

ARTICLE

Selection and estimation of the genetic gain in segregating generations of papaya

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ABSTRACT - In Brazil, papaya is sustained by a narrow genetic basis, with few genetically distinct cultivars for planting. Therefore, this study aimed to select and estimate the direct and combined genetic gains for commercial fruit yield (Yld Plr¹) in segregating generations of papaya. Six traits were simultaneously targeted in combined selection and were attributed weights associated to agronomic values. Direct selection however was based on Yld Plr¹ only. Results indicated genetic variability in the segregating generations for the evaluated traits and although combined selection achieved a lower genetic gain in Yld Plr¹, it offers greater chances of success in the following generations since favorable and unfavorable agronomic traits of papaya are considered. These results motivated the recommendation to advance generations with 30 plants, selected from a total of 345 plants, considering all segregating treatments.

Key words: Papaya, fruit yield, selection gain, carpelloidly, female sterility.

INTRODUCTION

Quite contrary to the fact that Brazil is the world's largest papaya (*Carica papaya* L.) producer (Nehmi et al. 2002), the alternatives in the choice of commercial cultivars and/or hybrids for planting that would meet national as well as international market demands are very limited. Few studies of improvement have been developed aiming at new superior cultivars and, consequently, the enlargement of the genetic basis for cultivation. Besides, the costliness of hybrid papaya seeds of the Formosa group, generally imported from Taiwan at 3000 to 4000 dollars per kilogram (Pereira 2003), has caused many fruit farmers to successively plant the hybrid generations F₂, F₃ and F₄, resulting in

numerous problems, above all the loss of vigor and segregation for fruit shape.

The genetic improvement of papaya in Brazil can, along with good management practices, contribute substantially to yield increase and improve fruit quality traits. This objective can be reached, partly, via basic information on inheritance of the main agronomic traits that one wishes to improve, as well as on the genetic variability available for improvement.

In connection with the computation of genetic variances and means, it is of fundamental importance to establish estimates of other genetic parameters, such as the coefficient of heritability and of genetic variation, index of variation and genetic correlations to predict gains, so the viability of determined improvement

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program can be evaluated and the most efficient selection strategy can be adopted (Vencovsky 1969).

In any selection program it is important to obtain favorable responses in all traits of importance for genetic improvement. By the classical selection index, as proposed by Smith (1936) and Hazel (1943), among others, different traits can be targeted simultaneously in the selection procedure. In plant improvement the application of the selection index is however still impaired, since breeders usually consider traits for which economic weights with an acceptable precision level can not be established (Rodríguez et al. 1998). According to these authors, one suggestion proposed in literature is to fix experimentally weights to the genetic values, related to the traits of interest for selection, thus allowing the identification of the selection units that provide gains in the desired sense and with greatest possible magnitude in all traits of interest.

In this context, the objective of our study was to select and estimate the genetic gain by direct and combined selection for commercial fruit yield within segregating generations. Six traits were simultaneously considered in combined selection to which weights were attributed, associated to the agronomic values of the traits.

MATERIAL AND METHODS

Plant material

Hermaphrodite plants of the following genotypes were used: 16BC₁S₁, 52BC₁S₁, 115BC₁S₁, SS 72/12 x 4BC₁, BC₂, SS 783, and Golden. The first five are segregating and the two latter are cultivars of the Solo group. The cultivars were included for comparative effects with the segregating generations and to allow the estimation of the environmental variance, since all phenotypic variation observed in these cultivars can be attributed to non-genetic causes.

The segregating generations were derived from the initial crossing between the dioecious genotype Cariflora and the cultivar Sunrise Solo 783 (SS 783). The SS 783 populations segregate for sex in a proportion of 2 hermaphrodite plants to 1 female plant and are denominated ginoic-andromonoic. Cariflora populations segregate for sex in a proportion of 1 male to 1 female plant and are called dioecious. The first three genotypes

were obtained by selfing BC₁ plants, originated by the first backcross with genotype Cariflora (BC₁) and the segregating BC₂ generation was obtained by a second backcross with Cariflora (BC₂). On the other hand, SS 72/12 x 4BC₁ was obtained by a cross between a segregating BC₁ plant and a plant of the cultivar Sunrise Solo 72/12 (SS 72/12).

