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Phenotypic evaluation to determine genetic merit in feijoa fruits

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Abstract – The objective of this work was to determine the viability of visual phenotypic evaluation to rank feijoa (*Feijoa sellowiana*) genotypes. A group of 59 feijoa genotypes was evaluated for length, diameter, and ellipsoid volume, as well as through a visual scale proposed by the authors. The best linear unbiased predictor (BLUP) was also used to estimate genetic parameters and rank the genotypes. The obtained results were compared to those of the phenotypic evaluation. All morphometric traits presented genetic variability, with moderate estimates of heritability. However, the fruit length trait showed the highest ratio between the genetic and experimental coefficients of variation, making it the most promising for selection based on fruit size. A common selection of 42 genotypes was possible using both BLUP and the visual scale, resulting in a coincidence of 89.3% between both methods. Therefore, phenotypic evaluation to determine genetic merit can be implemented in the early stages of feijoa breeding programs.

Index terms: best linear unbiased predictor (BLUP), fruit size, heritability, selection, visual scales.

Avaliação fenotípica para determinar o mérito genético em frutos de goiabeira-serrana

Resumo – O objetivo deste trabalho foi determinar a viabilidade da avaliação fenotípica visual para ranquear genótipos de goiabeira-serrana (*Feijoa sellowiana*). Um conjunto de 59 genótipos de goiabeira-serrana foi avaliado quanto a comprimento, diâmetro e volume da elipse, além de por meio de escala visual proposta pelos autores. O melhor preditor linear não viesado (BLUP) também foi utilizado para estimar parâmetros genéticos e classificar os genótipos. Os resultados obtidos foram comparados com os da avaliação fenotípica. Todos os caracteres morfométricos exibiram variabilidade genética, com estimativas moderadas de herdabilidade. Porém, o caráter comprimento de fruto apresentou a maior razão entre os coeficientes de variação genética e o experimental, sendo o mais promissor para seleção com base no tamanho de fruto. Foi possível uma seleção comum de 42 genótipos via BLUP e escala visual, o que resultou em uma coincidência de 89,3% entre os dois métodos. Portanto, a avaliação com base no fenótipo para determinar o mérito genético pode ser implementada nas fases iniciais de programas de melhoramento de goiabeira-serrana.

Termos para indexação: melhor preditor linear não viesado (BLUP), tamanho de fruto, herdabilidade, seleção, escalas visuais.

Introduction

Feijoa [*Feijoa sellowiana* (O.Berg) O.Berg], also commonly known as pineapple guava, is a fruit-bearing species originated from the Brazilian flora, specifically from the highlands of Southern Brazil (Santos et al., 2017). Its fruits are well accepted by consumers, emphasizing their potential for commercial use, which can lead to the popularization of their cultivation and conservation (Santos et al., 2021).

Despite this potential, the cultivation of feijoa in an agronomic system is still incipient, with a lack of production standardization due to the high genetic variability among the plants of this species (Souza et al., 2018). However, this genetic variability is essential for traits of interest, especially fruit yield, aiming to obtain superior new genotypes to expand cultivation areas and make the crop more commercially attractive to both producers and consumers (Costa et al., 2025). Once identified, the notable differences among genotypes, particularly regarding fruit size, rind thickness, sweetness, and acidity, can be used for the development of new and improved cultivars (Al-Harthy, 2010).

Generally, in the guava market, there is a preference for larger fruits associated with a greater weight (Souza et al., 2018). Given the variability in the forms and attributes of fruits, their size most likely exhibits a quantitative inheritance, similar to that verified in other fruit-bearing plants (Rawandoozi et al., 2021). In this scenario, the common approach to determine genetic merit is through estimates of parameters such as heritability (Silva et al., 2015).

The use of more refined genetic-statistical procedures, such as the methodology of mixed linear models, can also be applied in parameter estimation. This methodology makes it possible to obtain detailed information through the best linear unbiased prediction (BLUP), with a smaller standard deviation, which distinguishes it from other conventional methods (McLean et al., 1991). Therefore, the use of this tool helps in the direct selection of plants based on genetic merit.

