C_{21} & C_{22} \end{bmatrix}^{-1} = \begin{bmatrix} C^{11} & C^{12} \\ C^{21} & C^{22} \end{bmatrix}$ rank of the matrix X; whereas N and q are the total number of data and individuals, respectively.

The remaining estimates of variances and genetic parameters are given as follows: individual phenotypic variance, as $\hat{\sigma}_f^2 = \hat{\sigma}_a^2 + \hat{\sigma}_e^2$; estimated coefficients of variation, as $CVgi\% = \frac{100\sqrt{\hat{\sigma}_a^2}}{\hat{m}}$ (coefficient of individual genetic variability) and $CVe\% = \frac{100\sqrt{\hat{\sigma}_e^2}}{\hat{m}}$ (coefficient of experimental variation). The genetic correlation coefficients (G) between traits in the populations were estimated and the significance was tested using the non-parametric bootstrap method, performed by the Genes software (Cruz 2006). The selective accuracy ($r_{\hat{a}_i}$) of the individual i was obtained as follows: $r_{\hat{a}_i} = [1 - PEV_i / \hat{\sigma}_a^2]^{1/2}$, where $PEV_i = d_i \sigma_e^2$, and d_i is a diagonal element of C^{22} .

The characteristics of TSS and FF were considered of major importance in this study, so that the individuals were classified according to the highest values for these traits, regardless of weight, length and diameter of the fruit. Selection was based on TSS and FF traits, with a constraint that individuals should present predicted additive genetic value above the general mean for the two traits simultaneously.

This led to selection intensities of 16.1% and 27.9% for Calimosa and Tainung populations, respectively.

RESULTS AND DISCUSSION

The residual coefficients of variation presented a low magnitude (ranging from 7.98 to 24.78%), reaching good experimental precision. In addition, it agrees with the selection accuracy as a measure of experimental quality, according to Resende and Duarte (2007). Moreover, the genetic coefficients of variation at individual level (CVgi%), which express the amount of existing genetic variation in percentage of average, indicated values with small magnitude for FD, TSS and FF, whereas FL and FW values were significant, indicating greater variation in populations segregating for these traits (Table 1).

The populations showed high values of individual heritability (\hat{h}^2) for FL and FW, and moderate for FD. In addition, estimates of the accuracy of the individual selection ($r_{\hat{g}_g}$) were high for these traits. On the other hand, the \hat{h}^2 estimates for TSS and FF were lower, and also the accuracy of selection. In both cases, the possibility of successful selection among and within segregating populations was shown. However, the higher individual heritability, related to additive effects that are inheritable during the process of selection aiming to obtain new papaya lines, shows that the selection of individuals can be effective. The magnitude of heritability demonstrates the importance of carrying out the selection of genotypes based on their predicted genotypic values and not by their observed phenotypes.

Table 1. Estimates of parameters for fruit length (FL), fruit diameter (FD), fruit weight (FW), total soluble solids (TSS) and fruit firmness (FF) from the REML methodology

Parameters	Traits				
	CF	DF	PF	SST	FF
$\hat{\sigma}_a^2$	9.22	0.33	42143.68	0.38	0.07
$\hat{\sigma}_e^2$	3.34	0.43	19347.08	1.69	0.55
$\hat{\sigma}_f^2$	12.57	0.77	61490.76	2.07	0.63
\hat{h}^2	0.73±0.19	0.43±0.15	0.69±0.18	0.18±0.09	0.11±0.07
$r_{\hat{g}_g}$	0.99	0.80	0.99	0.52	0.41
CVgi%	16.96	6.97	36.58	5.37	6.74
CVe%	10.21	7.98	24.78	11.27	18.80
Maximum	23.22	10.76	1271.40	14.48	5.90
Minimum	12.70	6.60	303.00	7.48	2.45
General Mean	17.91	8.25	561.24	11.52	3.95

$\hat{\sigma}_a^2$: Genetic variance among individuals; $\hat{\sigma}_e^2$: residual variance; $\hat{\sigma}_f^2$: individual phenotypic variance; \hat{h}^2 : individual broad sense heritability; $r_{\hat{g}_g}$: accuracy of individual selection; CVgi%: coefficient of individual genetic variability; CVe%: coefficient of residual variation.