Genotype Cariflora is a dioecious selection with yellow pulp and moderately firm fruits, with a mean weight of around 1.67 kg and pleasant flavor and taste (Conover et al. 1986). According to the same authors, the tolerance level of this genotype to papaya ringspot virus (PRSV) is high, in the edaphoclimatic conditions of southern Florida, USA. The PRSV, also known as mosaic virus or papaya ringspot virus represents one of the strongest limitations on the maintenance of production centers of this crop, imposing a migratory character owing to the damages caused and the absence of resistant varieties (Oliveira et al. 1994). The cross of Cariflora with genotypes of the Solo group results in very vigorous and productive, although rather heterogeneous hybrids, owing to a high degree of loci in heterozygosis. On the other hand, SS 783 is a cultivar with pear-shaped fruit that weigh on average 0.52 kg, with red pulp and good quality (Marin et al. 2006).

Cultivar SS 72/12 presents good quality traits of fruits, which are pear-shaped, small-sized, weigh between 0.35 and 0.45 kg, with red-orange pulp, consistent and resistant to transport (Marin et al. 1986, Manica 1996).

Cultivar Golden was obtained by mass selection in the production fields of Sunrise Solo of the company Caliman Agrícola S/A, in the State of Espírito Santo. It has pear-shaped fruits with salmon-pink pulp and mean weight of about 0.45 kg.

Experiment installation and evaluation

The experiment was installed in the commercial plantations of the company Caliman Agrícola S/A (Fazenda Romana), municipality of Linhares, State of Espírito Santo, Brazil, on January 25, 2005.

The experiment was arranged in a randomized complete block design with seven treatments (16BC₁S₁, 52BC₁S₁, 115BC₁S₁, SS 72/12 x 4BC₁, BC₂, SS 783, and Golden) and two replications. The seedlings were transplanted to the field in double rows spaced 1.5 m x 2.0 m x 3.6 m. Originally, the plots consisted of 36, 33, 17, 24, 63, 15 and 15 plants of the treatments 16BC₁S₁,

52BC₁S₁, 115BC₁S₁, SS 72/12 x 4BC₁, BC₂, SS 783, and Golden, respectively. The variation of the number of plants per plot was related to the availability of seedlings and the plots with 63 BC₂ plants were basis for the selection required to establish the BC₃ generation. Fertilization, management, pest and disease control, and the routine cultural treatments in the commercial plantations of the company were applied.

Fruit and flower traits including yield components and qualitative fruit aspects were evaluated throughout 2005. For selection and to estimate the genetic gain, the following traits were considered here: **a) Number of carpeloid fruits (NCFr)**: determined by counting all carpeloid fruits of hermaphrodite plants individually, 140 days after transplanting (DAT) (NCFr1) and 240 DAT (NCFr2); **b) Number of pentandric fruits (NPFr)**: determined by counting all pentandric fruits of hermaphrodite plants individually, 140 DAT (NPFr1) and 240 DAT (NPFr2); **c) Number of sterile flowers (NSF)**: number of sterile female flowers (ovary suppression) was determined by counting all sterile flowers in hermaphrodite plants individually, 140 DAT (NSF1) and 260 DAT (NSF2); **d) Number of normal flowers (NNF)**: the number of normal hermaphrodite flowers (elongated) was determined by subtracting the sterile and deformed flowers (carpeloid and pentandra) from the total number of flowers, 140 DAT (NNF1) and 260 DAT (NNF2); **e) Plant yield (Yld Plt⁻¹)**: the fruit yield per plant was determined by multiplying the number of commercial fruits (total minus the carpeloid and pentandric), 240 DAT, by the mean weight of a three-fruit sample, expressed in kg; **f) Content of soluble solids (°Brix)**: obtained by a hand-held refratometer (Atago N1), expressed in °Brix, in a three-fruit sample per plant.

