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Bayesian and classical approaches for the estimation of genetic parameters and coefficients of repeatability of acerola quality traits

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ABSTRACT. Although acerola (*Malpighia emarginata* DC.) is a tropical fruit of high interest due to its high ascorbic acid content and attractive sensory attributes, fruit production is characterized by high genetic variability. Additionally, the use of new biometric tools for acerola breeding is scarce. This study aimed to estimate genetic parameters and the coefficient of repeatability, as well as determine the optimal number of fruits for quality trait analyses in different acerola genotypes, using different approaches. Twenty-three (Experiment I) and thirty-five (Experiment II) genotypes were evaluated in a randomized block design with four replicates and three plants per plot. Twenty fruits per plant were harvested and evaluated for the following quality traits: diameter, mass, skin color (lightness, chroma and hue), firmness, soluble solids (SS), titratable acidity (TA), SS/TA ratio, and ascorbic acid content. The genetic parameters and the coefficient of repeatability were estimated for each experiment using classical and Bayesian methods. Both approaches achieved similar results on estimating variance components, genetic parameters and the coefficient of repeatability. Genetic parameters showed favorable conditions for acerola selection. The coefficient of repeatability was high for all acerola quality traits. A total of 17 fruits are required for the effective selection of acerola genotypes with an accuracy of 95%.

Keywords: *Malpighia emarginata* DC.; analysis of variance; genetic variability; fruit quality; repeated measures.

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Introduction

Acerola (*Malpighia emarginata* DC.) is a tropical fruit well-known for its high ascorbic acid (vitamin C) content, attractive red color and high antioxidant activity (Delva & Schneider, 2013; Prakash & Baskaran, 2018). Acerola is usually consumed as fresh fruit or processed products (Ferreira et al., 2022; Gualberto et al., 2021).

Currently, Brazil is the global largest producer, consumer and exporter of acerola, which is cultivated in all states, but it is mainly concentrated in the Northeast region, which has tropical climatic conditions that favor the growth and development of acerola trees (Ferreira et al., 2021). Acerola commercial cultivation in Brazil started in the 1980s and is still characterized by high genetic variability that results in irregular fruit production, low productivity and poor fruit quality as a result of propagation by seeds (Ritzinger, Kobayashi, & Oliveira, 2003).

With the rising global appeal for fruit consumption, there is a need for genetic breeding programs to select genotypes with high yield and fruit quality to meet the demands of consumers, growers and exporters. In the breeding programs of fruit crops, the determination of physicochemical quality traits and their related genetic parameters is indispensable to improve the efficiency of the selection of superior genotypes and to efficiently preserve germplasm resources (Liu, Qi, Song, Li, & Li, 2018; Zaouay & Mars, 2014). Furthermore, the use of biometric tools optimizes genetic selection and allows the estimation of experimental accuracy.

In this context, the coefficient of repeatability has been extensively adopted in genetic breeding programs of several fruit species (Alcoforado, Pedrozo, Mayer, & Lima-Primo, 2019; Andrade Júnior et al., 2020; Catarina et al., 2020; Diel et al., 2020; Jesus, Lima, Souza, & Girdardi, 2021; Malikouski et al., 2021). The coefficient of repeatability indicates whether multiple measurements of a quality trait in a genotype are the same over time or

space, based on the contribution of the genotype to the total variance (Cruz, Regazzi, & Carneiro, 2012), which allows the estimation of an optimal number of fruits to ensure high accuracy in quality trait analysis.

In acerola, a previous study by Lopes, Bruckner, Cruz, Lopes, and Freitas (2001) estimated the coefficient of repeatability in some quality traits of sixteen genotypes and found values between 0.03 and 0.94 using four classical methods of determination (analysis of variance, principal component analysis based on the correlation and covariance matrices and structural analysis). However, there are no studies estimating genetic parameters and the coefficient of repeatability in acerola using Bayesian inference.

Bayesian inference is a data analysis approach based on Bayes' theorem that has been shown to be more informative and flexible in obtaining the components of variance to estimate genetic parameters than classical approaches because it allows the assessment of small samples and the inclusion of prior information, increasing selection accuracy (Evangelista et al., 2022; Valadares et al., 2022).

This work aimed to estimate genetic parameters and the coefficient of repeatability, as well as determine the optimal number of fruits for quality trait analyses in different acerola genotypes, using different approaches.

Material and methods

Plant material and experimental conditions

Two experiments were carried out in an experimental orchard in Petrolina, Pernambuco State, Brazil, situated at 9°09' S latitude and 40°22' W longitude at an altitude of 365 m. The local climate is BSh (semi-arid), according to Köppen's classification (Alvares, Stape, Sentelhas, Gonçalves, & Sparovek, 2013), and the soil is classified as a distrophic Yellow Argisol (Santos et al., 2018). The orchard was established in 2012, and cultural practices including micro-sprinkler irrigation, fertilization, pruning, and control of weeds, pests and diseases were carried out according to technical recommendations (Ritzinger et al., 2003).

Both experiments were conducted under a randomized complete block design, with four replications each. The experimental unit was composed of three plants, which were grown at a spacing of 4.0 × 3.0 m. Experiments I and II were composed of 23 and 35 genotypes, respectively, which were cultivated in the Active Germplasm Bank at the Brazilian Agricultural Research Corporation (Tropical Semi-Arid Embrapa), Petrolina, Pernambuco State, Brazil.

A total of 20 acerolas at the red-ripe maturity stage were collected per plant in September 2018 (Experiment I) and September 2019 (Experiment II). The climatic data during the fruit set period, i.e., 20–25 days from anthesis to harvest, depending on the genotype (Maranhão Ribeiro et al., 2018; Santos et al., 2019), were monitored at the experimental orchard weather station. Meteorological data for September 2018 and September 2019 were as follows: minimum/mean/maximum temperature 21.1/27.6/34.8°C and 21.3/27.4/34.0°C, rainfall 0 and 0.04 mm, relative humidity 56.7 and 55.3%, global solar radiation 26.0 and 24.4 MJ m^{-2} day^{-1}, and reference evapotranspiration of 6.9 and 6.8 mm day^{-1}, respectively.

