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Use of an index based on best linear unbiased prediction value for the selection of superior papaya lines for multiple traits

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ABSTRACT: Selection indexes represent the real efforts of a breeding program to obtain genetic gains for various significant traits simultaneously. As such, this study selected superior F_5 lines by combined selection for fruit quality using an index based on predicted genotypic values via residual or restricted maximum likelihood/best linear unbiased prediction (REML/BLUP) methodology weighted by agronomic weights. To do so, 97 F_5 papaya lines obtained by the single seed descent method, resulting from the biparental cross between the genotypes JS-12 and Sekati, were evaluated for the main traits related to fruit quality. Results of the analysis of deviance and the genetic parameters indicated that there was genetic variability, indicating possible success in the selection process. Based on the selection index, 29 lines were selected as superior for fruit quality with 'Formosa' pattern. The strategy of the selection index combining BLUPs of multiple traits of interest associated with agronomic weights allows maximizing genetic progress while discarding less-promising genotypes.

Key words: segregating population, mixed models, digital phenotyping, fruit market, genetic breeding.

INTRODUCTION

Papaya (*Carica papaya* L.) is a remarkably important fruit among the more than 1,000 tropical fruits found in North and South America (Paull and Duarte 2011), with an expressive economic value, since it is extensively cultivated and marketed in tropical and subtropical areas. Papaya has high nutritional value, providing a complex of carbohydrates, vitamins, proteins, and amino acids that are beneficial to health (Ming et al. 2008). In addition, it is a raw material for many utilizations in the industrial sector that uses papain, one of the main components of the mixture of enzymes extracted from the sap of the green fruit (Xiang et al. 2016).

Brazil is one of the largest producers and exporters of papaya providing fruits for fresh consumption and industrialized products (Cardoso et al. 2017). In the world ranking, Brazil ranks third among exporting countries (FAO 2022). It is the main fruit supplier to the European Union and has been conquering markets for 'Formosa' type fruits, such as the North American market, where 75% of the consumption is for larger fruits (Barbieri et al. 2019). Although the demand is continuously growing for the national and international markets, the productivity of the crop is hindered by factors related to climatic conditions, disease incidence, and the restricted number of cultivars available with larger fruit patterns.

Of all the plant breeders' skills, the most significant is the proper exploitation of plant resources with genetic variability, without which it is not possible to make progress in genetic breeding. In papaya crops, new cultivars are most often from the generation of segregating populations with such variability that allow identifying superior genotypes for traits of interest, such as disease resistance, productivity, and fruit quality (Cortes et al. 2018; Santa-Catarina et al. 2020). Therefore, it is pertinent to the work of breeders to explore segregating populations as genetic resources of high value for the identification of superior genotypes in the development of varieties that can be lines or hybrid combinations.

The most popular varieties in commercial production fields worldwide are from the 'Solo' group because of their fruits with desirable characteristics for export activities, with small size and weight between 300 and 650 g. On the other hand, hybrids of the 'Formosa' group presenting larger fruits, with an average weight between 1,000 and 1,300 g, have been gaining space in the Brazilian market and importing countries in Europe and North America (Barbieri et al. 2019; Oliveira and Vitória 2011). However, few hybrids of the 'Formosa' group are available for the larger fruit market, and there is still a strong dependence on hybrid seeds imported from Taiwan for the production of these fruits (Cortes et al. 2019).

Given that, genetic breeding programs with the fundamental purpose of obtaining superior genotypes for a set of economically important traits can use strategies with different approaches for simultaneous selection. To this end, the main desirable agronomic traits should be evaluated for the effective selection of superior materials that will originate new varieties. Therefore, the goal of this work was to select superior F_5 lines with 'Formosa' pattern by combined selection using predicted genotypic values via residual or restricted maximum likelihood/best linear unbiased prediction (REML/BLUP) methodology weighted by agronomic weights for traits relative to fruit quality.

MATERIAL AND METHODS

Plant material

The genetic material under evaluation was from a morphoagronomic evaluation trial that comprised 169 treatments, consisting of 97 F_5 lines, 62 topcross hybrids, and 10 controls (SS-72/12, 'Maradol', 'Waimanalo', 'Calimosa', 'Tainung', 'Golden', 'Aliança', 'UC10', JS-12, and Sekati).