To assist in genotype screening, phenotypic evaluation based on visual scales can also be used to identify characteristics associated with crop productivity from the beginning of selection (Silva et al., 2023). A trait that can be determined through this methodology is fruit size, considering simple variables such as length, diameter, volume, and weight, all with an immediate visual appeal, as observed at producer fairs and among fruit consumers (Barbosa et al., 2023). For this evaluation, the breeder collects a set of morphometric variables in the field that must be measured in the laboratory and, subsequently, analyzed statistically (Yangaza et al., 2024). Therefore, this process is labor-intensive, especially when dealing with large genetic collections that present an extensive genetic variability (Borém & Miranda, 2013).

Although phenotypic evaluations may present a high value in pre-breeding and in the enrichment of conservation and genetic breeding collections, there is still a lack of studies exploring the applicability of this type of intuitive selection in the genetic breeding of feijoa. Furthermore, the aimed results can only be achieved if phenotype and genotype present a high correlation, even if it is not as apparent for quantitative traits due to temporary environmental effects (Vencovsky et al., 2012).

The objective of this work was to determine the viability of visual phenotypic evaluation to rank feijoa genotypes.

Materials and Methods

The study was carried out at the Agriculture Experimental Area of Universidade Federal de Santa Catarina (UFSC), located in the municipality of Curitibanos, in the plateau region of the state of Santa Catarina, Southern Brazil (27º16'26"S, 50º30'13"W, at 1,000 m above sea level). This region is situated within the Atlantic Forest biome, specifically in the mixed Ombrophilous Forest. Its climate is classified as Cfb according to Köppen (Wrege et al., 2011), with an average annual temperature of 14ºC and an average annual precipitation ranging from 1,600 to 1,900 mm (Alvares et al., 2013).

The fruits used for evaluation were obtained from a collection of feijoa specimens established in 2014 at UFSC, in the municipality of Florianópolis, in the state of Santa Catarina, Brazil; fruiting began in 2018. Each specimen represents a distinct genotype, originated from crosses carried out at the São Joaquim Experimental Station of Empresa de Pesquisa Agropecuária e Extensão Rural de Santa Catarina and from open-pollinated specimens, whose fruits were collected in the municipality of Curitibanos.

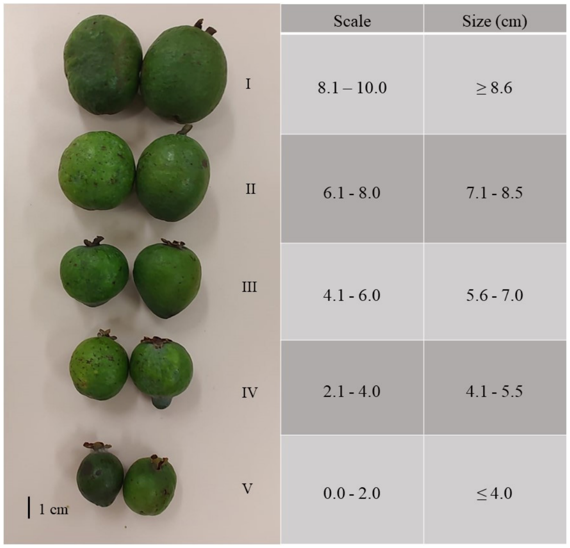
The individuals in the collection are arranged in rows, with a spacing of 3.0x4.0 m, under an agroecological production management (Brasil, 2003).

In March 2023, fruits were collected individually from 59 genotypes in the productive phase. These fruits were evaluated for the three following morphometric traits: length, distance between the point of attachment of the fruit peduncle and the opposite distal end, in centimeters; diameter, distance between the opposing points of the central width of the fruits, in centimeters, measured with a digital caliper; and elliptical volume, determined by the expression:

$$VE = \frac{(4 \times \pi) \times D \times \times (C/2)}{3},$$

where VE is the volume of the ellipse in cubic centimeters; and D and C are diameter and length, respectively, both in centimeters.