Estimations of genetic parameters enable the understanding of the nature of the gene action involved in trait inheritance and lead themselves to assessment of expected progress with selection, besides defining the best selection method to be adopted (Sampaio et al. 2002, Oliveira et al. 2008). Traits with higher heritability can be improved with the use of phenotypic mass selection, such as FL, FD and FW, whereas the selection for traits with low heritability are more efficient using progenies tests (Falconer and Mackay 1996), such as TSS and FF. On the other hand, in other crops, such as açai, even with low individual heritability, genetic gain above 25% was obtained for some quantitative traits (Farias Neto et al. 2007). In comparison to the results of the F₂ populations of papaya, the individual selection proposal for TSS and FF traits, with estimates of \hat{h}^2 of 0.18 and 0.11, respectively, may be feasible through BLUP procedure which uses family and individual information simultaneously.

According to Vencovsky and Barriga (1992), during the genetic studies for any measurable traits, the heritability has a key role in predicting the confidence of phenotypic value as a guide to the genetic value, or in the relationship degree between phenotypic value and the genetic value. In the case of papaya, estimates of heritability in broad sense are very close to those found for weight, length and fruit diameter and total soluble solids in S₂ populations originated from the 'Coorg Honey Dew' variety in papaya cultivars evaluated in India, as well as segregating backcross populations (Silva et al. 2008, Karunakaran et al. 2010, Singh and Kumar 2010). Also, according to Singh and Kumar (2010), heritability for fruit yield per plant is high (0.93), compared with number of fruits per plant (0.50). On the other hand, Silva et al. (2008) showed that heritability values for these two traits are very close (above 0.89) when measured at 240 days after planting. According to Singh et al. (1997), traits with high heritability associated with genetic variation have greater value in the selection process. Therefore, considering that estimates of selective accuracy, which correspond to the correlation between predicted genotypic value (selection criteria) and the true breeding value, they were classified as high for FL, FW and FD. For TSS and FF, the accuracy of the individual selection was lower. For fruits traits, the results showed the possibility of successful individual selection in segregating populations from Calimosa and hybrids.

Estimates of additive genetic correlations were high and positive for LF x (FD and FW) and FW x FD (Table 2). These results are in agreement with those obtained from papaya germplasm accessions studies (Oliveira et al. 2010b). On the other hand, the moderate and positive genotypic correlations for TSS x (FL, FD and FW) observed in this study are similar in magnitude, but they differ in direction from those

obtained by Oliveira et al. (2010b). Correlations of small magnitude were observed for FF x (FL, FD and FW). It was also identified high negative correlation (-0.81) between TSS and FF, which is one of the most important genetic correlation in papaya. Adverse genetic correlations between these traits are one of the main constraints in advancing papaya breeding program, since this work has the same direction of selection. This negative correlation has contributed to the use of lower intensity of selection in segregating populations, since it was used predicted additive genetic value above the general mean as default to select the best plants.

Table 2. Estimates of genotypic correlations between length of fruit (FL), fruit diameter (FD), fruit weight (FW), total soluble solids (TSS) and fruit firmness (FF) from two papaya segregating populations

Traits	FL	FD	FW	TSS
FL	0.98**			
FW	0.98**	0.99**		
TSS	0.55*	0.45	0.55*	
FF	-0.04	0.01	-0.06	-0.81**

* and **: significant at 5 and 1% of probability by the bootstrap method with 10,000 simulations, respectively.

Considering the overall mean from TSS and FF traits as a cutoff point for choosing the best individuals, 15 and 17 plants were selected from Calimosa-F₂ and Tainung-F₂ populations (Table 3 and 4). Therefore, a selection pressure of 20.7% for plants with the highest genotypic values for TSS and FF was used. Positive and negative genetic effects in different selected genotypes were observed for all the traits analyzed. The selection intensities of 16.1% and 27.9% for Calimosa and Tainung populations, respectively, are moderate. This is in line with the relative poor performance of the augmented block design for estimating variance components and prediction for selection purposes. Such selection intensity level ensures the inclusion of the truly best individuals among the selected ones.