Analysis of variance and estimation of genetic parameters

For the analysis of variance of the evaluated traits, in the experimental design type 1 (fixed model), which considers the treatment effect as fixed, we used software SAS (SAS Institute 1992) and the following statistical model: $Y_{ijk} = \mu + t_i + b_j + \varepsilon_{ij} + \delta_{ijk}$

Where: μ = overall treatment mean; t_i = fixed effect of the i -th treatment ($i = 1, 2, 3, \dots, t$);

b_j = effect of the j -th block ($j = 1$ and 2); ε_{ij} = experimental error associated to observation Y_{ij} , and δ_{ijk} = phenotypic effect of the variation among plants

within a plot. The genetic parameters were estimated according to Fehr (1987).

Combined and direct selection within treatment

The hermaphrodite superior plants were selected by the two procedures described, in December 2005. In view of the difficulty to compute the matrices of variance and covariance in this study, which are required for the classical selection indices, selection was initially performed for six traits simultaneously (combined selection): number of carpeloid fruits (NCFr), number of pentandric fruits (NPFr), number of sterile flowers (NSF), number of normal flowers (NNF), commercial fruit yield per plant (Yld Plt⁻¹) and content of soluble solids (°Brix). Weights associated to the agronomic values were attributed to these traits and the index obtained, as described below: NCFr (-10), NPFr (-10), NSF (-10), NNF (100), Yld Plt⁻¹ (100), and BRIX (50). The other traits were considered auxiliary and weighted with zero. This relation of weights, which has no economic connotation at all, was established experimentally based on the agronomic importance of the evaluated traits, as suggested in literature (Rodríguez et al. 1998).

For the combined selection, after establishing the index values in each treatment, the plants were classified in decreasing order and a selection pressure determined varying from 10 to 20 %, according to the number of plants available. It is worth emphasizing that in this phase, aside from commercial fruit yield (Yld Plt⁻¹), the other favorable traits for genetic improvement of papaya are being furthered while unfavorable traits are depreciated.

Direct selection was applied for Yld Plt⁻¹ considering the superiority of the plants in relation to this trait within each treatment, with the same selection pressure as used in combined selection.

Determination of genetic gain

To determine the combined and the direct genetic gain for Yld Plt⁻¹, the following formula was used:

$$\Delta_G = h^2 \times \Delta_S \text{ where,}$$

Δ_G = genetic gain; h^2 = broad-sense heritability; Δ_S = differential of selection.

The broad-sense heritability (h^2) was obtained as follows: $h^2 = (\hat{\sigma}_P^2 - \hat{\sigma}_E^2) / \hat{\sigma}_P^2$ where,

$\hat{\sigma}_P^2$ = Phenotypic variance of each treatment, where the variation can be attributed to genetic and

environmental causes; $\hat{\sigma}_E^2$ = Environmental variance, determined in treatment 6 (Golden) and 7 (SS 783), in which the variation is attributed entirely to non-genetic causes.

RESULTS AND DISCUSSION

The analysis of variance showed significant differences by the F test at 1 and 5% significance among the treatments, for most traits considered (Table 1).

The high and very high values of coefficient of variation (CV_e) observed here are partly due to the wide variation for these traits in the treatments, above all in the traits evaluated 140 DAT, where some plants within a treatment or even entire treatments presented complete absence of these traits. One must further take into consideration that the likewise high coefficients of genetic variations (CV_g) in most traits reflect a wide genetic variability for these traits, useful in the genetic improvement of papaya.