The 97 F_5 papaya lines obtained by the single seed descent method evaluated here resulted from the biparental cross between the genotypes JS-12 and Sekati, belonging to the Germplasm Bank of the UENF/Caliman program. Both genotypes belong to the heterotic 'Formosa' group and show high overall combining ability in crosses with genotypes from the 'Formosa' and 'Solo' groups (Cardoso et al., 2014). The genotype JS-12 was used for this cross as allelic source for the total soluble solid trait, and the Sekati genotype, as an allelic source for the firmness trait. The topcross hybrids were obtained by crossing lines in the F_4 generation with the SS-72/12 tester, from the heterotic 'Solo' group.

A flowchart depicts all the steps for obtaining F_5 lines and topcross hybrids (Fig. 1).

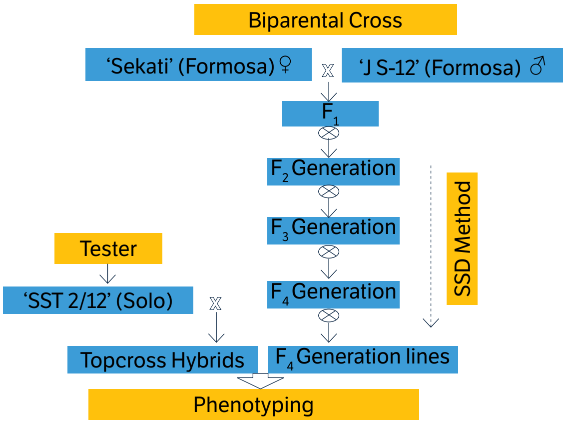

Figure 1. Flowchart of the steps for obtaining and conducting segregating populations of F_5 lines and topcross hybrids from the UENF/Caliman papaya genetic breeding program.

Note: The biparental cross between the genotypes JS-12 and Sekati created the F1 generation. This generation was conducted by the single seed descend method until the F4 generation, in which the lines were crossed with the SS-72/12 tester to obtain topcross hybrids, and the same lines were self-fertilized to obtain the lines in the F5 generation.

Conduction and experimental design

The experimental trial comprehensively evaluated agronomic aspects as to the quality, yield, and disease resistance of the F_5 lines and of the hybrids obtained by crossing the F_4 lines with the SS-72/12 tester. It was conducted in the commercial field of Caliman Agrícola S.A. company, located in Linhares, Espírito Santo state, Brazil, geographically between parallels 19°0' – 19°18' south latitude and between meridians 39°45' – 40°19' west longitude.

The experimental design was a lattice 13 × 13 with five repetitions, two plants per plot at 3.6 m spacing between rows and 1.5 m between plants. The seedlings were produced in plastic trays with 96 tubes using a commercial substrate. After 30 days of germination and acclimation, the seedlings were transplanted to the experimental unit. Four seedlings were planted per hole and, after three months, the sexing of the plants was done keeping only one hermaphrodite plant per hole. The fertilization, management, pest and disease control, and cultural treatments were the same as those used in the commercial plantations of the Caliman Agrícola S.A. company.

Evaluations were conducted at three different times: at 300 (January 2018), 390 (May 2018), and 450 (July 2018) days after planting in each season evaluated, when the fruits were at the same ripening stages RST1 (ripening stages on-tree), in which the fruit reaches its maximum physical development and can be harvested (Barragán-Iglesias et al. 2018).

Traits evaluated

The traits considered for fruit quality in the F_5 lines were: average fruit weight (AFW [g]); fruit firmness (FF [N]); flesh firmness (FLF [N]); soluble solids content (SSC [°Brix]); fruit length (FL [cm]); fruit diameter (FD [cm]); flesh thickness (FT [cm]); ovarian cavity length (OCL [cm]); ovarian cavity diameter (OCD [cm]); fruit volume (FV [cm^3]); ovarian cavity volume (OCV [cm^3]); flesh volume (FLV [cm^3]); and flesh yield (FYIE [%]).

Measurements of the FL, FD, FT, OCL, OCD, FV, OCV, FLV, and FYIE traits were performed at the Laboratory of Plant Genetic Breeding (LPGB) at UENF from a digital image taken from three fruits per plant according to image-based digital phenotyping methodology proposed by Santa-Catarina et al. (2018). As for the AFW, FF, FLF, and SSC traits, they were measured in the quality control laboratory of Caliman Agrícola S.A.