Segregating plants from Calimosa-F₂ population showed better performance for FF (4.25 pounds of fruit in average), when compared with Tainung-F₂ population. However, field observations indicate that Calimosa hybrid is known to have lower fruit firmness in comparison to Tainung and Golden. This can be evidenced by the average of Calimosa and Golden checks, with 4.00 and 4.21 pounds, respectively. However, even with high average, genotypes from Tainung-F₂ population showed predominantly negative genetic effects (Table 4). Therefore, 24.6% from Calimosa-F₂ were selected against 18.3% from Tainung-F₂; which shows that segregating populations from Calimosa hybrid could be more promising for selecting the best plants to continue the cycles of selfing, considering the FF trait.

Table 3. Phenotypic values (f), predicted genotypic effect (\hat{a}), genotypic values ($\hat{\mu} + \hat{a}$), genetic gain (G), new mean (NM), means of Calimosa-F₂, checks and 15 plants selected for length of fruit (LF), fruit diameter (FD), fruit weight (FW), total soluble solids (TSS) and external fruit firmness (FF). Values of the general mean ($\hat{\mu}$) are presented in Table 1

Genotype	FL					FD					FW				
	f	\hat{a}	$\hat{\mu} + \hat{a}$	G	NM	f	\hat{a}	$\hat{\mu} + \hat{a}$	G	NM	f	\hat{a}	$\hat{\mu} + \hat{a}$	G	NM
CalF2-1	18.30	-0.73	17.18	1.48	19.38	10.38	0.49	8.75	0.62	8.88	952.00	106.68	667.92	199.95	761.19
CalF2-2	17.10	0.06	17.97	2.05	19.95	8.58	0.17	8.43	0.37	8.62	590.40	-14.59	546.64	107.51	668.74
CalF2-9	21.08	2.78	20.69	3.87	21.77	9.90	0.45	8.71	0.58	8.83	933.60	218.87	780.10	341.71	902.95
CalF2-10	21.10	3.53	21.43	4.64	22.54	9.66	0.43	8.68	0.57	8.82	852.80	209.50	770.74	322.82	884.06
CalF2-27	18.70	0.37	18.28	2.25	20.16	8.22	0.25	8.50	0.43	8.68	619.60	91.44	652.67	183.89	745.13
CalF2-28	17.92	1.39	19.30	2.93	20.83	7.52	0.18	8.44	0.38	8.64	482.60	59.31	620.54	143.83	705.07
CalF2-34	19.60	1.35	19.26	2.88	20.79	8.48	0.12	8.37	0.33	8.59	586.80	-2.01	559.23	110.91	672.14
CalF2-35	17.04	0.25	18.15	2.11	20.02	7.76	0.31	8.57	0.46	8.72	505.60	82.72	643.96	168.41	729.65
CalF2-38	16.70	0.00	17.90	1.89	19.80	8.14	0.18	8.44	0.38	8.63	497.20	4.30	565.54	119.38	680.62
CalF2-45	16.64	0.61	18.51	2.32	20.23	8.92	0.30	8.56	0.46	8.71	618.40	87.95	649.19	178.33	739.57
CalF2-46	17.82	0.05	17.96	2.01	19.92	8.22	0.00	8.25	0.27	8.52	542.00	-62.79	498.45	40.74	601.97
CalF2-50	20.98	3.80	21.71	4.80	22.70	7.30	0.01	8.26	0.28	8.53	547.20	69.22	630.46	150.80	712.04
CalF2-51	20.10	1.87	19.78	3.18	21.09	8.58	0.20	8.46	0.40	8.65	668.00	84.90	646.14	173.15	734.39
CalF2-52	19.20	1.67	19.57	2.97	20.88	9.52	0.47	8.73	0.61	8.86	772.20	152.32	713.56	236.73	797.96
CalF2-53	21.48	2.48	20.39	3.57	21.48	8.38	-0.04	8.21	0.24	8.50	714.00	27.18	588.41	131.90	693.13
$\bar{X}_{Cal F_2}$	19.05	1.26	19.17	2.83	20.73	8.62	0.28	8.53	0.46	8.71	641.13	79.62	640.86	179.67	740.90
\bar{X}'_{Cal}	20.88	3.81	21.72	4.72	22.62	9.49	0.58	8.83	0.71	8.96	910.05	249.94	811.17	324.79	886.03
\bar{X}'_{Gol}	13.45	-3.84	14.06	0.03	17.93	7.90	-0.77	7.49	0.04	8.30	393.65	-271.20	290.03	5.64	566.87
\bar{X}_{Selec}	18.16	0.48	18.39	2.31	20.21	8.49	0.03	8.29	0.29	8.55	605.66	8.84	570.08	130.40	691.64
\bar{X}	17.61	-0.23	17.68	1.77	19.68	8.36	0.04	8.29	0.30	8.55	562.81	-5.30	555.94	115.44	676.68