Additionally, the fruits were visually assessed using a visual scale proposed by the authors, ranging from 0 to 10 (Figure 1). These numbers correspond to the actual length of the fruits in centimeters, i.e., the highest range, from 8.1 to 10, for example, indicates fruits with a length of 8.6 cm or greater. Nine untrained individuals used this scale to carry out phenotypic evaluations, recording their assessments to obtain averages for each genotype. Between five and ten fruits (replicate) of each genotype were evaluated by each evaluator, depending on fruit availability on the plant and evaluation conditions. The genotypes were ranked according to their average scores, based on the visual scale.



	Scale	Size (cm)
I	8.1 – 10.0	≥ 8.6
II	6.1 - 8.0	7.1 - 8.5
III	4.1 - 6.0	5.6 - 7.0
IV	2.1 - 4.0	4.1 - 5.5
V	0.0 - 2.0	≤ 4.0

Figure 1. Scale proposed by the authors for visual evaluation of feijoa (*Feijoa sellowiana*), as well as the corresponding sizes equivalent to fruit length in centimeters. Photo by Ingrid Maira de Freitas.

The morphometric data of the fruits were subjected to the deviance analysis according to Resende (2002). The significance of the difference in the fit of different models was tested using the likelihood ratio test proposed by Wilks, defined by the model: $\lambda = 2[\text{Log}_e L_{p+1} - \text{Log}_e L_p]$, where L_{p+1} and L_p correspond to the peaks of the likelihood function associated with the full and reduced models, respectively. Therefore, λ should be compared with the probability density function for a given number of degrees of freedom and error probability (Dobson, 1990).

The variance components were estimated using the restricted maximum likelihood (REML) method, ideal for unbalanced data, as in the case of the present work, and phenotypic and genotypic values were predicted using the BLUP (Resende, 2002). Statistical model 83 of the SELEGEN software (Resende, 2016) was applied, since it is the model used for a completely randomized design for an evaluation at a single location and in a single harvest. The used statistical model was expressed as: $y = Xu + Wg + e$, where: y is the data vector, u is the scalar representing the overall mean (assumed as fixed), g is the vector of genotypic effects (assumed as random), e is the vector of errors or residuals (random), and X and W represent the incidence matrices for these effects. The genetic correlation between the analyzed traits was also estimated. The SELEGEN-REML/BLUP statistical software was used in the data analysis.

To detect the genetic variability of the traits in the studied population, the $\hat{b}$ index was calculated using the formula: $\hat{b} = CVgi/CVe$, which represents the ratio between the coefficient of genetic variation (CVgi) and the coefficient of experimental variation (CV_e), unaffected by the mean of the trait. The average components (individual BLUPs), founded on the permanent phenotypic effect of the 59 evaluated genotypes, were obtained with the aim of classifying/ranking and identifying superior genotypes for each variable. To determine the genotypic values for each evaluated individual, each genotypic effect was added to the overall mean of the experiment. Therefore, genetic gain equates to the average of the predicted genetic effect vectors for each selected genotype, and the overall mean plus genetic gain resulted in an improved population mean for each variable. The relative performance of each genotype was determined using the ratio between the improved population means and the mean of the genotype with the highest genetic value.

The rankings obtained using the BLUP method and the visual evaluation of each variable were compared to determine commonly highlighted genotypes. The genotypes selected using the BLUP method were those in which the genotypic value for each variable showed a relative performance greater than 80%. For genotype selection based on visual evaluation, the considered criteria were: minimum classification of III on the proposed scale, i.e., minimum fruit length of 5.6 cm (Figure 1); and relative performance greater than 80% for one of the evaluated morphometric variables.

Results and Discussion

The deviance analysis revealed that the 59 evaluated feijoa genotypes differed in terms of fruit length, diameter, and elliptical volume (Table 1). The values of the likelihood ratio test indicated that both genotypic and environmental effects were significant for all variables, suggesting that the full model is more suitable for fitting the data than the reduced model. Therefore, the former type of model is the most appropriate for genetic estimation and, therefore, has been used for the selection of other perennial species such as black wattle (*Acacia mearnsii* De Wild.) by Bisognin et al. (2022) and gray laurel [*Cordia trichotoma* (Vell.) Steud.] by Avinio et al. (2023). In addition, the significance of the likelihood ratio test is the first indication of the existence of genetic variability in fruit dimensions among the evaluated feijoa genotypes.