The digital images were obtained from the fruits cut longitudinally scanned on an Optico Pro A320 model scanner. From these images, the values of the digital measurements of the fruits were obtained for the FL, FD, OCL, OCD, FT, FV, OCV, FLV, and FYIE traits. The FT trait was measured by the Straight and Wand tools. The FL, OCL, FD, and OCD traits were measured using the major and minor parameters provided by the ImageJ v1.50c software.

The measurement of the AFW trait was obtained by weighing the fruit using a Toledo model 9094 digital electronic analytical balance. The measurement of the SSC trait was made with juice extracted by a hand press from a sample of the flesh of the median region using a portable refractometer Mettler Toledo Densito 30PX Density meter model.

The FF trait was measured by perforating three equidistant points in the equatorial region of the fruit. For the FLF trait, the measurement was made by slicing the fruit into two equal parts, transversely, and perforating three equidistant points in the fruit flesh. The firmness of the fruit and flesh was evaluated by the resistance to penetration, using a Digital Bench Penetrometer (Fruit Pressure Tester, Italy, Model 53205) with a 3.0 × 3.0 cm adapter (height × diameter).

The FLV trait was obtained by the difference between FV and OCV using the measurements of the lengths and diameters of the fruit and ovarian cavity, following Eq. 1.

$$V_e = \pi(L \, x \, D^2/6) \tag{1}$$

in which V_e is the estimated volume; L, the length; and D, the diameter, as described by Santa-Catarina et al. (2018), adapted from Koc (2007). The FYIE trait was calculated from Eq. 2

$$FYIE = (FLV \times 100)/FV \tag{2}$$

Statistical analysis

The data from the evaluation of the F_5 lines were analyzed using the linear mixed model methodology, via the REML/BLUP procedure, considering the lattice design. Estimation of variance components and genetic parameters were conducted via REML (restricted maximum likelihood), and genotypic values were estimated by the BLUP procedure by using the Selegen-REML/BLUP software presented by Resende (2016). Equation 3 shows the statistical model used to evaluate the data genetically:

$$y = X\mathrm{m} + Z\mathrm{g} + W\mathrm{b} + T\mathrm{p} + e \tag{3}$$

in which y is the vector of data, m is the vector of effects of measurement-repeat combinations (assumed to be fixed) added to the overall mean, g is the vector of genotypic effects (assumed to be random), b is the vector of block effects (assumed to be random), p is the vector of permanent environmental effects (plots in this case) (random), and e is the vector of errors or residuals (random). The capital letters (X, Z, W, and T) represent the incidence matrices for these effects, respectively.

The statistical model 70 from the Selegen software was applied in this study taking into account that the materials were derived from self-fertilization, and the model is appropriate for evaluating genotypes (accessions, cultivars, clones, hybrids, lines, and families) in multiple replications in a lattice experimental design.

The selection ranking graph was made using the radar graph in the Microsoft Excel software. The correlogram and selection gain boxplot was made using the corrplot and ggplot2 packages, respectively in the R software (R Core Team 2018).

Selection index

The combined selection was performed with the mean of the plot of the F_5 lines evaluated in three different seasons to identify the best genotypes. To do so, the predicted genotypic values estimated by the BLUP procedure were standardized and weighted by agronomic weights according to the interest of each trait. The index based on multiple traits (combined selection) suggested by Ramos et al. (2014), referred here as PGVI-predicted genotypic value index, was as described in Eq. 4.

$$\mathrm{PGVI} = (\mathrm{GV}_1 \times \mathrm{p}_1) + (\mathrm{GV}_2 \times \mathrm{p}_2) + \ldots + (\mathrm{GV}_n \times \mathrm{p}_n) \tag{4}$$

in which GV is the standardized predicted genotypic value, and p is the agronomic weight established for each trait. For standardizing the GVs, the equation used was Eq. 5:

$$GV = \left(\frac{X_g - \bar{X}_g}{SX_g}\right) \tag{5}$$

in which X_g is the value measured in the individual for variable x, $\bar{X}_g$ is the overall mean of the variable, and SX_g, the standard deviation.

Agronomic weights were used for AFW (1), FF (100), FLF (100), SSC (100), and FT (70) traits described by Ramos et al. (2014). For all other traits, such as FLV (100) and FYIE (100), agronomic weights were attributed based on their relevance to the papaya crop.

