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# Selection of pineapple hybrids via genotypic values (REML/BLUP) for fruit mass and total soluble solids

José Severino de Lira Júnior <sup>1,\*</sup>, João Emmanoel Fernandes Bezerra <sup>2</sup> and Domingos Eduardo Guimarães Tavares de Andrade <sup>3</sup>

<sup>1</sup> Researcher, Experimental Station of Itambé , Department of Research and Development, Agronomic Institute of Pernambuco - IPA, Itambé, Pernambuco State, Brazil.

<sup>2</sup> Researcher, Administrative headquarters, Department of Research and Development, Agronomic Institute of Pernambuco - IPA, Recife, Pernambuco State, Brazil.

<sup>3</sup> Researcher, Experimental Station of Itapirema , Department of Research and Development, Agronomic Institute of Pernambuco - IPA, Goiana, Pernambuco State, Brazil.

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#### Abstract

The ranking of hybrids via genotypic values stands out due to its maximum selective accuracy in relation to ordering based on phenotypic values, which incorporate environmental effects, causing changes in the final classification. The aim of this study was to pre-select cloned pineapple hybrids based on genotypic values for higher total soluble solids (TSS) and larger fruit mass without crown (FMWC). It was evaluated with 364 hybrids propagated vegetatively, in a Federer's Augmented Blocks. Genotypic values were estimated by REML/BLUP procedure. High proportion of the phenotypic variance was explained by genotypic effects, due to heritabilities in broad sense of 0.9786 (TSS) and 0.4929 (FMWC). IPA 04-60, IPA 125-363, IPA 125-85, and IPA 04-92 hybrids present FMWC greatest than 2.20 kg. IPA 125-218, IPA 125-95, IPA 125-188, and IPA 125-97 hybrids achieve TSS greatest than 20.0 °Brix. These hybrids exhibit promising traits to proceed a second evaluation cycle via vegetative propagation.

#### Keywords: Ananas comosus var. comosus; Genetic breeding; Heritability; Mixed model

#### 1. Introduction

Pineapple (*Ananas comosus* var. *comosus*) is a fruit of economic importance, standing out among the most cultivated tropical fruit species around the world. In 2019, world pineapple production was estimated at 28,179,348 tons, harvested in an area of 1,125,307 ha, distributed about 80 countries [1]. The largest producing countries were the Costa Rica (3,328,100 tons), Philippines (2,747,856 tons) and Brazil (2,426,526 tons), harvested, respectively, about 40,000 ha, 66,048 ha and 67,167 ha.

In Brazil, almost all production supplies the national market for fresh consumption. Pineapple fruit is sold by the unit, classified by size or weight at the Supply Centers and exposed to consumers on supermarket shelves, greengrocers and open markets. Flavor pulp, fruit mass and its dimensions are indispensable attributes to convince wholesale and retail customers. Usually, the highest prices are paid for larger fruits with a mass greater than 1.5 kg and total soluble solids of 14-16 °Brix [2, 3].

\* Corresponding author: José Severino de Lira Júnior; Email: lira.junior@ipa.br

Researcher, Experimental Station of Itambé , Department of Research and Development, Agronomic Institute of Pernambuco - IPA, Itambé, Pernambuco State, Brazil. PE 75, km 32, CEP 55.920-000 - Itambé – PE, +55 81 36353912.

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Just as reported by Cabral et al. [4] and Cabral et al. [5] to many important traits for the genetic breeding of pineapples in Brazil, the selection was performed from minimum values defined for fruit mass without crown (FMWC) and total soluble solids (TSS). The pineapple growing in Brazil is still based on 'Pérola' cultivar, that although susceptible to fusariosis and totally spiny leaf margin, presents wide adaptation, vigorous plant growth, excellent fruit quality for fresh national market and average weight of 1.6 kg [2, 3].

The selection of seedlings based on the genotypic value for greater fruit mass and better fruit quality allows it possible to expand the development of cultivars more adapted to the edaphoclimatic variations and better adjusted to different production systems. The ranking of hybrids via Best Linear Unbiased Prediction (BLUP) genotypic values estimated by Restricted Maximum Likelihood (REML) variance components stands out for its maximum selective accuracy in relation to the ordering based on phenotypic values, which incorporate environmental effects, causing changes in the final classification [6].

According to Piepho et al. [7] and Thompson [8], REML/BLUP procedure results in less error or residue variation, as a result of its 'shrinkage' statistical property, which promotes increased accuracy, offset by a significant reduction in variance and leading to a smaller mean square error. This procedure maximizes the correlation between predicted and real genotypic values, which in essence is the main target of plant breeding for ranking of individuals and practicing selection based on their genetic values [7, 8].