After harvest, the fruit was washed, sanitized, dried and selected based on uniformity of color, size, shape, and absence of damage and fungal infection. Ten fruit quality traits were analyzed, as described below.

Acerola quality traits

Fruit diameter (mm) was determined with 0.01 mm precision using a digital caliper model CD-6 CS (Mitutoyo Corp., Japan). The weight (g) was evaluated with an accuracy of 0.1 g using a semi-analytic balance model VI 2400 (Acculab, USA).

Skin color was analyzed with a colorimeter model CR-400 (Konica Minolta, Japan), according to the three-dimensional CIEL*C*h space, which records the following measurements: lightness (L^*), varying from black (0) to white (100); chroma (C^*), which indicates the color intensity; and hue angle ($°h$), which indicates the color, where 0/360° represents red, and 90°, 180°, and 270° represent yellow, green, and blue, respectively (Pathare, Opara, & Al-Said, 2013).

Pulp firmness (N) was measured with a texture analyzer (model TA.XT Plus, Stable MicroSystem, UK) equipped with a P/75 compression plate. Firmness was determined using the compression test, which recorded fruit resistance against 10% deformation in its volume.

Soluble solid (SS) content (%) was measured with an accuracy of 0.2% using a digital refractometer model PAL-1 (Atago, Japan). Titratable acidity (TA) (% of malic acid) was determined by titrating 5 mL of juice with 0.1 M NaOH until reaching a pH of 8.1. The SS/TA ratio was calculated for each sample by dividing the SS value by its respective TA value.

The ascorbic acid content (AsA, in mg 100 g^{-1}) was determined using Tillman's method according to AOAC method no. 942.15 (Association of Official Analytical Chemists [AOAC], 2016). One milliliter of juice was diluted in 100 mL of 0.5% oxalic acid, which was titrated with 0.02% 2,6-dichlorophenol indophenol (DFI).

Frequentist and Bayesian analysis

In each experiment, genetic parameters were estimated using the frequentist method, i.e., analysis of variance (ANOVA) and Bayesian inference. The model for the frequentist approach was $Y_{ij} = \mu + g_i + a_j + \varepsilon_{ij}$, where Y_{ij} is the observation of the i-th genotype in the j-th environment; μ is the overall mean; g_i is the random effect of the i-th genotype under the influence of the permanent environment; a_j is the fixed effect of the temporary environment in the j-th measurement; and ε_{ij} is the experimental error established by the temporary environmental effect of the j-th measurement in the i-th genotype (Cruz et al., 2012).

Bayesian inference was applied using Monte Carlo via Markov chains (MCMC) through the Gibbs sampling algorithm. Bayesian inference analysis was carried out using the *MCMCglmm* package (Hadfield, 2010) of R (R Foundation for Statistical Computing, Austria). A total of 1,500,000 iterations were generated per trait. A burn-in of 100,000 and a thin sampling interval of 1,000 iterations, where the variance components were obtained (*a posteriori* distribution), were used. Different degrees of freedom (nu) (0.002, 0.02, 2, 4, and 7) were adopted to test informative *priors* (Resende & Alves, 2020). Chain convergence was tested using the Geweke test without autocorrelation ($p > 0.05$) in the *boa* package (Smith, 2007). After confirming these criteria for each quality trait, genetic parameters and the coefficient of repeatability were estimated.

Estimation of genetic parameters and coefficient of repeatability

The following genetic parameters were estimated: genetic coefficient of variation ($CV_g = \sqrt{\sigma_g^2} / \mu \times 100$); residual (experimental) coefficient of variation ($CV_e = \sqrt{\sigma_e^2} / \mu \times 100$); variation index ($I_v$) = CV_g/CV_e; phenotypic variance (σ_p^2); genetic variance (σ_g^2); environmental (residual) variance (σ_e^2); and heritability ($h^2 = \sigma_g^2 / \sigma_p^2 \times 100$). The phenotypic and genotypic correlations were evaluated using a t-test at a 5% probability level.

The coefficient of repeatability (ρ) was estimated with four classical methods, according to Cruz et al. (2012): a) analysis of variance (ANOVA) ($\rho = \frac{\sigma_g^2}{\sigma_{g^{2+}}\sigma_e^2}$); b) principal component analysis based on a correlation matrix (PCA-Cor); c) principal component analysis based on a covariance matrix (PCA-Cov) (Abeywardena, 1972); and d) structural analysis based on a correlation matrix (SA-Cor) (Mansour, Nordheim, & Rutledge, 1981). The coefficient of repeatability from Bayesian inference was calculated using variance components and the same formula as the ANOVA method.

After the estimation of the coefficient of repeatability in all methods, for all quality traits, the minimum required number of fruit (η_0) for prediction of the real value of the individuals was calculated based on predefined R^2 values of 0.80, 0.85, 0.90, and 0.95, as follows:

$$\eta_0 = \frac{R^2 (1 - \rho)}{(1 - R^2) \rho}$$

Results

Genetic parameters of acerola genotypes determined by the frequentist method, represented by the genetic coefficient of variation, environmental coefficient of variation, variation index, phenotypic variance, genetic variance, environmental variance and heritability are shown in Table 1.

In Experiment I, the CVg ranged between 5.90 and 31.59%, while those for Experiment II were between 7.62 and 35.28%. In both experiments, lightness was the trait with the lowest CVg, while pulp firmness and fruit mass had the highest CVg in Experiments I and II, respectively. The CVg was higher in Experiment II for all quality traits, except for the pulp hue. In 80% of quality traits (considering both experiments together), CVg was higher than 10%, considering the desired variability for genotype selection.

The CVe ranged between 2.13 and 6.20% in Experiment I and between 2.19 and 5.32% in Experiment II. All CVe values were considered low (<10%). Fruit mass and pulp firmness were the traits with the lowest and highest CVe, respectively, in both experiments.