The predicted genotypic values were obtained from the Selegen REML/BLUP software (Resende, 2016). The construction of the selection index and ranking chart were made using the Microsoft Office Excel 2016 software. A 30% selection intensity was practiced for the indication of the superior lines regarding fruit quality.

RESULTS

Analysis of deviance

Significant genotype effects were observed by the likelihood ratio test (LRT) at 1% probability for all morphoagronomic traits related to fruit quality, except for FYIE (Table 1). In contrast, there was a significant difference at 1% probability for block effect in the AFW, FLF, FT, OCD, and FLV traits, and there was a significant difference at 5% probability for the other traits. No significant difference was found among the three seasons evaluated (300, 390, and 450 days after planting) for fruit and FLF and SSC.

Table 1. Analysis of deviance and likelihood ratio test (LRT) for papaya population for traits related to fruit quality.

Effect	AFW		FF		FLF	
	Deviance	**LRT (χ^2)**	**Deviance**	**LRT (χ^2)**	**Deviance**	**LRT (χ^2)**
Genotype	18943.5310	261.5212**	8070.3161	75.006**	7822.6920	98.0254**
Block	18701.8958	19.886**	7999.5130	4.2029*	7731.3875	6.7209**
Season	18702.7587	20.7489**	7995.3609	0.0508^{ns}	7724.7506	0.084^{ns}
Model	18682.0098		7995.3101		7724.6666	
Effect	**SSC**		**FT**		**OCL**	
	Deviance	**LRT (χ^2)**	**Deviance**	**LRT (χ^2)**	**Deviance**	**LRT (χ^2)**
Genotype	3203.6521	102.6973**	-1887.1415	194.6753**	4595.1176	362.0778**
Block	3105.1797	4.22*	-2067.9230	13.8968**	4239.0731	6.0333*
Season	3101.0336	0.0788^{ns}	-2071.8505	9.9693**	4249.7677	16.7279**
Model	3100.9548		-2081.8198		4233.0398	
Effect	**OCD**		**FLV**		**FYIE**	
	Deviance	**LRT (χ^2)**	**Deviance**	**LRT (χ^2)**	**Deviance**	**LRT (χ^2)**
Genotype	1070.6991	254.8002**	18261.7523	319.75**	13827.6642	0.0604^{ns}
Block	829.7110	13.8121**	17954.5740	12.5717**	13851.0396	23.4358**
Season	822.1710	6.2721*	17955.4185	13.4162**	13827.6179	0.0141^{ns}
Model	815.8989		17942.0023		13827.6038	

Deviance of the adjusted model without the corresponding effects, ns: non-significant; * and **: Significant by Chi-square test (χ^2) at 5% (3.84) and 1% (6.63), respectively. AFW: average fruit weight (g); FF: fruit firmness (N); FLF: flesh firmness (N); SSC: soluble solids content (°Brix); FT: flesh thickness (cm); OCL: ovarian cavity length (cm); OCD: ovarian cavity diameter (cm); FLV: flesh volume (cm^3); FYIE: flesh yield (%).

Components of variance and genetic parameters

The components of variance and genetic parameters associated with the study are presented in Table 2. The highest estimated values of genotypic variance (σ_g^2) were the AFW and FLV traits, while the lowest values of this component were referred to by SSC, flesh thickness, and OCD. The values regarding the residual variance (σ_e^2) of the FF, FLF, and SSC traits were higher than the genotypic variance for such traits. The values of selective accuracy (r) ranged from low to high magnitude. The highest values of the heritability parameter (h^2) were associated with the AFW and FLV, and the lowest were related to the FF, FLF, and FYIE.

Table 2. Estimation of genetic parameters and mean for nine morphoagronomic traits related to fruit quality in papaya lines by REML/BLUP procedure.

Trait	σ^2_g	σ^2_f	σ^2_e	*r*	*h*^{2}	Mean
AFW	69111.290	150475.444	62060.564	0.587	0.459	1166.002
FF	14.292	81.005	64.445	0.204	0.176	125.968
FLF	13.510	68.717	53.083	0.227	0.196	84.802
SSC	0.636	3.117	2.397	0.231	0.204	10.098
FT	0.045	0.120	0.062	0.482	0.379	2.682
OCL	5.381	10.222	3.916	0.617	0.526	17.630
OCD	0.353	0.862	0.436	0.494	0.410	5.187
FLV	50078.039	97407.526	38690.115	0.602	0.514	831.546
FYIE	8.060	3779.614	3547.337	0.061	0.002	77.386

AFW: average fruit weight (g); FF: fruit firmness (N); FLF: flesh firmness (N); SSC: soluble solids content (°Brix); FT: flesh thickness (cm); OCL: ovarian cavity length (cm); OCD: ovarian cavity diameter (cm); FLV: flesh volume (cm3), FYIE: flesh yield (%).