The objective of this paper was to select cloned pineapple hybrids based on the ordering of predicted genotypic values via mixed REML/BLUP models, prioritizing higher fruit mass without crown and total soluble solids under rainfed cultivation system.

## 2. Material and methods

The experiment was carried out during 18 months (May 2017 - October 2018) in the Experimental Station of Itambé (lat 7° 24' 16.80" S, long 35° 10' 54.00" W, alt 190 m asl), belonging to Agronomic Institute of Pernambuco State (IPA). The municipality of Itambé is located in North region of the 'Zona da Mata'. The climate of the region is hot and humid As (Köppen), with an average annual temperature of 25 °C, and average rainfall of 1.200 mm.year<sup>-1</sup>.

#### 2.1. Plant materials

Plant materials of this study (first clonal evaluation) consisted of 364 vegetatively propagated hybrids by slips and stem shoots, that were collected from a half-sib progeny. This progeny was developed by IPA's Pineapple Genetic Breeding Program via pollination among 'Pérola' cultivar (female genitor) that received a pollen mix from 'MD-2', 'BRS Imperial', and 'BRS Vitória' cultivars (male genitors). The pollination procedures were performed according to Cabral et al. [4]. These cultivars were chosen due to their contrasting and complementary traits, such as resistance to fusariosis, spinescence, fruit mass and shape, pulp color and total soluble solids concentration (Table 1).

Tuoita	Cultivars				
Traits	'Pérola'	'MD-2'	'BRS Imperial'	'BRS Vitória'	
Fusariosis	susceptible	susceptible	Resistant	resistant	
Leaf margin	spiny	spiny tip or base	Piping	piping	
Fruit mass (kg)	0.9 - 1.6	1.3 - 2.5	0.9 - 1.3	1.5	
Fruit shape	conical	cylindrical	cylindrical	Cylindrical	
Pulp color	white	yellow	Yellow	White	
Soluble solids (°Brix)	13 - 16	15 - 17	14 - 18	15.8	

Table 1 Agronomic information about the cultivars used as genitors

Source: Sanewski et al. [2], Junghans [3].

#### 2.2. Experimental design

Federer's Augmented Blocks experimental design was used, with 364 cloned individuals (non-common treatments) and two cultivars 'Pérola' and 'BRS Imperial' (common treatments), distributed in 10 incomplete blocks. The

experimental plot was composed from 3 to 12 plantlets for non-common treatments and 6 plantlets for common treatments. One observation per plot for statistical analysis was used.

### 2.3. Planting

Slips and stem shoots were planted in simple rows (0.9 m x 0.4 m) and management in a rainfed cultivation system. Adult plants did not receive artificial treatment for induced flowering. The natural flowering occurred gradually between 2018-May and 2018-August. The fertilizers were performed according to the technical recommendations of Bezerra et al. [9], considering the following results of the fertility analysis of soil:  $P = 5 \text{ mg.dm}^{-3}$ ;  $PH = 5.7 (H_2O)$ ;  $Ca = 3.7 \text{ cmol}_c\text{.dm}^{-3}$ ;  $Mg = 1.00 \text{ cmol}_c\text{.dm}^{-3}$ ;  $Na = 0.03 \text{ cmol}_c\text{.dm}^{-3}$ ;  $K = 0.27 \text{ cmol}_c\text{.dm}^{-3}$ ;  $Al = 0.00 \text{ cmol}_c\text{.dm}^{-3}$ ;  $H = 5.36 \text{ cmol}_c\text{.dm}^{-3}$ ;  $S = 5.00 \text{ cmol}_c\text{.dm}^{-3}$ ;  $CTC = 10.40 \text{ cmol}_c\text{.dm}^{-3}$ .

According to Agência Pernambucana de Águas e Clima – APAC, monthly distribution of rainfall during the field cultivation period are presented as follow: 2017-may 147.0 mm; 2017-jun 191.0mm; 2017-jul 380.0mm; 2017-aug 83.0mm; 2017-sep 63.0mm; 2017-oct 40.0mm; 2017-nov 5.0mm; 2017-dec 8.0mm; 2018-jan 201.9mm; 2018-feb 217.0mm; 2018-mar 105.0mm; 2018-apr 235.0mm; 2018-may 175.0mm; 2018-jun 136.8mm; 2018-jul 124.0mm; 2018-aug 2.0mm; 2018-sep 4.5mm; 2018-oct 3.0mm.