The heritability was very high (>80%) for all quality parameters. Fruit lightness had the lowest h^2 in Experiment I (84.58%) and hue in Experiment II (89.06%). The highest h^2 values were observed for fruit mass in both experiments, at 96.84 and 98.60% in Experiments I and II, respectively.

Table 1. Estimates of genetic parameters of 10 postharvest physicochemical fruit traits from acerola genotypes using the frequentist method.

Parameter	FD	FM	L	C	h	PF	SS	TA	SS/TA	AsA
Experiment I (23 genotypes)										
CV_g	8.04	25.47	5.90	10.08	18.36	31.59	8.83	14.31	17.54	19.05
CV_e	2.13	4.60	2.52	3.77	5.57	6.20	3.58	3.75	4.73	5.78
CV_g/CV_e	3.77	5.53	2.34	2.67	3.29	5.10	2.47	3.82	3.71	3.30
σ^2_p	3.78	2.79	5.82	19.26	26.19	12.99	0.78	0.046	1.42	105894
σ^2_g	3.53	2.70	4.92	16.89	23.98	12.51	0.67	0.043	1.32	96968
σ^2_e	0.25	0.09	0.90	2.36	2.21	0.48	0.11	0.003	0.10	8926
h^2	93.42	96.84	84.58	87.72	91.56	96.30	85.90	93.59	93.22	91.57
Experiment II (35 genotypes)										
CV_g	11.66	35.28	7.62	12.92	13.62	33.79	18.88	19.96	23.35	26.84
CV_e	2.19	4.21	2.54	3.09	4.78	5.32	3.08	3.97	4.26	4.98
CV_g/CV_e	5.33	8.38	3.00	4.18	2.85	6.35	6.13	5.03	5.48	5.39
σ_p^2	6.51	3.46	10.06	33.80	16.93	11.99	2.85	0.080	2.42	181331
σ_g^2	6.29	3.41	9.06	31.97	15.08	11.70	2.77	0.077	2.34	175304
σ_e^2	0.22	0.05	1.01	1.83	1.85	0.29	0.07	0.003	0.08	6027
h^2	96.60	98.60	89.99	94.59	89.06	97.58	97.40	96.20	96.78	96.68

FD: fruit diameter; FM: fruit mass; L: lightness; C: chroma; h: hue angle; PF: pulp firmness; SS: soluble solids; TA: titratable acidity; AsA: ascorbic acid. CV_g: genetic coefficient of genetic variation; CV_e: residual (experimental) coefficient of variation; σ_p^2: phenotypic variance; σ_g^2: genetic variance; σ_e^2: environmental (residual) variance; h^2: heritability.

Genetic parameters were also estimated using Bayesian inference and are shown in Table 2. The estimates of the variance components (σ_g^2 and σ_p^2) were higher using the Bayesian method, with a slight increase in CV_g and CV_e when compared to the frequentist method. CV_g ranges of acerola genotypes were 6.02–33.14% (Experiment I) and 7.92–36.50% (Experiment II) using the Bayesian approach.

Table 2. Estimates of genetic parameters of 10 postharvest physicochemical fruit traits from acerola genotypes using the Bayesian method.

Parameter	FD	FM	L	C	h	PF	SS	TA	SS/TA	AsA
Experiment I (23 genotypes)										
CV_g	8.32	26.22	6.02	10.48	19.16	33.14	9.04	14.52	18.06	19.43
CV_e	2.16	4.70	2.56	3.88	5.77	6.26	3.65	3.76	4.80	5.84
CV_g/CV_e	3.86	5.58	2.35	2.70	3.32	5.29	2.48	3.86	3.76	3.33
σ^2_p	4.03	2.95	6.04	20.75	28.50	14.25	0.82	0.05	1.50	109951
σ^2_g	3.78	2.86	5.12	18.24	26.13	13.76	0.70	0.044	1.40	100847
σ^2_e	0.25	0.09	0.92	2.51	2.37	0.49	0.11	0.003	0.10	9104
h^2	93.71	96.89	84.70	87.92	91.70	96.56	86.02	93.71	93.40	91.72
Experiment II (35 genotypes)										
CV_g	11.84	36.50	7.92	13.17	13.76	34.79	19.35	20.84	24.26	27.37
CV_e	2.26	4.38	2.65	3.15	4.92	5.45	3.10	4.03	4.39	5.15
CV_g/CV_e	5.23	8.34	2.98	4.18	2.80	6.38	6.25	5.17	5.53	5.32
σ^2_p	6.72	3.70	10.88	35.15	17.35	12.70	2.99	0.09	2.61	188765
σ^2_g	6.48	3.65	9.78	33.25	15.38	12.40	2.91	0.084	2.53	182316
σ^2_e	0.24	0.05	1.10	1.90	1.96	0.30	0.07	0.003	0.08	6449
h^2	96.47	98.58	89.90	94.59	88.68	97.61	97.50	96.40	96.83	96.58

FD: fruit diameter; FM: fruit mass; L: lightness; C: chroma; h: hue angle; PF: pulp firmness; SS: soluble solids; TA: titratable acidity; AsA: ascorbic acid. CV_g: genetic coefficient of genetic variation; CV_e: residual (experimental) coefficient of variation; σ_p^2: phenotypic variance; σ_g^2: genetic variance; σ_e^2: environmental (residual) variance; h^2: heritability.

In both experiments, h^2 was slightly higher when estimated by Bayesian inference for most quality traits. In Experiment I, the lowest and highest h^2 were 84.70 (lightness) and 96.89% (fruit mass), respectively. In Experiment II, h^2 varied between 88.68 (lightness) and 98.58% (hue).