Genotype	TSS					EFF				
	f	\hat{a}	$\hat{\mu} + \hat{a}$	G	NM	f	\hat{a}	$\hat{\mu} + \hat{a}$	G	NM
CalF2-1	13.45	-0.31	11.22	-0.04	11.49	3.45	0.23	4.18	0.28	4.23
CalF2-2	13.68	-0.32	11.20	-0.05	11.48	2.75	0.21	4.16	0.27	4.23
CalF2-9	12.84	-0.30	11.23	-0.03	11.49	2.95	0.19	4.15	0.27	4.23
CalF2-10	11.80	-0.34	11.19	-0.06	11.47	2.95	0.22	4.17	0.28	4.23
CalF2-27	11.36	-0.32	11.21	-0.04	11.49	3.25	0.26	4.21	0.29	4.24
CalF2-28	12.96	-0.37	11.16	-0.06	11.47	3.25	0.17	4.13	0.27	4.23
CalF2-34	12.68	-0.27	11.26	-0.03	11.50	3.00	0.21	4.17	0.27	4.23
CalF2-35	14.04	-0.22	11.31	-0.02	11.51	4.45	0.29	4.24	0.30	4.26
CalF2-38	13.24	-0.37	11.16	-0.07	11.46	2.80	0.21	4.17	0.28	4.23
CalF2-45	13.72	-0.34	11.19	-0.05	11.48	2.80	0.24	4.20	0.28	4.24
CalF2-46	12.84	-0.24	11.29	-0.02	11.51	3.50	0.26	4.22	0.29	4.25
CalF2-50	13.24	-0.32	11.21	-0.04	11.49	4.60	0.30	4.26	0.31	4.27
CalF2-51	10.52	-0.35	11.18	-0.06	11.47	4.95	0.26	4.22	0.29	4.25
CalF2-52	12.04	-0.29	11.24	-0.03	11.50	4.45	0.26	4.22	0.29	4.25
CalF2-53	10.84	-0.33	11.20	-0.05	11.48	5.65	0.33	4.29	0.33	4.29
$\bar{X}_{Cal F_2}$	11.06	-0.45	11.08	-0.11	11.42	4.24	0.27	4.23	0.30	4.25
\bar{X}'_{Cal}	14.02	0.78	12.31	0.82	12.34	3.39	-0.18	3.78	0.04	4.00
\bar{X}'_{Gol}	12.16	-0.22	11.31	-0.02	11.51	3.89	0.02	3.97	0.26	4.21
\bar{X}_{Selec}	11.91	-0.21	11.32	0.00	11.56	4.10	0.07	4.03	0.25	4.21
\bar{X}	11.37	-0.18	11.31	0.07	11.53	3.96	0.02	3.98	0.18	4.13

$\bar{X}_{Cal F_2}$, mean from genotypes of Calimosa-F₂ population; \bar{X}'_{Cal} and \bar{X}'_{Gol} = means from Calimosa and Golden, respectively; \bar{X}_{Selec} and \bar{X} , the average of selected genotypes and general mean, respectively.