The means and respective minimal significant differences (MSD) of the morpho-agronomic and fruit quality traits are presented in Table 2. Note that the mean NSF was higher 140 DAT than 260 DAT in all treatments, and significantly superior in treatment 115BC₁S₁. In spite of the marked variation of the NSF between the two evaluations, in all treatments, the mean NNF varied little in the treatments 16BC₁S₁ and 115BC₁S₁, indicating greater stability in the expression of this trait in these treatments.

The mean values of the traits NCFr and NPFR were highest in the treatments 52BC₁S₁ and BC₂ and lowest in 115BC₁S₁. Nevertheless, these traits were not relevant in the treatments SS 783 and Golden, that are genetically very close. Considering that the segregating treatments were originated by the initial cross between SS 783 and genotype Cariflora, it may be inferred that the greater expression of the carpelloid and pentandric fruits, verified in the treatments 52BC₁S₁ and BC₂, are probably inherited from parent Cariflora since in the dioecious (segregating) condition these traits would never have found expression in this genotype (Silva et al. 2007a and Silva et al. 2007b).

Female sterility and carpelloid and pentandric fruits in hermaphrodite plants affect the commercial fruit yield. This calls for the conduction of segregating generations to select plants with a minimal expression of these traits in the main papaya producing regions of Brazil (Silva et al. 2007a).

The Yld Plt⁻¹ (kg) was significantly higher in treatment 115BC₁S₁, followed by SS 783 and SS 72/12 x 4BC₁. But all segregating treatments were significantly or slightly superior to Golden, one of the most widely planted cultivars in the papaya producing regions of Espirito Santo. The mean fruit weight, used to calculate Yld Plt⁻¹, indicated that within segregating genotypes there is a potential for the selection of plants for production for both the national market (that demands fruits that weigh between 0.80 and 1.50 kg) as well as for the foreign market (requiring a standard fruit weight of around 0.50 kg).

Table 1. Summary of the analysis of variance of the morpho-agronomic and fruit quality traits in papaya segregating generations and cultivars, considered in the selection procedures and estimation of the genetic gain, with the mean square values of genotype (MSG) and respective significances, means, coefficient of experimental variation (CV_e), and coefficient of genetic variation (CV_g)

Trait	MSG	Mean	CV_e (%)	CV_g (%)
NSF ₁	9459.92**	19.63	28.67	64.33
NSF ₂	986.64**	4.09	41.92	106.01
NNF ₁	1869.01	27.25	19.14	16.83
NNF ₂	623.09**	10.06	13.50	34.26
NCFr ₁	0.88	0.15	66.67	66.67
NCFr ₂	22.46**	0.85	23.53	78.04
NPFR ₁	1.49	0.13	133.23	108.78
NPFR ₂	110.68*	1.13	66.25	124.21
Yld Plt ⁻¹	818.03**	20.13	10.46	22.06
°Brix	9.88	11.40	3.28	3.82

NSF₁ = number of sterile flowers 140 DAT; NSF₂ = number of sterile flowers 260 DAT; NNF₁ = number of normal flowers 140 DAT; NNF₂ = number of normal flowers 260 DAT; NCFr₁ = number of carpelloid fruits 140 DAT; NCFr₂ = number of carpelloid fruits 240 DAT; NPFR₁ = number of pentandric fruits 140 DAT; NPFR₂ = number of pentandric fruits 240 DAT; Yld Plt⁻¹ = plant yield in kg; °Brix = content of soluble solids of the fruit pulp

** = significant at 1 % probability; * = significant at 5 % probability

Table 2. Mean values and respective standard deviations related to the morpho-agronomic and fruit quality traits in papaya segregating generations and cultivars, and the respective minimal significant differences at 5 % probability (MSD)