The phenotypic and genotypic correlations for the ten quality traits in acerola genotypes are shown in Table 3. A total of 9 and 11 significant phenotypic correlations were found in Experiments I and II, respectively, with coefficient ranges (in modulus) of 0.41–0.96 and 0.34–0.90. Of these, two were strong correlations ($0.90 < |r| < 1.00$), nine were strong correlations ($0.60 < |r| \leqslant 0.90$), and nine were medium correlations ($0.30 < |r| \leqslant 0.60$). When considering genotypic correlations, nine significant correlations were found in Experiment I and eleven in Experiment II. Most significant genotypic correlations were classified as strong (50%) or medium (40%).

For both experiments, fruit mass and diameter had strong and positive phenotypic (0.96 and 0.90) and genotypic (0.97 and 0.91) correlation coefficients. All correlations between color traits (L^*, C^*, and $°h$) were significant and positive, and most of them were strong. Other significant phenotypic and genotypic correlations in both experiments included FM × (PF and SS) and L × AsA. As expected, the SS/TA ratio was

positively correlated with TA and negatively correlated with SS. In Experiment II, AsA was negatively correlated with SS/TA ratio, considering phenotypic (-0.47) and genotypic (-0.48) correlations.

Table 3. Estimates of phenotypic (upper diagonal) and genotypic (lower diagonal) correlations for 10 postharvest physicochemical fruit traits from acerola genotypes.

	FD	FM	L	C	h	PF	SS	TA	SS/TA	AsA
Experiment I (23 genotypes)										
FD		0.96**	-0.19	-0.27	-0.22	0.33	-0.36	-0.12	-0.08	-0.25
FM	0.97**		-0.15	-0.34	-0.09	0.43*	-0.41*	-0.03	-0.17	-0.28
L	-0.22	-0.18		0.77**	0.78**	0.13	-0.18	-0.02	-0.12	-0.52*
C	-0.32	-0.38	0.75**		0.58**	-0.06	0.05	-0.03	0.01	-0.12
h	-0.25	-0.10	0.77**	0.57**		0.33	-0.23	0.14	-0.25	-0.24
PF	0.36	0.44*	0.10	-0.09	0.32		-0.36	-0.16	-0.04	-0.03
SS	-0.38	-0.44*	-0.14	0.12	-0.22	-0.38		-0.15	0.61**	0.34
TA	-0.15	-0.04	-0.04	-0.04	0.14	-0.18	-0.19		-0.87**	0.37
SS/TA	-0.06	-0.17	-0.10	0.05	-0.24	-0.03	0.62**	-0.88**		-0.10
AsA	-0.27	-0.31	-0.62**	-0.16	-0.28	-0.05	0.38	0.40	-0.11	
Experiment II (35 genotypes)										
FD		0.90**	-0.11	-0.26	0.05	0.34*	-0.25	-0.16	-0.08	-0.23
FM	0.91**		-0.04	-0.24	0.18	0.36*	-0.26	-0.09	-0.15	-0.09
L	-0.12	-0.04		0.71**	0.72**	-0.31	-0.14	-0.18	0.07	-0.14
C	-0.27	-0.25	0.73**		0.68**	-0.41	0.03	-0.14	0.16	-0.05
h	0.06	0.20	0.74**	0.70**		-0.11	-0.12	-0.18	0.10	-0.11
PF	0.35*	0.36*	-0.34*	-0.43	-0.13		-0.08	0.24	-0.31	0.23
SS	-0.25	-0.26	-0.14	0.04	-0.11	-0.07		0.39*	0.47**	0.24
TA	-0.18	-0.08	-0.18	-0.15	-0.20	0.26	0.39*		-0.60**	0.72**
SS/TA	-0.08	-0.16	0.08	0.18	0.12	-0.32	0.48	-0.60**		-0.47**
AsA	-0.23	-0.09	-0.14	-0.05	-0.12	0.24	0.24	0.74**	-0.48**	

FD: fruit diameter; FM: fruit mass; L: lightness; C: chroma; h: hue angle; PF: pulp firmness; SS: soluble solids; TA: titratable acidity; AsA: ascorbic acid.* and **: significant correlations at 5 and 1% by the t-test, respectively.

Variation between quality traits was observed for the coefficient of repeatability, whose values ranged from 0.58 for lightness in Experiment I to 0.95 for fruit mass in Experiment II. Estimates of the coefficient of repeatability in our study are considered high since all quality traits except lightness in Experiment I showed a coefficient of repeatability greater than or equal to 0.60 (Table 4).

Table 4. Estimates of the coefficient of repeatability (ρ) and its coefficient of determination (R^2) for 10 postharvest physicochemical fruit traits from acerola genotypes.

Quality trait	ANOVA		PCA-Cor		PCA-Cov		AS-Cor		Bayesian	
	ρ	R^2	ρ	R^2	ρ	R^2	ρ	R^2	ρ	R^2
Experiment I (23 genotypes)										
FD	0.78	93.42	0.80	93.96	0.79	93.86	0.79	93.83	0.78	93.29
FM	0.88	96.84	0.90	97.24	0.90	97.22	0.90	97.22	0.88	96.79
L	0.58	84.58	0.62	86.90	0.58	84.80	0.61	86.29	0.53	81.94
C	0.64	87.72	0.68	89.44	0.67	88.97	0.67	89.09	0.61	86.27
h	0.73	91.56	0.75	92.47	0.75	92.28	0.75	92.29	0.72	90.95
PF	0.87	96.30	0.87	96.46	0.87	96.36	0.87	96.42	0.87	96.43
SS	0.60	85.90	0.66	88.45	0.61	86.11	0.65	87.90	0.56	83.74
TA	0.78	93.59	0.83	94.98	0.81	94.62	0.82	94.86	0.78	93.28
SS/TA	0.77	93.22	0.81	94.43	0.79	93.94	0.81	94.30	0.77	92.94
AsA	0.73	91.57	0.75	92.47	0.77	92.90	0.75	92.19	0.72	90.97
Experiment II (35 genotypes)										
FD	0.88	96.60	0.88	96.82	0.88	96.81	0.88	96.79	0.87	96.34
FM	0.95	98.60	0.95	98.66	0.95	98.63	0.95	98.66	0.94	98.56
L	0.69	89.99	0.72	91.29	0.70	90.13	0.72	90.99	0.66	88.77
C	0.81	94.59	0.82	94.93	0.82	94.64	0.82	94.84	0.80	94.29
h	0.67	89.06	0.70	90.25	0.69	89.92	0.68	89.65	0.63	87.23
PF	0.91	97.58	0.92	97.84	0.92	97.94	0.92	97.82	0.91	97.55
SS	0.90	97.40	0.91	97.61	0.91	97.61	0.91	97.59	0.90	97.44
TA	0.86	96.20	0.87	96.34	0.86	96.21	0.87	96.30	0.87	96.26
SS/TA	0.88	96.78	0.89	96.89	0.88	96.85	0.89	96.85	0.88	96.73
AsA	0.88	96.68	0.88	96.82	0.88	96.74	0.88	96.79	0.87	96.07