Combined selection

The combined selection was carried out by using the PGVI selection index to rank the F$_5$ lines (Fig. 2). The selection intensity practiced was 30%. A total of 29 lines were indicated for selection according to the PGVI selection index, which used standardized agronomic weights and predicted genotypic values.

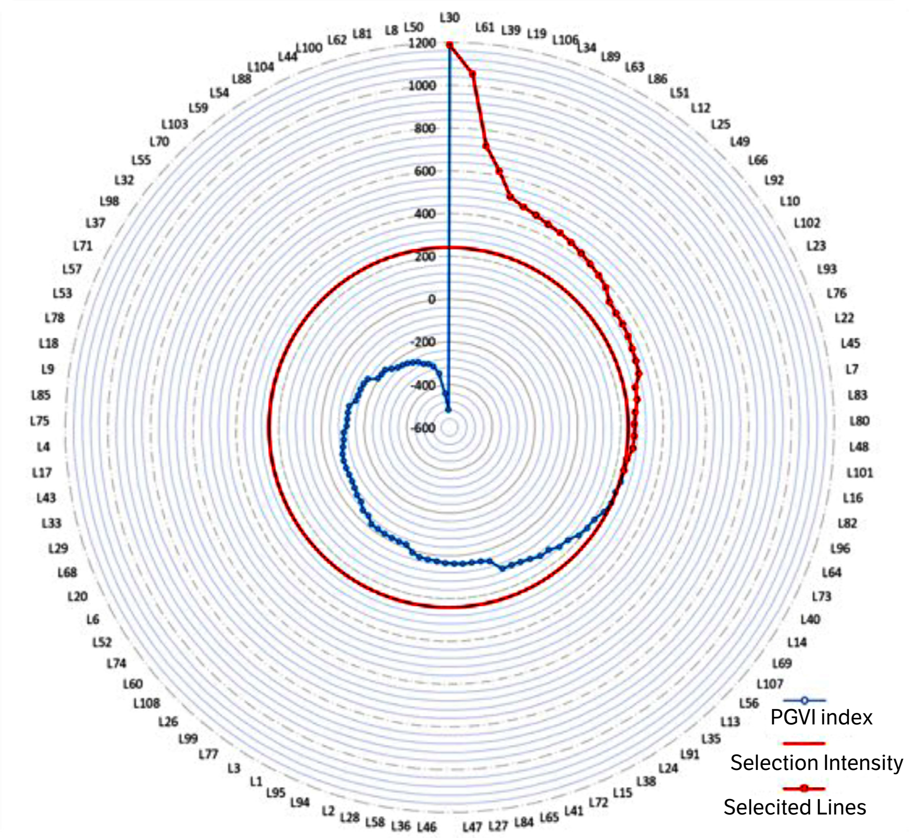

Figure 2. Ranking, selection intensity and lines selected by the PGVI index.

Note: The axis of the graph shows the score* of the lines, the dashed circle depicts the minimum score of the selected lines. *Value originated by the calculation of the PGVI index for each line evaluated.

The F_5 lines indicated for selection had predicted means from 1,211.22 to 1,993.92 g for the AFW trait and a mean of 1,573.17 g, higher than the predicted means of their parents JS-12 and Sekati (Table 3). For FF, the predicted means varied from 126.84 to 136.83 N with a mean of 131.04 N exceeding 9 of the evaluated controls. The predicted means for FLF ranged from 86.43 to 91.78 N with a mean of 89.13 N, which did not exceed only the JS-12 control. The SSC trait showed a range of 10.19 to 10.91 °Brix with a mean of 10.63 °Brix, exceeding the predicted means of the Sekati, 'Maradol', 'Waimanalo', 'Calimosa', 'Tainung', and 'UC10' controls.