Trait	Treatments						MSD (t. 5%)	
	16BC ₁ S ₁	52BC ₁ S ₁	115BC ₁ S ₁	SS 72/12 x 4BC ₁	BC ₂	Golden		SS 783
NSF ₁	23.82±22.75	21.80±21.03	52.48±29.63	16.08±15.33	16.16±17.10	3.53±2.79	4.70±2.76	19.50
NSF ₂	9.61±13.83	2.42±2.96	14.94±11.76	1.48±3.20	2.54±4.53	0.83±0.98	0.93±1.46	5.94
NNF ₁	17.60±10.84	28.56±13.36	23.03±15.10	29.91±12.19	31.69±15.40	26.47±5.63	30.43±9.98	-
NNF ₂	14.62±8.41	10.51±7.80	18.12±8.89	8.63±5.66	7.53±10.16	7.40±3.40	6.90±2.83	4.71
NCFr ₁	0.04±0.21	0.26±0.60	0.00±0.00	0.07±0.45	0.28±0.58	0.00±0.00	0.07±0.36	-
NCFr ₂	0.58±1.26	1.27±1.70	0.05±0.22	0.13±0.61	1.62±2.26	0.17±0.53	0.33±1.06	0.68
NPFr ₁	0.00±0.00	0.12±0.77	0.00±0.00	0.00±0.00	0.35±1.15	0.00±0.00	0.00±0.00	-
NPFr ₂	0.18±0.68	1.29±3.62	0.00±0.00	0.00±0.00	3.11±5.73	0.00±0.00	0.00±0.00	2.59
Yld Plt ⁻¹	16.23±8.62	20.67±9.88	31.40±19.58	23.92±8.76	19.00±12.13	13.29±3.81	26.96±9.63	7.29
°Brix	11.62±1.38	11.50±0.94	12.27±1.21	11.86±1.39	11.33±1.35	11.23±0.69	10.24±0.56	-

NSF₁ = number of sterile flowers 140 DAT; NSF₂ = number of sterile flowers 260 DAT; NNF₁ = number of normal flowers 140 DAT; NNF₂ = number of normal flowers 260 DAT; NCFr₁ = number of carpelloid fruits 140 DAT; NCFr₂ = number of carpelloid fruits 240 DAT; NPFr₁ = number of pentandric fruits 140 DAT; NPFr₂ = number of pentandric fruits 240 DAT; Yld Plt⁻¹ = plant yield in kg; °Brix = content of soluble solids of the fruit pulp; - = traits with non-significant difference by the F test

For the content of soluble solids (°Brix), determined in maturation stage I (green fruits with a yellow stripe), there was no significant difference among the treatments, but the segregating genotypes were moderately superior to the cultivars Golden and SS 783. With exception of SS 783, the treatments presented mean °Brix values close to the ones found by Jacomino et al. (2002) in fruits of cultivar Sunrise Solo 72/12; where °Brix values varied from 11.15 to 12.01.

Owing to the low number of segregating treatments (five), the selection was performed within treatments only. The results of Table 3 express satisfactory genetic gains in all treatments, when selection was underlaid with an index based on the combination of six simultaneous traits (combined selection). Treatment 3 (115BC₁S₁) was the most outstanding with a percentage genetic gain of 99.24 %. With exception of treatment 4 (SS 72/12 x 4BC₁), the genetic gain in all treatments was over 40 %. However, these gains reflect the trait combination and do not inform precisely on the magnitude of gains in terms of commercial fruit yield (Yld Plt⁻¹). Therefore, the combined genetic gain for Yld Plt⁻¹ was estimated (Table 4), considering only plants selected based on combined selection index.

The selection within and among is based on the family means and deviations from the individual value and is more easily applied. On the other hand, the combined selection is based on the index that considers, simultaneously, the performance of a plant and its family (Costa et al. 2000). Thus, according to the weighting factors attributed to a plant and to its family, it is possible to select superior plants in families of intermediary performance, or to select plants of intermediary performance in superior families (Falconer 1987).

The results of the genetic gains estimated by direct and combined selection for Yld Plt⁻¹ are shown in Table 4. In a first estimation, all plants selected in the treatment were considered together (direct selection) while the second estimation considered only the plants selected based on the selection index combining six traits simultaneously (combined selection). This strategy made a comparison of the direct with the combined genetic gain for Yld Plt⁻¹ possible.