#### 2.4. Evaluated traits

Ripe fruits were harvested for evaluations of the fruit mass without crown (FMWC) and total soluble solids (TSS). Fruit shape (FS), pulp color (PC) and leaf margin spinescence (LMS) were evaluated as complementary information for the selected hybrids. Ripening point for harvesting was determined when at least 50% of shell color has changed with flattening and increase of the spaces between individual fruitlets. Hybrids with the following anomalies were excluded: fruits without crown; mini crown; multiple crown; fasciation; slips inserted at fruit base; or without slips, stem shoots, and ground shoots.

Plot values were used for estimation of Restricted Maximum Likelihood (REML) variance components and prediction of BLUP (Best Linear Unbiased Prediction) genotypic values, using the model 76 of the SELEGEN-REML/BLUP software [10], disregarding the half-sib parentage among the cloned individuals, according to reported by Resende [11].

#### 2.5. Statistical analysis

The mixed linear model was used:  $y=Xf+Zg+Wb+\epsilon$ , with: y is the vector of phenotypic data; f is the vector of fixed effects (overall average); g is the vector of genotypic effects (random); b is the vector of block effects (random); and  $\epsilon$  is the vector of errors or residuals (random). Letters X, Z and W represent incidence matrices that associate to elements of vectors f, g and b with vector y, respectively. The variance components were estimated: genotypic variance (Vg), environmental variance between blocks (Vbloc), residual variance (Ve), and individual phenotypic variance (Vf). The genetic parameters were predicted: heritability of individual plots in broad sense (h<sup>2</sup>); determination coefficient of the block effects (C<sup>2</sup>bloc); and the genotype selection's accuracy (ACgen). Individual genotypic value (u+g) was predicted, with: u is overall average; and g is the predicted genotypic effects. The equations of mixed model, estimators of REML variance components and BLUP predictors are described by Resende [11].

Deviance analysis to verify the significance of random effects via the Likelihood Ratio Test (LRT) was performed according to Resende [11]. Deviance values based on Log of the maximum point of the residual likelihood function (L) were obtained, whose subtraction between the models without and with the effect to be tested was submitted to chi-square test, with 1 degree of freedom, considering the probabilities of 1% and 5%.

Firstly, two groups according to genotypic values greatest than overall averages were obtained: TSS group > 15.90  $^{\circ}$ Brix; and FMWC group > 1.60 kg. This adopted criterion corresponded to a selection rate of approximately 20 %, in relation to the total number of 364 evaluated hybrids. Posteriorly, within of the TSS and FMWC groups, respectively, hybrids with genotypic values of FMWC < 1.60 kg and TSS < 15.90  $^{\circ}$ Brix were discarded, resulting in the ultimate select rate of 10.44%.

#### 3. Results and Discussion

Two groups with 38 hybrids were selected for higher fruit mass without crown (FMWC) and total soluble solids (TSS), from 364 hybrids evaluated. The first group with 22 hybrids (Table 2) was selected in descending order for FMWC and TSS > 15.90 ° Brix, equivalent to the overall average. The selected hybrids reached predicted genotypic values (u + g)

between 2.72 kg and 1.83 kg for FMWC and 20.87 ° Brix and 15.98 ° Brix for TSS. This group presented increments of 28.12% for FMWC and 8.68% for TSS, respectively, in relation to overall averages.

**Table 2** Predicted genotypic values (u+g) of 22 pineapple hybrids, selected in descending order for fruit mass without crown (FMWC) and total soluble solids (TSS) > 15.90 °Brix, with complementary information about fruit shape (FS), pulp color (PC) and leaf margin spinescence (LMS).