Table 4. Phenotypic values (f), predicted genotypic effect (\hat{a}), genotypic values ($\hat{\mu} + \hat{a}$), genetic gain (G), new mean (NM), means of Tainung-F₂, checks and 17 plants selected for length of fruit (LF), fruit diameter (FD), fruit weight (FW), total soluble solids (TSS) and external fruit firmness (FF). Values of the general mean ($\bar{\mu}$) are presented in Table 1

Genotype	FL					FD					FW				
	f	\hat{a}	$\hat{\mu} + \hat{a}$	G	NM	f	\hat{a}	$\hat{\mu} + \hat{a}$	G	NM	f	\hat{a}	$\hat{\mu} + \hat{a}$	G	NM
TaiF2-1	22.86	6.47	24.37	6.68	24.59	10.76	0.39	8.65	0.53	8.78	1271.40	467.03	1028.27	501.15	1062.39
TaiF2-3	14.02	-3.59	14.32	-0.09	17.82	7.50	-0.47	7.78	0.06	8.31	349.60	-319.77	241.47	-2.34	558.89
TaiF2-4	15.26	-1.32	16.59	0.56	18.47	7.60	-0.43	7.82	0.07	8.32	384.80	-181.67	379.57	12.02	573.26
TaiF2-6	20.78	0.26	18.17	2.15	20.05	9.32	0.10	8.35	0.32	8.57	852.40	99.12	660.36	190.03	751.27
TaiF2-9	16.40	-2.76	15.15	0.15	18.05	8.60	-0.29	7.97	0.09	8.34	537.60	-199.96	361.28	5.53	566.77
TaiF2-10	15.34	-3.50	14.41	-0.07	17.84	8.48	-0.27	7.99	0.09	8.35	474.00	-190.60	370.64	6.86	568.09
TaiF2-13	20.94	0.92	18.83	2.53	20.43	8.14	-0.30	7.95	0.08	8.34	599.20	-98.24	463.00	28.52	589.76
TaiF2-22	21.38	4.23	22.14	5.86	23.77	8.02	-0.20	8.06	0.11	8.36	623.60	58.82	620.06	142.20	703.43
TaiF2-28	15.26	-1.36	16.54	0.53	18.44	7.64	-0.02	8.24	0.26	8.52	379.60	-40.40	520.84	96.87	658.11
TaiF2-34	17.00	-1.32	16.58	0.55	18.45	8.92	0.04	8.30	0.30	8.55	596.40	20.92	582.16	130.01	691.25
TaiF2-36	17.86	0.03	17.93	1.92	19.83	7.44	-0.26	8.00	0.10	8.35	429.60	-118.93	442.31	26.51	587.75
TaiF2-38	16.06	0.03	17.93	1.95	19.86	8.26	-0.02	8.24	0.26	8.51	495.20	14.60	575.84	121.18	682.41
TaiF2-43	16.98	-0.32	17.59	1.64	19.55	8.12	-0.16	8.10	0.12	8.37	440.00	-60.77	500.47	42.45	603.69
TaiF2-45	15.12	-0.58	17.33	1.56	19.47	8.40	-0.14	8.11	0.12	8.38	462.80	-69.05	492.19	36.54	597.77
TaiF2-56	16.76	0.40	18.31	2.29	20.19	8.62	0.03	8.29	0.29	8.54	534.00	15.91	577.15	122.87	684.11
TaiF2-60	16.46	-2.51	15.40	0.23	18.13	7.78	-0.33	7.92	0.08	8.33	449.20	-182.75	378.48	10.74	571.97
TaiF2-61	18.98	0.84	18.75	2.49	20.40	8.46	-0.17	8.08	0.11	8.36	619.20	-46.39	514.85	91.65	652.89
$\bar{X}Cal F_2$	16.71	-1.20	16.71	1.05	18.95	8.14	-0.12	8.14	0.18	8.44	500.43	-60.83	500.40	68.81	630.05
$\bar{X}'Cal'$	20.88	3.81	21.72	4.72	22.62	9.49	0.58	8.83	0.71	8.96	910.05	249.94	811.17	324.79	886.03
$\bar{X}'Gol'$	13.45	-3.84	14.06	0.03	17.93	7.90	-0.77	7.49	0.04	8.30	393.65	-271.20	290.03	5.64	566.87
$\bar{X}Selec$	18.16	0.48	18.39	2.31	20.21	8.49	0.03	8.29	0.29	8.55	605.66	8.84	570.08	130.40	691.64
\bar{X}	17.61	-0.23	17.68	1.77	19.68	8.36	0.04	8.29	0.30	8.55	562.81	-5.30	555.94	115.44	676.68