The genetic gain was greater in all treatments that did not involve the selection index combining six traits simultaneously, above all treatment 3, where the

Table 3. Estimate of the genetic gain based on selection index combining six traits of agronomic interest, simultaneously, in the different segregating treatments

Treat.	Xs	Xo	Δ_s	$\hat{\sigma}_p^2$	$\hat{\sigma}_G^2$	h^2	Δ_G	$\Delta_G(\%)$
1	8234.66	4388.06	3846.60	4612533.04	2583796.78	0.56	2154.09	49.10
2	9682.54	6049.58	3632.96	6603751.20	4575014.94	0.69	2506.74	41.44
3	7662.20	3221.58	4440.62	7212752.73	5184016.47	0.72	3197.25	99.24
4	9092.80	6517.50	2575.30	4269233.21	2240496.95	0.52	1339.16	20.55
5	8957.90	4466.35	4491.55	6136507.35	4107771.09	0.67	3009.34	67.38

Treat. = treatment; 1 = 16BC₁S₁; 2 = 52BC₁S₁; 3 = 115BC₁S₁; 4 = SS 72/12 x 4BC₁; 5 = BC₂; Xs = mean of selected plants; Xo = original treatment mean; Δ_s = differential of selection; $\hat{\sigma}_p^2$ = phenotypic variance; $\hat{\sigma}_G^2$ = genotypic variance; h^2 = coefficient of heritability; Δ_G = genetic gain; $\Delta_G(\%)$ = genetic gain in percent

Table 4. Estimate of the direct genetic gain (Δ_G), and combined genetic gain (Δ_{Gi}) for commercial fruit yield (Yld Plt⁻¹), in the different segregating treatments

Treat.	Xs	Xsi	Xo	Δ_s	Δ_{Si}	h^2	Δ_G	Δ_{Gi}	$\Delta_G(\%)$	$\Delta_{Gi}(\%)$
1	30.30	22.45	16.24	14.05	6.21	0.28	3.93	1.74	24.20	10.71
2	35.76	33.78	20.67	15.09	13.11	0.45	6.79	5.90	32.85	28.54
3	49.33	42.30	31.40	17.92	10.89	0.86	15.41	9.36	49.08	28.81
4	36.75	33.52	23.92	12.83	9.59	0.30	3.85	2.88	16.09	12.04
5	32.21	27.43	19.01	13.20	8.42	0.63	8.32	5.30	43.77	27.88

Treat. = treatment; 1 = 16BC₁S₁; 2 = 52BC₁S₁; 3 = 115BC₁S₁; 4 = SS 72/12 x 4BC₁; 5 = BC₂; Xs = mean of selected plants (direct selection); Xsi = means of the selected plants based on index (combined selection); Xo = original treatment mean; Δ_s = differential of direct selection; Δ_{Si} = differential of selection based on index (combined); h^2 = coefficient of heritability; Δ_G = direct genetic gain; Δ_{Gi} = combined genetic gain, based on index; $\Delta_G(\%)$ = direct genetic gain in percent; $\Delta_{Gi}(\%)$ = combined genetic gain in percent, based on index

difference was of 20.27 percentage units (Table 4). One must however bear in mind that, in spite of this reduction in the genetic gain, the estimate considering the combined selection index furthers, besides yield, the other favorable traits and depreciates the unfavorable traits for genetic improvement of papaya.

The high genetic gain verified in treatment 3, considering the combined selection index (Table 3), can be attributed partly to the high index of sterile flowers of the plant (Table 2) and to the fact that during the evaluations for fruit yield, some plants had not even fructified. Therefore, the genetic gain estimated in this treatment, considering a selection pressure of 15.50%, was very close to the value of the original mean and indicates that the selection is effective to reduce the undesirable traits, above all female sterility and favor desirable traits in the following generation. This tendency is most clearly shown in a comparison of the genetic gain of direct with the genetic gain of combined selection for Yld Plt⁻¹. In this comparison, the percentage genetic gain of 49.08%, considering direct selection, sinks to 28.81%, considering combined selection based on combined selection index (Table 4).