ANOVA: analysis of variance; PCA-Cor: principal component analysis based on correlation matrix; PCA-Cov: principal component analysis based on covariance matrix; SA-Cor: structural analysis based on correlation matrix; FD: fruit diameter; FM: fruit mass; L: lightness; C: chroma; h: hue angle; PF: pulp firmness; SS: soluble solids; TA: titratable acidity; AsA: ascorbic acid.

Classical methods for estimating the coefficients of repeatability showed very similar values. Bayesian estimation resulted in similar coefficients of repeatability for most quality traits. In a few quality traits, the Bayesian approach revealed values slightly lower than the other methods for this parameter, such as for SS in the first experiment (0.56 in Bayesian inference × 0.66 in PCA-Cor method).

Based on classical methods for estimating the coefficient of repeatability, the minimum required number of measurements for prediction of the real value of the individuals was 13.86, 11.46, 13.62, and 12.07 fruit in the first experiment, and 9.34, 8.21, 8.52, and 8.78 in the second experiment, considering ANOVA, PCA-Cor, PCA-Cov and SA-Cor methods, respectively, with an R^2 of 95%. For the same accuracy, the number of measurements estimated by Bayesian inference was 16.75 and 11.12 fruit in Experiments I and II, respectively. The diameter, mass, pulp firmness, titratable acidity and SS/TA ratio determined by the PCA-Cor and PCA-Cov approaches required the smallest number of fruit (<6) to predict the real value with a 95% accuracy for both experiments independent of the adopted approach (Figure 1).

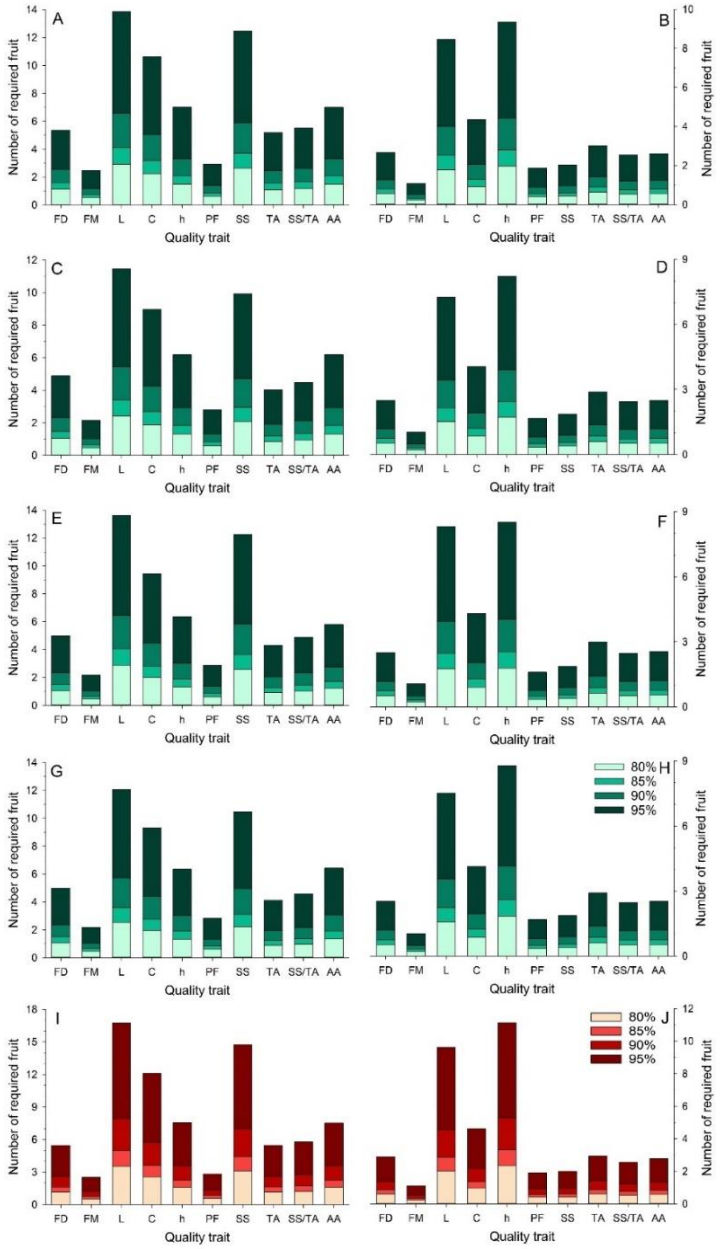

Figure 1. Number of fruit required for different R^2 values (80, 85, 90, and 95%) estimated by analysis of variance (A and B), principal component analysis based on correlation matrix (C and D), principal component analysis based on covariance matrix (E and F), structural analysis based on correlation matrix (G and H), and Bayesian inference (I and J) for 10 postharvest physicochemical traits of fruit from 53 acerola genotypes. Figures on the left represent Experiment I (23 genotypes), and those on the right represent Experiment II (35 genotypes). FD: fruit diameter; FM: fruit mass; L: lightness; C: chroma; h: hue angle; PF: pulp firmness; SS: soluble solids; TA: titratable acidity; AA: ascorbic acid.