Genotype	TSS					EFF				
	f	\hat{a}	$\hat{\mu} + \hat{a}$	G	NM	f	\hat{a}	$\hat{\mu} + \hat{a}$	G	NM
TaiF2-1	10.12	-0.34	11.19	-0.05	11.48	4.45	-0.08	3.88	0.22	4.18
TaiF2-3	11.48	-0.14	11.39	0.00	11.53	4.85	-0.06	3.90	0.24	4.19
TaiF2-4	12.84	0.02	11.54	0.21	11.73	4.55	-0.09	3.86	0.21	4.16
TaiF2-6	11.76	-0.01	11.52	0.18	11.71	5.60	-0.06	3.90	0.24	4.20
TaiF2-9	10.68	-0.20	11.33	-0.01	11.52	4.95	-0.05	3.91	0.25	4.21
TaiF2-10	10.36	-0.16	11.37	0.00	11.53	4.15	-0.07	3.88	0.22	4.18
TaiF2-13	12.20	-0.06	11.47	0.03	11.56	4.40	-0.11	3.85	0.18	4.14
TaiF2-22	10.76	-0.13	11.40	0.01	11.54	4.20	-0.11	3.85	0.19	4.15
TaiF2-28	12.00	-0.13	11.40	0.01	11.53	5.75	-0.03	3.92	0.25	4.21
TaiF2-34	9.92	-0.23	11.29	-0.02	11.51	4.40	-0.07	3.89	0.23	4.19
TaiF2-36	10.76	-0.12	11.41	0.01	11.54	3.75	-0.10	3.86	0.20	4.16
TaiF2-38	12.35	-0.13	11.40	0.01	11.54	4.05	-0.07	3.88	0.23	4.18
TaiF2-43	11.32	-0.07	11.46	0.03	11.55	4.30	-0.09	3.87	0.21	4.17
TaiF2-45	12.16	-0.17	11.36	0.00	11.53	3.25	-0.10	3.86	0.20	4.16
TaiF2-56	11.96	-0.03	11.50	0.14	11.67	4.75	-0.09	3.87	0.22	4.17
TaiF2-60	10.80	-0.10	11.43	0.02	11.55	4.20	-0.11	3.85	0.19	4.14
TaiF2-61	10.32	-0.05	11.48	0.12	11.65	4.70	-0.10	3.85	0.20	4.15
$\bar{X}Cal F_2$	11.47	-0.06	11.47	0.11	11.64	3.82	-0.13	3.83	0.11	4.07
$\bar{X}'Cal'$	14.02	0.78	12.31	0.82	12.34	3.39	-0.18	3.78	0.04	4.00
$\bar{X}'Gol'$	12.16	-0.22	11.31	-0.02	11.51	3.89	0.02	3.97	0.26	4.21
$\bar{X}Selec$	11.91	-0.21	11.32	0.00	11.56	4.10	0.07	4.03	0.25	4.21
\bar{X}	11.37	-0.18	11.31	0.07	11.53	3.96	0.02	3.98	0.18	4.13

$\bar{X}Tai F_2$, mean from genotypes of Tainung-F₂ population; $\bar{X}'Cal'$ and $\bar{X}'Gol'$ = means from Calimosa and Golden, respectively; $\bar{X}Selec$ and \bar{X} , the average of selected genotypes and general mean, respectively.

Fruit firmness indicates the stage of fruit ripening, and nowadays it is one of the main attributes related to papaya quality since fruits with low firmness showed less resistance to transportation, storage and handling, therefore, less acceptability by consumers (Fagundes and Yamanishi 2001). Some studies indicate fruit firmness ranging from 1.23 to 2.29 pounds in varieties from the Solo group, and 3.95 to 6.31 pounds in varieties from the Formosa group, when evaluated at different harvest times (Fagundes and Yamanishi 2001). Considering that the fruits were evaluated at more advanced stages of maturation (note 5), it is expected that fruit firmness estimates are underestimated in the present study, when compared with the results mentioned above. In addition, the genotypes selected in these two segregating populations have high potential to develop superior lines for this trait.