Treatment 4 was generally the one with lowest estimates of percentage genetic gains. This is probably

due to the similar performance of this treatment to the F₁ generation, in view of the configuration of the cross made to obtain it (SS 72/12 x 4BC₁). Nevertheless, it is likely that an evaluation of the next generations derived from the plants selected in this phase will state greater segregation for the traits evaluated and, therefore, higher estimates of genetic gains.

Comparing the direct and combined genetic gains for Yld Plt⁻¹ in treatments 2 and 4, differences of 4.31 and 4.05 percentage units, respectively, were verified (Table 4). This indicates that direct selection for commercial fruit yield in these treatments was as effective as combined selection, which considered the selection index of six simultaneous target traits. On the other hand, for commercial fruit yield, a significant reduction of the genetic gain from the direct to combined selection was estimated in the other treatments.

In spite of the reduction of the genetic gain estimated by combined selection, compared with the genetic gain estimated by direct selection for Yld Plt⁻¹, in higher or lower proportion, it must be considered that the combined selection for Yld Plt⁻¹, based on the combined selection index, is probably more effective, since it is to be expected that the unfavorable traits are diminished and the favorable traits furthered.

According to the literature, the direct selection is the easiest and most practical way to obtain gains for a given trait; the response to direct selection modifies the original mean of the trait considered in a given population, in consequence of the selection practiced in the proper trait (Maêda et al. 2001). Nevertheless, the selection, when performed for one trait only, can give rise to undesirable changes in other important traits, due to the association among them. In this context, Cruz and Regazzi (1997) described that a way of increasing the chances of success in an improvement program is by means of simultaneous selection of a set of important traits for the crop.

According to the genetic gains obtained by the different selection strategies, it can be inferred that there is genetic variability in the segregating genotypes for the study traits, which are therefore promising for the advance of generations with the expectation of developing superior lines in the short and medium term. Although the selection criterion combining six traits,

considered those of greatest agronomic importance, had provided the lowest genetic gain for Yld Plt⁻¹, we concluded that chances of success thereby are greater in the following generations since the group of favorable traits is promoted while the group of unfavorable traits for papaya is derogated. Therefore, based on these results, 30 plants were selected from a total of 345 plants to advance the generations. Since there was no selection among segregating treatments, they were all considered with varying proportions according to the selection pressure determined in each treatment.

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Seleção e estimação do ganho genético em gerações segregantes de mamoeiro

RESUMO - *A cultura do mamoeiro, no Brasil, sustenta-se em uma estreita base genética, resultando em poucas cultivares geneticamente distintas para o plantio. Portanto, este trabalho objetivou selecionar e estimar os ganhos genéticos direto e combinado para produção de frutos comerciais em gerações segregantes de mamoeiro. A seleção combinada foi realizada combinando-se seis variáveis simultaneamente, às quais foram atribuídos pesos associados aos valores agrônomicos. Já a seleção direta foi realizada com base apenas na produção. Os resultados indicaram que as gerações segregantes dispõem de variabilidade genética para as variáveis avaliadas e embora a seleção combinada tenha propiciado um menor ganho genético para produção, esta gera uma maior expectativa de êxito nas próximas gerações por considerar variáveis agrônomicas favoráveis e desfavoráveis à cultura do mamoeiro. Com base nestes resultados foram recomendados o avanço de gerações com 30 plantas, selecionadas em um total de 345 plantas, contemplando todos os tratamentos segregantes.*

Palavras-chave: Mamão, produção de frutos, ganho de seleção, carpeloidia, esterilidade feminina.

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