Discussion

The commercial cultivation of acerola in Brazil started in the late 1980s and was mostly focused on the production of ascorbic acid (vitamin C) for the food and pharmaceutical industries. At that time, acerola trees were mainly propagated by seeds (sexual method), which resulted in a high genetic variability in Brazilian acerola orchards (Ritzinger, Ritzinger, Fonseca, & Machado, 2017) that has been observed until the present day and reported in studies that have evaluated the fruit quality of different acerola genotypes cultivated in different regions (Farinelli et al., 2021; Ferreira et al., 2021; Ferreira et al., 2022; Magalhães et al., 2018). In this context, the use of biometric tools is key for genotype characterization to optimize selection.

The assessment of genotypes in fruit breeding programs requires time, labor and expenses. Therefore, the study of experimental parameters, such as the coefficient of correlation and repeatability, can optimize genotype selection by estimating an ideal number of measurements required to ensure high quality characterization accuracy (Alcoforado et al., 2019; Jesus et al., 2021).

In this study, the high values of genetic coefficients of variance (CV_g) (> 10%) and high heritability (h^2) (> 60%) for most quality traits indicate favorable conditions for selection as a result of high genetic variability (Jesus et al., 2021). The environmental coefficient of variation (CV_e) was lower than 10% for the ten studied quality traits. When assessing quality parameters of eight acerola genotypes, Mariano-Nasser et al. (2017) found low CV_e values (3.0–7.9%) for skin lightness, soluble solids, titratable acidity and ascorbic acid and medium CV_e values (13.8–19.9%) for skin chroma and hue. Furthermore, the relative CV (CV_g/CV_e) was higher than 1 for all quality traits, which is recommended for genotype selection (Azevedo et al., 2021; Vasconcelos et al., 2020).

Fruit mass and pulp firmness presented the highest CV_g among all quality traits assessed in both experiments, confirming exploitable and desirable genetic variability. Larger and firmer fruit are strongly desirable in acerola breeding programs to improve pulp yield and facilitate processing, as well as to reduce fruit losses due to higher resistance to postharvest handling, storage, and shipping (Ferreira et al., 2022). However, lightness showed the lowest CV_g in both experiments. Lightness is part of the CIEL*C*h color space system that can range from dark (0) to light (100), which varies less than other color parameters, such as chroma and hue angle (Lazaro, Boada, Villarino, & Girbau, 2019).

Some significant correlations in acerola quality traits include those between both physical traits (diameter and mass) and between pairs of skin color parameters (lightness, chroma and hue), confirming previous results observed in 103 acerola trees (phenotypes) evaluated by Farinelli et al. (2021) and in 24 genotypes evaluated by Magalhães et al. (2018). The genetic coefficients of correlation for acerola were higher than phenotypic ones, which confirms the high genetic variability in the studied genotypes.

The coefficient of repeatability was estimated for each quality trait in each experiment using four classical methods and Bayesian inference. In all methods, the variance components (genetic and environmental variances) were the basis for calculating the coefficient of repeatability. A higher repeatability coefficient (close to 1) means that multiple measurements of a quality trait in one evaluated genotype are consistent in different times or spaces (Cruz et al., 2012), and thus, not many fruit are required to assess this trait with high accuracy in genetic breeding programs. A high coefficient of repeatability (>0.60) was observed for the ten quality traits, similar to Lopes et al. (2001) with 16 acerola genotypes evaluated for similar traits, including fruit diameter (0.88), mass (0.92), titratable acidity (0.81) and ascorbic acid (0.84).

The estimates of genetic parameters found in this study indicate similar results for different approaches (Bayesian × classical methods), which agrees with studies on kale (Brito et al., 2019) and physic nut (*Jatropha curcas* L.) (Evangelista et al., 2022). Some advantages of Bayesian inference in relation to frequentist determination of variance components (and consequently coefficients of repeatability) include the feasibility of using previous data information (*priori*), the lower sensitivity to outliers and lower data assumptions, such as experimental balance and high sample size (Singh, L-Yassin, & Omer, 2015), resulting in more accurate estimates of variance, as reported in guava (Silva et al., 2020) and soybean (Volpato et al., 2019).

Despite several studies on the genotypic variability of acerola quality, only a few studies have involved the evaluation of repeated measures in acerola breeding. Furthermore, Bayesian inference was applied for the first time as an alternative method for estimating genetic parameters in acerola.

Conclusion

Frequentist and Bayesian approaches achieved similar results in estimating variance components and genetic parameters of acerola quality traits. The coefficient of repeatability was high for all acerola quality

traits and varied little when estimated using five different methods. A total of 17 fruits are required for the effective selection of acerola genotypes with an accuracy of 95%.

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References

Abeywardena, V. (1972). An application of principal components analysis in genetics. *Journal of Genetics*, *61*, 27–51. DOI: https://doi.org/10.1007/BF02984099

Alcoforado, A. T. W., Pedrozo, C. Â., Mayer, M. M., & Lima-Primo, H. E. (2019). Repeatability of morpho-agronomic characters of *Theobroma grandiflorum* fruits. *Revista Brasileira de Fruticultura*, *41*(2), e142. DOI: https://doi.org/10.1590/0100-29452019142

Alvares, C. A., Stape, J. L., Sentelhas, P. C., Gonçalves, J. L. M., & Sparovek, G. (2013). Köppen's climate classification map for Brazil. *Meteorologische Zeitschrift*, *22*(6), 711–728. DOI: https://doi.org/10.1127/0941-2948/2013/0507

Andrade Júnior, V. C., Oliveira, A. J. M., Guimarães, A. G., Ferreira, M. A. M., Cavalcanti, V. P., & Fernandes, J. S. C. (2020). Repeatability and heritability of production characters in strawberry fruits. *Horticultura Brasileira*, *38*(1), 89–93. DOI: https://doi.org/10.1590/s0102-053620200114

Association of Official Analytical Chemists [AOAC]. (2016). *Official methods of analysis of AOAC International* (20th ed.). Rockville, MD: AOAC International.