Table 3. Predicted mean (PM) of the lines indicated for selection for the principal traits of papaya fruit quality, ranked by the PGVI index.

Genotype	AFW (g)	FF (N)	FLF (N)	SSC (°Brix)
L030	1731.20	129.47	91.09	10.20
L061	1993.92	134.36	91.78	10.59
L039	1571.56	136.83	88.87	10.64
L019	1698.41	131.82	88.23	10.60
L106	1893.03	130.06	88.09	10.69
L034	1349.24	135.28	91.35	10.68
L089	1621.38	128.10	89.61	10.85
L063	1666.55	133.77	88.45	10.46
L086	1935.99	126.84	88.02	10.79
L051	1630.86	133.39	89.95	10.27
L012	1708.06	129.39	90.31	10.67
L025	1381.15	131.48	90.04	10.63
L049	1280.82	131.57	90.91	10.81
L066	1512.32	130.90	89.73	10.31
L092	1676.09	129.56	89.80	10.44
L102	1779.94	129.74	88.54	10.50
L010	1556.93	130.23	87.39	10.68
L023	1523.82	132.54	88.91	10.51
L093	1399.40	127.50	86.89	11.37
L076	1579.02	130.69	90.12	10.47
L022	1276.74	132.08	88.83	10.91
L045	1612.45	131.13	87.79	10.56
L007	1446.74	132.94	91.69	10.19
L083	1761.53	131.74	87.82	10.35
L080	1455.45	131.39	87.00	10.67
L048	1211.22	132.28	88.34	10.52
L101	1603.53	127.08	86.43	11.30
L016	1295.08	130.12	90.58	10.84
L082	1469.53	127.87	88.19	10.81
Mean	1573.17	131.04	89.13	10.63
		Controls		
Sekati	1416.28	126.72	88.05	10.25
JS12	1442.61	131.22	91.78	10.63
SS 7212	1166.00	126.13	85.19	10.85
Maradol	2082.73	127.31	86.72	10.28
Waimanalo	1640.22	127.45	85.16	10.23
Calimosa	1387.16	126.60	88.99	10.55
Tainung	1718.90	130.01	88.30	10.17
Golden	1169.98	128.41	85.67	10.70
Aliança	1179.16	130.43	85.13	10.65
UC10	1745.15	130.30	88.66	10.53

AFW: average fruit weight (g); FF: fruit firmness (N); FLF: flesh firmness (N); SSC: soluble solids content (°Brix).

The lines recommended for selection exhibited genetic gains varying from −22.82 to 59.30% for AFW; from −2.85 to 12.09% for FF; from −3.60 to 7.91% for FLF; and from −11.79 to 10.75% for SSC (Fig. 3). The mean gains were 12.62%, 3.18%, 1.75%, and 1.45% for AFW, FF, SSC, and FLF traits, respectively.

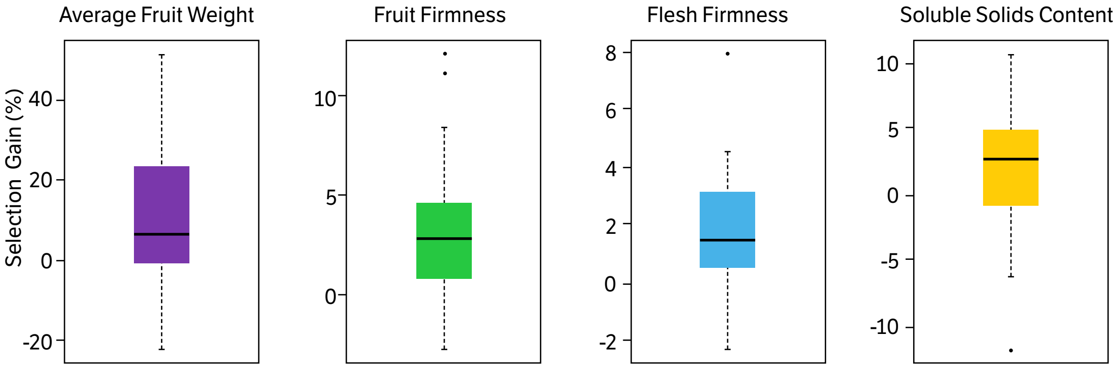

Figure 3. Selection gain in percentage of lines indicated for selection for main traits related to fruit quality in papaya trees.