Hybrid	FMWC (kg)	TSS (°Brix)	FS	РС	LMS
IPA 04-60	2.72	16.18	con.	yel.	irr.
IPA 125-363	2.54	15.98	con.	gol. yel.	spi.
IPA 125-85	2.37	17.95	con.	yel.	spi.
IPA 04-92	2.21	18.35	con.	gol. yel.	pip.
IPA 125-320	2.11	20.69	con.	whi.	spi.
IPA 125-257	2.08	20.87	con.	whi.	spi.
IPA 125-20	2.07	15.99	con.	yel.	spi.
IPA 125-256	2.07	17.36	con.	gol. yel.	spi.
IPA 125-150	2.06	17.55	cyl. bas.	yel.	spi.
IPA 04-11	2.03	17.16	con.	gol. yel.	spi.
IPA 125-71	2.03	17.94	con.	gol. yel.	irr.
IPA 125-364	2.02	16.96	con.	yel.	spi.
IPA 125-338	2.01	16.20	cyl.	gol. yel.	spi.
IPA 125-369	1.91	17.36	cyl. bas.	gol. yel.	spi.
IPA 04-84	1.88	16.58	con.	yel.	irr.
IPA 04-19	1.88	16.58	cyl.	gol. yel.	spi.
IPA 125-178	1.87	17.16	cyl. bas.	gol. yel.	spi.
IPA 125-106	1.86	15.98	cyl. bas.	yel.	spi.
IPA 04-95	1.86	16.20	con.	gol. yel.	spi. tip.
IPA 125-310	1.85	17.35	cyl.	yel.	pip.
IPA 125-62	1.84	16.87	con.	whi.	spi.
IPA 125-151	1.83	16.96	cyl.	whi.	spi.
Overall average	1.60	15.90	-	-	-
Selected average	2.05 (+28.12%)	17.28 (+8.68%)	-	-	-

FS - cyl. = cylindrical, cyl. bas. = cylindrical base, con = conical, irr. = irregular; PC – yel. = yellow, gol. yel. = golden yellow, whi. = white; LMS - irr. = irregular, spi. = spiny, pip. = piping, spi. tip. = spiny tip.

The second group with 16 hybrids (Table 3) was selected in descending order for TSS and FMWC > 1.60 kg, that equivalent to the overall average. The selected hybrids reached predicted genotypic values (u + g) between 21.86 ° Brix and 17.94 ° Brix for TSS and 1.82 kg and 1.60 kg for FMWC. This group presented increments of 20.31% for FMWC and 5.00% for SST, respectively, in relation to overall averages (Table 3). Both FMWC and TSS groups were selected to compose a second cycle of vegetative propagation in the field conditions, considering larger number of plantlets per plot and focusing on the yield and fruit quality stabilities. The remaining hybrids non-selected within both groups were eliminated, because they presented genotypic values of FMWC <1.60 kg and TSS <15.90 °Brix.

IPA 04-60, IPA 125-363, IPA 125-85 and 04-92 hybrids presented the highest (> 2.20 kg) genotypic values for FMWC, while IPA 125-218, IPA 125- 95, IPA 125-188 and IPA 125-97 hybrids reached the highest (> 20.0 ° Brix) genotypic values for TSS. Cabral et al. [5], analyzing phenotypic values observed a decrease in fruit weight from selected genotypes in most of the crossings and an increase of total soluble solids in all crossings, in relation to own parents. This result

was attributed to the fact that only individuals with fruit weight between 0.9 kg – 2.5 kg and total soluble solids higher than 13 °Brix were selected, occurring discard of all genotypes with more than 2.5 kg.

Basically, selection process via vegetative propagation enables to fix in a given individual the integral vigor or genetic gain (additivity, dominance and epistasis) in any phase of the breeding program, just as it has been using for sugarcane, cassava, potato, and fruit trees, including pineapple [12]. The advantage this process is enable to immediate cloning of the best hybrids, through vegetative propagation for use per se. Therefore, within each selective cycle there is non-recombination of these selected genotypes until the final phase of evaluation for release of the new cultivar. After this release, some cultivars also may be indicated as parents for hybridizations in with each other, and thus allow feedback to the initial phase (sexual cycle) of the breeding program.

**Table 3** Predicted genotypic values (u+g) of 16 pineapple hybrids, selected in descending order for total soluble solids (TSS) and fruit mass without crown (FMWC) > 1.5 kg, with complementary informations about fruit shape (FS), pulp color (PC) and leaf margin spinescence (LMS).

Hybrid	TSS (ºBrix)	FMWC (kg)	FS	РС	LMS
IPA 125-218	21.86	1.63	con.	gol. yel.	spi.
IPA 125-95	21.07	1.74	con.	gol. yel.	spi.
IPA 125-188	20.48	1.60	irr.	whi.	spi.
IPA 125-97	20.10	1.69	con.	gol. yel.	spi.
IPA 125-36	19.89	1.62	cyl.	gol.	spi.
IPA 125-133	19.70	1.60	con.	gol. yel.	spi.
IPA 125-217	19.12	1.82	con.	whi.	spi.
IPA 125-211	18.52	1.78	con.	whi.	spi.
IPA 125-302	18.52	1.65	con.	gol.	pip.
IPA 125-65	18.44	1.72	cyl. bas.	whi.	irr.
IPA 04-54	18.33	1.73	con.	gol.	spi.
IPA 125-142	18.15	1.62	con.	gol. yel.	spi.
IPA 125-148	18.14	1.68	cyl. bas.	gol. yel.	spi.
IPA 125-304	17.94	1.66	cyl.	gol. yel.	pip.
IPA 125-210	17.94	1.72	cyl. bas.	gol. yel.	spi.
IPA 03-26	17.94	1.61	con.	whi.	spi.
Overall average	15.90	1.60	-	-	-
Selected average	19.13 (+20.31%)	1.68 (+5.00%)	-	-	-