A contrary situation was observed for TSS, comparing with FF, where Calimosa hybrid has more TSS content than Tainung, but the analysis of segregating populations revealed higher predicted values for TSS for Tainung- F_2 population than for Calimosa- F_2 (11.42 versus 11.64 °brix). The predicted values of TSS for checks (Calimosa and Golden) were 12.34 and 11.51 °brix, respectively (Tables 3 and 4).

Genotypic values correspond to the observed values without the environmental effect. Therefore, in vegetatively propagated species, the genotypic values may capitalize the additive and dominance effects completely; whereas in allogamous species or autogamous segregating populations, where progeny tests are performed, only additive effects are transmitted to the offspring and should be taken into account at the moment of the selection of genotypes to be crossed or selfed (Resende 2002). The genetic gain is equal to the average of the genetic predicted values for the selected genotypes, and the overall mean plus the genetic gain results in the improvement of the average population.

Since the prediction of genetic values of superior materials is one of the main problems in the breeding of any species, once it requires the true values of variance components, the use of more sophisticated methods, such as BLUP, allows obtaining better estimates for these parameters (Resende

2002). This approach takes into account the treatment effects as random, which enables to carry out the genotypic selection instead of the phenotypic one (Resende and Duarte 2007).

The approach of treatment as random effects and their implications in plant selection is presented by several authors in the literature (Duarte and Vencovsky 2001, Resende and Duarte 2007). As one of the criteria of this method, the use of multiple comparison tests is not recommended, since they are derived from assumptions from a fixed model, and also because they are applied and produce inferences about phenotypic instead of genotypic means (Resende 2002). Therefore, direct selections were made for the desired genotypes with higher predicted genotypic values obtained by the BLUP method, which corrects for identified environmental effects and presents greater accuracy than the phenotypic selection.

Comparing the average of 32 selected genotypes with the overall average of the two populations, small gains for TSS and FF and small reductions in FL, FD and FW, were observed. Regarding Calimosa check, a reduction in the size of the fruit in relation to FL, FD, FW and TSS, was shown. On the other hand, there were gains for FF. Regarding Golden check, higher predicted values for FL, FD, FW and TSS, and lower average for FF (Tables 3 and 4) were observed.

Since TSS and FF traits had more emphasis in the choice of genotypes to be selfed, the average gains from the 32 selected plants were not so high, due to the high negative correlation (-0.81) between these traits (Table 2).

The prediction of the genotypic effects using BLUP in early generations of breeding programs has shown satisfactory results for several crops such as common beans and peanuts (Coimbra et al. 2008, Luz et al. 2010). This statement can be extended to the evaluation of papaya F_2 segregating populations.

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Seleção de plantas em populações F_2 segregantes de mamoeiros híbridos comerciais

Resumo – *Objetivou-se estimar parâmetros genéticos e valores genotípicos em populações segregantes de mamoeiro com o método de modelos mistos. Foram avaliadas duas populações segregantes F_2 dos híbridos Tainung e Calimosa. O delineamento experimental foi em blocos aumentados com quatro repetições, utilizando como testemunhas as cultivares Golden e Calimosa. As estimativas de herdabilidade individual foram altas para comprimento (CF) e peso do fruto (PF), moderadas para diâmetro (DF) e menores para sólidos solúveis totais (SST) e firmeza do fruto (FF). Considerando SST e FF como principais características para seleção, genótipos da população Calimosa- F_2 apresentaram melhor desempenho em relação à FF, porém pior em relação à SST. Foram selecionados*

18,30 e 24,61% dos indivíduos da população Tainung-F₂ e Calimosa-F₂, respectivamente. A existência de correlação negativa entre SST e FF não dificultou a obtenção de ganhos genéticos. Foi demonstrado que populações segregantes do híbrido Calimosa são mais promissoras para seleção de linhagens de mamoeiro.

Palavras-chave: herdabilidade, melhoramento, parâmetros genéticos.

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