Correlogram

Correlation analysis demonstrated important correlations between the measured traits (Fig. 4). Positive correlation coefficients using BLUP values were observed between FF and FLF (r = 0.51); AFW and FF (r = 0.21); AFW and FLF (r = 0.14) and negative correlation coefficients were observed for SSC and AFW (r = −0.19); SSC and FLF (r = −0.04) and SSC and FF (r = −0.01). Likewise, positive correlation coefficients using phenotypic values were also observed for FF and FLF (r = 0.48); AFW and FF (r = 0.19); AFW and FLF (r = 0.11) and negative correlation coefficients were observed for SSC and AFW (r = −0.14); SSC and FF (r = −0.09) and SSC and FLF (r = −0.06).

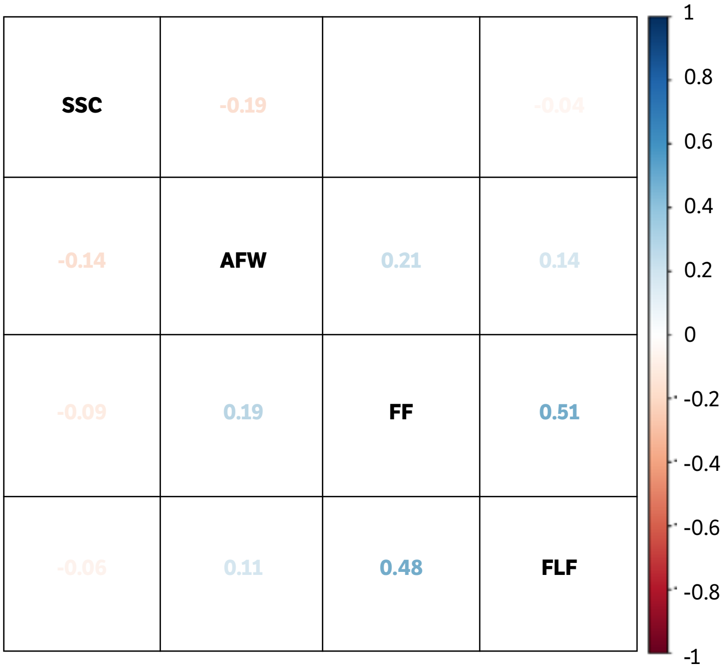

Figure 4. Correlogram of F$_5$ lines with BLUP values (upper) and phenotypic values (lower) for main traits related to fruit quality in papaya trees.

Note: AFW: average fruit weight (g); FF: fruit firmness (N); FLF: flesh firmness (N); SSC: soluble solids content (°Brix).

DISCUSSION

The results of the analysis of variance corroborate the existence of adequate genetic variability among the genotypes evaluated, suggesting the possibility of obtaining a successful selection process based on morphoagronomic traits related to fruit quality.

The F_5 papaya lines evaluated presented higher estimates of genotypic variance for the AFW and FLV traits (Table 2). This indicates that the lines have significant variability, from genetic causes, linked to these traits, enabling genetic progress by selection. In turn, FF, FLF, and SSC traits gave the lowest estimates of genotypic variance, revealing that they were influenced predominantly by environmental conditions, as seen in their residual variances (Falconer and Mackay 1989).

The magnitude of the heritability estimates of the traits analyzed suggest a structure of correlation between phenotype and genotype that may provide a favorable scenario for selection (Alves et al. 2019). In terms of heritability, what was seen in the F_5 lines is a more favorable scenario for selection average fruit weight and flesh volume traits since most of the variability comes from genetic causes.

The low heritability estimates may be attributed not only to environmental circumstances but also to the structure of the population being evaluated (Barros et al. 2017; Falconer and Mackay 1989; Moreira et al. 2019; Pinto et al. 2013; Resende et al. 2016). The F_5 lines showed the lowest expectations of response to selection for FF, FLF, and SSC, given that this population was derived from a biparental cross belonging to the same heterotic group and that there is probably low allelic variability for the physical-chemical traits concerned.

It is difficult to find genotypes that simultaneously express genetic gains of high magnitude for several traits in the breeding of papaya (Ide et al. 2009; Miranda et al. 2021). These authors explained that this difficulty is due to the presence of a negative correlation structure present between the traits considered in the selection, as observed in the correlogram with BLUP and phenotypic values (Fig. 4).