FS - cyl. = cylindrical, cyl. bas. = cylindrical base, con = conical, irr. = irregular; PC – yel. = yellow, gol. yel. = golden yellow, whi. = white; LMS - irr. = irregular, spi. = spiny, pip. = piping, spi. tip. = spiny tip.

Genotypic values (u + g) presented for FMWC and TSS (Tables 2 and 3) are more adequate for the genetic breeding programs due to do not incorporate the environmental effects differently than conventional procedures established on phenotypic values, which integrate the environmental effects and your interactions versus genotypes, that may cause lower selective accuracy. Essentially, all the following phases of the Brazilian programs of pineapple genetic breeding are based on phenotypic values for plant and fruit traits [4, 13]. The first field evaluation for dozens traits (Phase I - sexual cycle); evaluation of phenotypic stability by two cycles of vegetative propagation (Phase II); competition experiment, including standard cultivar as control (Phase III).

As an example of the strong interaction between genotypes and environments, we can mention the 'BRS Imperial' and 'BRS Vitória' cultivars, both are resistants to fusariosis, piping leaf margin, and with excellent sensory qualities of the pulp were evaluate by Cabral and Matos [14] in the municipalities of Itambé and Vitória de Santo Antão, Pernambuco State. These cultivars did not present agronomic satisfactory results, when they were compared with a 'Pérola' traditional cultivar. Following phenotypic averages were obtained, respectively, for fruit mass with crown, titratable

acidity and ratio: 550 g, 0.7% and 31 ('BRS Imperial'); 842 g, 0.5% and 40 ('BRS Vitória'); 946 g, 0.4% and 44 ('Pérola'). The pineapple growing in Brazil is still based on 'Pérola', which even susceptible to fusariosis (dependent of the chemical control by fungicides) and with totally spiny leaf margin presents wide adaptation, vigorous growth and great acceptance in the domestic market for fresh fruit consumption [2, 3].

However, "BRS Imperial" cv., for example, showed excellent results in Bahia State - Brazil with 1.8 kg of fruit mass with crown [15]. One way to get around this unfavorable situation for the success of the genetic improvement would be to implement the regionalization of the selection stages, from the initial stages (sexual cycle), in addition to adopting the estimate of genotypic values (REML / BLUP) for studies of genotype x environment interactions, adaptability and stability.

Deviance analysis revealed that the genotypic effects were significant for FMWC (p<0.05) and TSS (p<0.01). This result indicates high genetic variability among 364 cloned hybrids, as well as favorable conditions for the improvement of both evaluated traits (Table 4). According to Cabral et al. [16] and Sanewski et al. [2] the hybridization of heterozygous genitors is responsible for most of the widely variable genotypes through gene recombination.

**Table 4** Analysis of deviance and likelihood ratio test (LRT) for fruit mass without crown (FMWC) and total soluble solids (TSS) of 364 pineapple's cloned hybrids.

	FMWC		TSS		
Effect	Deviance	LRT $(\chi^2)$	Deviance	LRT $(\chi^2)$	
genotypic	-37.6800+	3.9650*	1,073.8013	36.2341**	
Blocks	-16.1747+	25.4703**	1,037.6151	0.04779ns	
Residue	-	-	-	-	
Complete model	-41.6450	-	1,037.5672	-	

+Deviance of the adjusted model without the corresponding effects; \* and \*\*Significant by the chi-square test at 5% (3.84) and 1% (6.63), respectively; ns: non-significant.

Significance for FMWC (p < 0.01) were detected regarding the block effects. This result indicates existence of differences among blocks influencing the evaluated trait. In this case, the statistical design (augmented blocks) was efficient to detect heterogeneity due to environment. However, there was no significance in the block effects (p < 0.05) for TSS indicating that such effects did not differ from each other and contributed in a homogeneously to the referred trait. Therefore, it is not necessary to adopt the statistical principle of local control, whose experimental units or plots do not need to be distributed within each block to assess TSS.