Azevedo, C. V. G., Val, B. H. P., Araújo, L. C. A., Juhász, A. C. P., Di Mauro, A. O., & Unêda-Trevisoli, S. H. (2021). Genetic parameters of soybean populations obtained from crosses between grain and food genotypes. *Acta Scientiarum. Agronomy*, *43*(1), e46968. DOI: https://doi.org/10.4025/actasciagron.v43i1.46968

Brito, O. G., Andrade Júnior, V. C., Azevedo, A. M., Donato, L. M. S., Silva, L. R., & Ferreira, M. A. M. (2019). Study of repeatability and phenotypical stabilization in kale using frequentist, Bayesian and bootstrap resampling approaches. *Acta Scientiarum. Agronomy*, *41*(1), e42606. DOI: https://doi.org/10.4025/actasciagron.v41i1.42606

Catarina, R. S., Pereira, M. G., Vettorazzi, J. C. F., Cortes, D. F. M., Poltronieri, T. P. S., Azevedo, A. O. N., ... Viana, A. P. (2020). Papaya (*Carica papaya* L.) S1 family recurrent selection: Opportunities and selection alternatives from the base population. *Scientia Horticulturae, 260*, 108848. DOI: https://doi.org/10.1016/j.scienta.2019.108848

Cruz, C. D., Regazzi, A. J., & Carneiro, P. C. S. (2012). *Modelos biométricos aplicados ao melhoramento genético* (4. ed.). Viçosa, MG: Editora UFV.

Delva, L., & Schneider, R. G. (2013). Acerola (*Malpighia emarginata* DC): production, postharvest handling, nutrition, and biological activity. *Food Reviews International*, *29*(2), 107-126. DOI: https://doi.org/10.1080/87559129.2012.714433

Diel, M. I., Lúcio, A. D., Olivoto, T., Pinheiro, M. V. M., Krysczun, D. K., Sari, B. G., & Schmidt, D. (2020). Repeatability coefficients and number of measurements for evaluating traits in strawberry. *Acta Scientiarum. Agronomy*, *42*(1), e43357. DOI: https://doi.org/10.4025/actasciagron.v42i1.43357

Evangelista, J. S. P. C., Peixoto, M. A., Coelho, I., Alves, R., Resende, M. D. V., Silva, F. F., ... Bhering, L. L. (2022). Genetic evaluation and selection in *Jatropha curcas* through Frequentist and Bayesian inferences. *Bragantia*, *81*, 1-12. DOI: https://doi.org/10.1590/1678-4499.20210262

Farinelli, D., Portarena, S., Silva, D. F., Traini, C., Silva, G. M., Silva, E. C., ..., Villa, F. (2021). Variability of fruit quality among 103 acerola (*Malpighia emarginata* D. C.) phenotypes from the subtropical region of Brazil. *Agriculture, 11*(11), e2722. DOI: https://doi.org/10.3390/agriculture11111078

Ferreira, I. C., Silva, V. P., Vilvert, J. C., Souza, F. F., Freitas, S. T., & Lima, M. S. (2021). Brazilian varieties of acerola (*Malpighia emarginata* DC.) produced under tropical semi-arid conditions: Bioactive phenolic compounds, sugars, organic acids, and antioxidant capacity. *Journal of Food Biochemistry*, *45*(8), e13829. DOI: https://doi.org/10.1111/jfbc.13829

Ferreira, M. A. R., Vilvert, J. C., Silva, B. O. S., Ferreira, I. C., Souza, F. F., & Freitas, S. T. (2022). Multivariate selection index of acerola genotypes for fresh consumption based on fruit physicochemical attributes. *Euphytica, 218*(25). DOI: https://doi.org/10.1007/s10681-022-02978-1

Gualberto, N. C., Oliveira, C. S., Nogueira, J. P., Jesus, S., Caroline, H., Araujo, S., ... Narain, N. (2021). Bioactive compounds and antioxidant activities in the agro-industrial residues of acerola (*Malpighia emarginata* L.), guava (*Psidium guajava* L.), genipap (*Genipa americana* L.) and umbu (*Spondias tuberosa* L.) fruits assisted by ultrasonic or shaker. *Food Research International*, *147*, 110538. DOI: https://doi.org/10.1016/j.foodres.2021.110538

Hadfield, J. D. (2010). MCMC methods for multi-response generalized linear mixed models: the MCMCglmm R package. *Journal of Statistical Software*, *33*(2), 1–22. DOI: https://doi.org/10.18637/jss.v033.i02

Jesus, O. N., Lima, L. K. S., Souza, P. U., & Girardi, E. A. (2021). Genetic parameters, correlation and repeatability of agronomic characters of yellow passion fruit genotypes in three harvest cycles. *Bragantia*, *80*, e1621. DOI: https://doi.org/10.1590/1678-4499.20200294

Lazaro, A., Boada, M., Villarino, R., & Girbau, D. (2019). Color measurement and analysis of fruit with a battery-less NFC sensor. *Sensors*, *19*(7). DOI: https://doi.org/10.3390/s19071741

Liu, C., Qi, X., Song, L., Li, Y., & Li, M. (2018). Species identification, genetic diversity and population structure of sweet cherry commercial cultivars assessed by SSRs and the gametophytic self-incompatibility locus. *Scientia Horticulturae, 237*, 28–35. DOI: https://doi.org/10.1016/j.scienta.2018.03.063

Lopes, R., Bruckner, C. H., Cruz, C. D., Lopes, M. T. G., & Freitas, G. B. (2001). Repetibilidade de características do fruto de aceroleira. *Pesquisa Agropecuária Brasileira, 36*(3), 507–513. DOI: https://doi.org/10.1590/S0100-204X2001000300015

Magalhães, D. S., Rufni, J. C. M., Alburquerque, A. S., Viol, R. E., Fagundes, M. C. P., & Menezes, T. P. (2018). Genetic diversity among accessions of acerola based on the quality of fruits. *Comunicata Scientiae*, *9*(2), 133–141. DOI: https://doi.org/10.14295/CS.v9i2.2961