Cortes et al. (2019) state that the difficulty of selecting simultaneously papaya progenies with a high magnitude of selection gains relies on the difference in the magnitudes of heritability of the traits involved in the selection process. It was difficult to find genotypes that presented a high magnitude of gains for fruit quality and other traits in the present study with F_5 lines since the traits FF, FLF, and SSC had low heritability estimates when compared to the others.

One of the main advantages of using selection indices is related to the weighting of higher weights for the traits that showed low genotypic variation, because according to the genetic parameters, these traits would not present satisfactory gains. Among the main traits related to fruit quality (AFW, FF, FLF and SSC) only AFW showed high genotypic variability, reflecting a high proportion of heritability and greater genetic gain obtained with the selection. According to Miranda et al. (2021), assigning equivalent weights to firmness (FF and FLF) and SSC in selection index makes it possible to obtain positive genetic gains for the three traits in papaya breeding, even if they present a negative correlation.

Another important point is genetic assessment based on REML/BLUP has received special attention because of the potential for outstanding genetic progress and great accuracy in the selection process (Lima and Silva et al. 2017). This way, the genetic-statistical procedure of mixed models via REML/BLUP has been a strategy adopted to rank genotypes considering the predicted genotypic values of various traits (Alves et al. 2019; Imai et al. 2016; Lima and Silva et al. 2017; Moreira et al. 2019; Pinto et al. 2013). The most indicated practice in papaya breeding programs is, however, the use of selection indexes, which, together with the predicted genotypic values (BLUP), are more efficient as a strategy to obtain genotypes with favorable responses to the maximum number of traits in a combined selection (Cortes et al. 2019; Ramos et al. 2014).

A total of 29 lines were selected as superior for fruit quality with 'Formosa' pattern using the PGVI index and a selection intensity of 30%. From this selection, these promising lines may be used as varieties on their own or as parents in hybrid combinations. This choice will depend on the specific combining ability (SCA) for each trait.

Estimates of SCA refer to nonadditive interactions arising from gene complementation between the parents, enabling the prediction of genetic gain responses with heterotic effect. The SCAs show the existence of dominance deviations. When positive, they lead to genes that increase trait expression; when negative, they lead to similarly dominant genes that reduce the expression (Vettorazzi et al. 2021). Hence, the SCA estimates indicate which lines should be considered excellent options for the development of hybrids. Besides, these superior lines can also compose a new population in recurrent selection programs, allowing the continuity of the genetic advance in papaya breeding.

Moreover, it is expected that opportunities will be exploited to benefit farmers with the development of hybrid combinations from the superior lines selected here, which belong to the heterotic group 'Formosa', reducing the dependence on seeds imported from Taiwan and increasing papaya exports, especially in European and North American markets, where there is high consumption of large fruits, meeting consumer preferences for fruit quality.

It should also be emphasized that, in breeding programs, both genetic parameters and selection efficiency are inherent to the population involved and to the experimental conditions established for a particular study.

CONCLUSION

The genetic variability among F_5 lines, the proportion of heritability, and BLUPS accuracy were the main factors that enabled genetic gains with the combined selection strategy weighted by agronomic weights. It should be efficient to obtain superior genotypes with favorable responses to the highest number of traits regarding fruit quality.

AUTHORS' CONTRIBUTION

Conceptualization: Pereira, M. G.; **Methodology:** Pereira, M. G.; Ramos, H. C. C.; Santa-Catarina, R.; **Investigation:** Santana, J. G. S.; Vettorazzi, J. C. F.; Santa-Catarina, R.; Miranda, D. P.; Pirovani, A. A. V.; Poltronieri, T. P. S. ;Azevedo, A. O. N.; Duarte, R. P.; Bohry, D.; **Formal Analysis:** Santana, J. G. S.; **Writing – Original Draft:** Santana, J. G. S. and Ramos, H. C. C.; **Writing – Review and Editing:** Santana, J. G. S.; Ramos, H. C. C. ; Vettorazzi, J. C. F.; Santa-Catarina, R.; Miranda, D. P.; **Funding Acquisition:** Pereira, M. G. and Ramos, H. C. C.; **Resources:** Pereira, M. G. and Ramos, H. C. C.; **Supervision:** Pereira, M. G. and Ramos, H. C. C.

DATA AVAILABILITY STATEMENT

All dataset were generated and analyzed in the current study.

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