**Table 5** Estimated variance components and genetic parameters for fruit mass without crown (FMWC) and totalsoluble solids (TSS) from 364 pineapple hybrids.

Parameters	FMWC	TSS
Genotypic variance (Vg)	0.1770	6.4972
Environmental variance between blocks (Vbloc)	0.0399	0.0021
Residual variance (Ve)	0.1421	0.1394
Phenotypic variance (Vf)	0.3591	6.6388
Heritability of individual plots in broad sense $(h_g^2)$	0.4929	0.9786
Determination coefficient of the block effects $(c_{bloc}^2)$	0.1112	0.0003
Genotype selection's accuracy ( $Ac_{gen}$ )	0.7021	0.9892
Overall average	1.6087	15.9083

Genotypic variances  $(V_g)$  reached higher proportions (Table 5) in relation to environment variances between blocks  $(V_{bloc})$  and residual variances  $(V_e)$  for FMWC and TSS. These results indicated that genotypic variances were determinant to the expression of the phenotypic values observed for FMWC and TSS. High proportion of the phenotypic variance was explained by genotypic effects, due to heritability in broad sense, indicating existence of variability for evaluated traits and high perspective for selection of superior individuals.

Possibility of to pre-select cloned hybrids with higher genotypic values, in relation to overall averages, was evidenced by the higher proportions of estimated genotypic variances for both traits (FMWC and TSS) (Table 5). These evaluated hybrids are descendants of 'Pérola', 'MD-2', 'BRS Imperial' and 'BRS Vitória' that have a high variation to the various traits on related to plant and fruit [5, 3]. Cabral et al. [16] highlighted this segregation for traits of agronomic importance is due to the majority of heterozygous loci of cultivars used as direct hybridization parents.

Heritability estimates  $(h^2_g)$  reached medium and high magnitudes, respectively, for FMWC and TSS (Table 5), indicating a good genetic control in the expression of these traits among evaluated hybrids. These results enabled high precision for selection of hybrids, with high accuracy (AC<sub>gen</sub>) for TSS and moderate for FMWC. The selective accuracy represents the correlation between predicted genotypic values and true genotypic values of the evaluated hybrids. These results are similar to those obtained by Abreu et al. [17], who reported heritability coefficients of 0.6379 for fruit mass without crown and 0.7052 for total soluble solids, estimated for pineapple clones of 'Turiaçu', via REML / BLUP method.

Determination coefficients for block effects ( $c_{bloc}$ ) reached low values (Table 5) for evaluated traits, indicating low environment heterogeneities, associated to the statistical design adopted in Federer Augmented Blocks. According to Resende [18] the  $c_{bloc}^2$  coefficients must be interpreted in combination with the block effects. For FMWC the significant block effects and with low value of  $c_{bloc}^2$  indicate that the design was efficient and the precise capacity of the Likelihood Ratio Test (LRT). For TSS the bloc effects were no significant and with low value of  $c_{bloc}^2$  indicate great environmental homogeneity and that any statistical design will be efficient, but the test capacity was not as efficient. In general, in the early stages of genetic breeding, it is difficult to find uniform experimental areas of adequate size to accommodate hundreds of genotypes [19]. Combined with the low availability of propagative materials for the formation of experimental units with complete blocks, it is associated with plant losses, which impose the need to choose incomplete block designs.

## 4. Conclusion

The selection criteria resulted in a rate of 10.44%, include a total of 38 hybrids with values higher and/or equal to the genotypic averages of 1.60 kg for fruit mass without crown and 15.90 ° Brix for total soluble solids;

First group contains 22 hybrids with genotypic values that range from 2.72 kg to 1.83 kg for fruit mass without crown and from 20.87 °Brix to 15.98 °Brix for total soluble solids. Second group comprises 16 hybrids with genotypic values ranging from 21.86 °Brix to 17.94 °Brix for total soluble solids and from 1.82 kg to 1.60 kg for fruit mass without crown.

IPA 04-60, IPA 125-363, IPA 125-85 and IPA 04-92 hybrids have genotypic values greater than 2.20 kg for fruit mass without crown. In relation to total soluble solids, IPA 125-218, IPA 125-95, IPA 125-188 and IPA 125-97 hybrids reach genotypic values greater than 20.0 °Brix. These selected hybrids exhibit promising traits to proceed a second clonal selection focusing on the yield and fruit quality stabilities.

#### **Compliance with ethical standards**

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## Disclosure of conflict of interest

There is no conflict of interest.

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