For the three studied variables, the values obtained for genotypic variance and residual variance were close, indicating that genetic and environmental factors contribute, in a balanced manner, to the phenotypic variation of these traits. The balanced contribution of the environmental component to phenotypic variance resulted in heritability estimates considered moderate in magnitude for length, diameter, and elliptical volume. From this perspective, it is evident that these variables are shaped by multiple genes and are substantially influenced by environmental factors. Similarly, Degenhardt et al. (2002) found that environmental effects significantly impacted traits such as fruit diameter and length of a same species, with variability between years. This pattern of a greater environmental variance affecting estimated heritability has also been verified in other perennial fruit species, such as fig (*Ficus carica* L.) by Almeida et al. (2022), passion fruit (*Passiflora edulis* Sims) by Preisigke et al. (2020), peach [*Prunus persica* (L.) Batsch] by Rawandoozi et al. (2021), and mango (*Mangifera indica* L.) by Paranhos et al. (2022).

The morphometric characteristics of the analyzed feijoa fruits presented moderate to high heritability values. Heritability was high for fruit length, but moderate for diameter and volume according to Resende (2015). In a study conducted by Degenhardt et al. (2002), fruit diameter showed a repeatability (heritability) of 0.63, which was higher than that obtained for fruit length (0.29), an unexpected result

Table 1. Deviance analysis and genetic parameters (obtained through individual restricted maximum likelihood) estimated for fruit length, fruit diameter, and ellipse volume of feijoa (*Feijoa sellowiana*) genotypes.

Variable(1)	Length (cm)	Diameter (cm)	Ellipse volume (cm^{-3})
Effect			
H^2	118.13	-168.9	4,179.53
Full model	-90.85	-335.35	3,987.58
LRT	208.98**	166.45**	191.95**
Genetic parameter			
Vg	0.24	0.12	1,321.96
Ve	0.23	0.14	1,434.14
Vf	0.47	0.26	2,756.10
h^2g	0.52±0.09	0.47±0.09	0.48±0.09
CVgi%	12.91	10.12	32.17
CVe%	12.47	10.67	33.50
$\hat{b}$	1.04	0.95	0.96
Overall mean	3.82	3.47	113.03

(1)H^2, model without genotype effect; LRT, likelihood ratio test; Vg, genotypic variance; Ve, residual variance; Vf, individual phenotypic variance; h^2g, broad-sense heritability of individual plots; CVgi%, genotypic coefficient of variation in percentage; CVe%, residual coefficient of variation in percentage; and $\hat{b}$, ratio between the coefficient of genetic variation and the coefficient of environmental variation. **Significant at 0.01 probability according to the chi-squared test with one degree of freedom.

given that the authors considered these traits to be similar in their variation within the evaluated population. Moderate to high values of heritability and genetic variation are associated with a high genetic variability and selective precision, as well as with the potential for a successful selection of accessions with desirable agronomic traits (Sayd et al., 2019).

Fruit length showed the highest heritability value of 52%, as well as a genetic variance slightly exceeding environmental variance, indicating that this variable has the greatest potential for use in the selection of feijoa genotypes. Therefore, this trait is relevant for fruit selection since morphometric variables associated with fruit yield are preferred for the evaluation of fruit-bearing species. Moreover, the measurement of fruit length is operationally simple compared to that of elliptical volume or total weight, which facilitates its large-scale application, especially in participatory or agroecological breeding programs.

There were significant genetic correlations between fruit length and elliptical volume (r = 0.95) and fruit diameter (r = 0.61). This reveals the potential of fruit length as a trait for the selection of feijoa genotypes, resulting in indirect genetic gains for other yield components. For peach, fruit weight and length were also strongly correlated (r = 0.92), a predictable result given that both are fruit size measures (Rawandoozi et al., 2021).

When examining the coefficients of variation in isolation, the CVgi (%), which measures pure genetic variation unaffected by the trait mean, exceeded 7% for all variables (Table 1). In addition to being considered high by Sebbenn et al. (1998), this value supports the existence of genetic variability among the studied genotypes and the potential for selection and genetic improvement of feijoa for fruit size. Furthermore, the CVe (%) was relatively low for fruit length and diameter when compared to the values above 20% considered high by Couto et al. (2013). This is an indicative that fruit shape is a genetic parameter with a weaker environmental effect than the other traits.