Malikouski, R. G., Peixoto, M. A., Morais, A. L., Elizeu, A. M., Rocha, J. R. A. S. C., Zucoloto, M., & Bhering, L. L. (2021). Repeatability coefficient estimates and optimum number of harvests in graft/rootstock combinations for 'tahiti' acid lime. *Acta Scientiarum. Agronomy*, *43*(1), e51740. DOI: https://doi.org/10.4025/actasciagron.v43i1.51740

Mansour, H., Nordheim, E. V., & Rutledge, J. J. (1981). Estimators of repeatability. *Theoretical and Applied Genetics*, *60*(3), 151–156. DOI: https://doi.org/10.1007/BF00264520

Maranhão Ribeiro, C. M. C., Sousa, T. P. A., Holschuh, H. J., Ribeiro, M. T. J. B., Silva, S. M., & Maciel, M. I. S. (2018). Fruit development and ripening of acerola 'Okinawa' cultivar. *Acta Horticulturae, 1198*, 199–204. DOI: https://doi.org/10.17660/ActaHortic.2018.1198.32

Mariano-Nasser, F. A. D. C., Nasser, M. D., Furlaneto, K. A., Ramos, J. A., Vieites, R. L., & Pagliarini, M. K. (2017). Bioactive compounds in different acerola fruit cultivares. *Semina: Ciências Agrárias*, *38*(4), 2505–2514. DOI: https://doi.org/10.5433/1679-0359.2017v38n4Supl1p2505

Pathare, P. B., Opara, U. L., & Al-Said, F. A.-J. (2013). Colour measurement and analysis in fresh and processed foods: a review. *Food and Bioprocess Technology*, *6*, 36–60. DOI: https://doi.org/10.1007/s11947-012-0867-9

Prakash, A., & Baskaran, R. (2018). Acerola, an untapped functional superfruit: a review on latest frontiers. *Journal of Food Science and Technology*, *55*(9), 3373–3384. DOI: https://doi.org/10.1007/s13197-018-3309-5

Resende, M. D. V., & Alves, R. S. (2020). Linear, generalized, hierarchical, Bayesian and random regression mixed models in genetics/ genomics in plant breeding. *Functional Plant Breeding Journal*, *3*(2), 121–152. DOI: https://doi.org/10.35418/2526-4117/v2n2a1

Ritzinger, R., Kobayashi, A. K., & Oliveira, J. R. P. (2003). *A cultura da aceroleira*. Cruz das Almas, BA: Embrapa Mandioca e Fruticultura.

Ritzinger, R., Ritzinger, C. H. S. P., Fonseca, N., & Machado, C. F. (2017). Advances in the propagation of acerola. *Revista Brasileira de Fruticultura*, *40*(3), e928. DOI: https://doi.org/10.1590/0100-29452018928

Santos, C. P., Batista, M. C., Saraiva, K. D. C., Roque, A. L. M., Miranda, R. S., Silva, L. M. A., ... Costa, J. H. (2019). Transcriptome analysis of acerola fruit ripening: insights into ascorbate, ethylene, respiration,

and softening metabolisms. *Plant Molecular Biology*, *101*(3), 269–296. DOI: https://doi.org/10.1007/s11103-019-00903-0

Santos, H. G., Jacomine, P. K. T., Anjos, L. H. C., Oliveira, V. A., Lumbreras, J. F., Coelho, M. R., ... Cunha, T. J. F. (2018). *Brazilian Soil Classification System* (5th ed.). Brasília, DF: Embrapa.

Silva, F. A., Viana, A. P., Corrêa, C. C. G., Carvalho, B. M., Sousa, C. M. B., Amaral, B. D., ... Glória, L. S. (2020). Impact of Bayesian inference on the selection of *Psidium guajava*. *Scientific Reports*, *10*(1). DOI: https://doi.org/10.1038/s41598-020-58850-6

Singh, M., Al-Yassin, A., & Omer, S. O. (2015). Bayesian estimation of genotypes means, precision, and genetic gain due to selection from routinely used barley trials. *Crop Science*, *55*(2), 501–513. DOI: https://doi.org/10.2135/cropsci2014.02.0111

Smith, B. J. (2007). boa: an R package for MCMC output convergence assessment and posterior inference. *Journal of Statistical Software*, *21*(11), 1–37. DOI: https://doi.org/10.18637/jss.v021.i11

Valadares, N. R., Fernandes, A. C. G., Rodrigues, C. H. O., Brito, O. G., Paula Gomes, L. S., Magalhães, J. R., ... Azevedo, A. M. (2022). Bayesian approach to estimate genetic parameters and selection of sweet potato half-sib progenies. *Scientia Horticulturae*, *294*, 110759. DOI: https://doi.org/10.1016/j.scienta.2021.110759

Vasconcelos, U. A. A., Dias, L. A. D. S., Corrêa, T. R., Rosmaninho, L. B. C., Silva, D. R. M., & Zaidan, I. R. (2020). Estimates of genetic parameters and path analysis of crambe: An important oil plant for biofuel production. *Acta Scientiarum. Agronomy*, *42*(1), e42490. DOI: https://doi.org/10.4025/actasciagron.v42i1.42490

Volpato, L., Alves, R. S., Teodoro, P. E., Resende, M. D. V., Nascimento, M., Nascimento, A. C. C., ... Borém, A. (2019). Multi-trait multi-environment models in the genetic selection of segregating soybean progeny. *PLoS ONE*, *14*(4), e0215315. DOI: https://doi.org/10.1371/journal.pone.0215315

Zaouay, F., & Mars, M. (2014). Phenotypic variation and estimation of genetic parameters to improve fruit quality in Tunisian pomegranate (*Punica granatum* L.) accessions. *Journal of Horticultural Science and Biotechnology*, *89*(2), 221–228. DOI: https://doi.org/10.1080/14620316.2014.11513072