Only fruit length displayed a $\hat{b}$ index greater than 1, which may result in selection gains. According to Vencovsky (1978), indices greater than 1 are attributed to a high genetic variance i.e., are likely minimally influenced by the environment, indicating a high potential for a successful selection. That index considers the environmental effect and detects more precisely the specific genetic variability of a trait through the CVgi/CVe ratio (Silva Júnior et al., 2022). Therefore, it provides an estimate of the proportion of phenotypic variation attributable to genetic variation relative to non-genetic variation (Holland, 2006), and can also be used as an additional parameter to indicate significant genetic gains through the selection of superior genotypes (Cruz et al., 2012). In this sense, the CVgi/Cve ratio can serve as an index to facilitate the selection of genotypes for a specific trait (Leite et al., 2016).

Considering fruit length as the most appropriate morphometric trait for genotype selection, the 59 feijoa genotypes were ranked based on average components, that is, on individual BLUPs. To assess the potential of visual phenotypic evaluation, the genotypes were also ranked according to the scores assigned to each of them through this method.

Based on the BLUP values, 47 genotypes exhibited a relative performance greater than 80%, resulting in a selection intensity of 79.7% (Table 2). Using visual phenotyping by score assignment based on fruit length, 42 out of these 47 genotypes were also chosen. This indicates an 89.3% of coincidence between both evaluation methods. This value is in agreement with that obtained by Moreira et al. (2019), who compared selection indices based on phenotypic and genotypic values and observed up to an 80% correspondence between selection methods for papaya (*Carica papaya* L.) fruit characteristics. Yamada et al. (2024) also applied this selection strategy to pineapple [*Ananas comosus* (L.) Merr.] genotypes for four fruit traits, reporting selection efficiency. Considering the phenotypic classification scale, genotypes 373/29-2A07 (ranking index - IC 48), C527X0403-14 (IC 54), Ntv-Vd-3R2 (IC 49), FS-nov15-4 (IC 53), and C527x0403-7 (IC 51) would not be selected and, therefore, do not match the genotypic classification.

The direct and indirect selection gains for fruit size according to visual assessment were slightly lower than those of 4.7 and 10.1% obtained via BLUP for fruit length and ellipse volume, respectively (Table 3). This result can be attributed to the low selection intensity applied within the population. The selection values observed in the present study were comparable to those of 6.24 to 4.99% and 28.70 to 22.64% for fruit weight per plant and fruit number, respectively, found in passion fruit (Preisigke et al., 2020).

Table 2. Ranking of feijoa (*Feijoa sellowiana*) genotypes for the fruit length trait according to best linear unbiased prediction (BLUP) and visual evaluation through rating scales(1).

Genotype	BLUP			Rating scale	
	g	RP (%)	RI	Size	RI
Ntv-Vd-2R2	1.15	100.0	1	8.58	1
CL-3	1.10	99.54	2	6.33	13
C04103X387-B	0.80	97.36	3	8.17	2
373A29-35	0.79	96.2	4	6.58	10
FS-out16-1	0.67	95.03	5	4.75	41
FS-nov15-3	0.65	94.17	6	5.00	35
C0403X527-17	0.59	93.41	7	6.83	6
FS-nov15-7	0.54	92.69	8	6.67	8
CL-7	0.52	92.09	9	5.92	17
527/35-2B45	0.51	91.59	10	5.75	19
Ntv-1	0.42	91.02	11	7.08	3
CL-5	0.35	90.44	12	5.42	26
373/29-2V38	0.23	89.76	13	5.58	23
522/14-2B27	0.23	89.16	14	6.87	5
C527X0403-10	0.19	88.60	15	6.67	7
FS-nov15-10	0.19	88.10	16	6.00	16
FS-nov15-6	0.18	87.65	17	6.17	15
FS-nov15-2	0.17	87.24	18	5.17	31
FS-nov15-12	0.16	86.87	19	4.83	38
C527X0403-6	0.16	86.53	20	6.48	12
C103X0403	0.14	86.21	21	4.67	43
C0403X527-15	0.14	85.92	22	6.50	11
527/35-2B11	0.14	85.65	23	5.08	34
Branc-36	0.14	85.40	24	5.33	28
373/29-2A07	0.14	85.18	25	4.17	48(2)
C527X0403-14	0.14	84.97	26	3.50	54(2)
Ntv-Vd-3R2	0.05	84.71	27	4.00	49(2)
C2316X387	0.04	84.46	28	5.50	24
C527X0403-2	0.03	84.22	29	6.65	9
C527X0403-1	0.00	83.97	30	4.67	42
FS-nov15-1	0.00	83.74	31	4.75	40
127/21-3A14	-0.02	83.51	32	5.58	22
FS-nov15-4	-0.06	83.28	33	3.67	53(2)
C527X387-1	-0.06	83.06	34	7.00	4
FS-nov15-9	-0.07	82.84	35	4.92	36
C527x0403-7	-0.09	82.62	36	3.92	51(2)
C527X387-2	-0.11	82.41	37	5.83	18
C527X387-3	-0.12	82.20	38	5.08	33
C527X0403-8t	-0.16	81.98	39	5.25	29
C527X0403-5	-0.17	81.76	40	5.12	32
CL-2	-0.19	81.55	41	5.42	25
C527X0403-4	-0.20	81.34	42	5.58	21
CL-4	-0.22	81.13	43	5.33	27
C527X0403-9	-0.22	80.94	44	6.17	14
FS-nov15-11	-0.32	80.70	45	5.25	30
C04103X387-A	-0.41	80.44	46	4.33	46
C527X0403-3	-0.42	80.18	47	5.58	20

(1)g, estimated predicted genotypic effect; RP, relative performance; and RI, size according to the rating scale and ranking index. (2)Genotypes that would not be selected by the phenotypic classification scale and, therefore, do not match the genotypic classification.

Table 3. Original mean (MO), improved mean (MM), selection gain (GS), and selection gain in percentage (GS%) for the variables: fruit length (CF), fruit diameter (DF), and ellipse volume (VE) of feijoa (*Feijoa sellowiana*) genotypes based on selection for length using the best linear unbiased predictor (BLUP) method and visual evaluation.

Variable	BLUP			Visual evaluation		
	CF (cm)	DF (cm)	VE (cm^3)	CF (cm)	DF (cm)	VE (cm^3)
MO	3.83	3.47	112.69	3.82	3.47	112.69
MM	4.01	3.58	125.33	4.01	3.58	125.14
GS	0.19	0.11	12.65	0.19	0.11	12.45
GS%	4.70	3.04	10.09	4.62	3.14	9.95

Although it is a subjective method, the field-based phenotypic evaluation shows substantial alignment with more accurate selection methods, resulting in important applications in pre-breeding and in the enrichment of germplasm banks and breeding populations through a facilitated rescue of genetic variability. This is an indicative that phenotypic selection is advantageous for the classification and selection of superior genotypes in populations of fruit species, since the collection and evaluation of a large number of fruits is comparatively time-consuming and expensive. In addition to capturing genetic variability that is potentially useful for breeding programs, phenotypic evaluation, alsow known as primary selection, is appropriate to avoid discarding target genotypes for the traits of interest (Yamada et al., 2024). Therefore, even though visual phenotypic evaluation based on fruit length scales does not replace traditional biometric methods, it shows potential as an additional tool that could facilitate the recovery of genotypes of interest for the enrichment of germplasm banks or be used in participatory breeding processes.

The observations presented here were made for a single harvest, which indicates the need for further studies aimed at assessing the repeatability of morphometric responses over time. Therefore, the results obtained in the present study do not yet constitute a validation of a selection method, but rather a strong indication of the potential use of phenotypic selections associated with genotypic selections for significant genetic gains in numerous crops of interest.

Conclusions

1. There is wide genetic variability in feijoa (*Feijoa sellowiana*) genotypes for fruit morphometric traits, among which fruit length presents the highest heritability value and potential as a variable for genotype selection.

2. Phenotypic evaluation is promising as a strategy for the selection of feijoa genotypes in the initial stages of breeding programs.

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No generative artificial intelligence (AI) was used in this study.

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The authors declare no conflicts of interest.

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