Euphytica (2023) 219:35
https://doi.org/10.1007/s10681-023-03163-8

Estimates of genetic parameters and the selection of table grape hybrids in semiarid regions of Brazil

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Received: 24 November 2022 / Accepted: 28 January 2023

Abstract The objective of this study was to estimate the repeatability coefficients, optimal number of harvests, and genetic gains and to select superior hybrids of table grapes for the development of cultivars adapted to semiarid conditions in Brazil. The mixed model methodology REML/BLUP was used to estimate the variance components and predict the genotypic values. Two hundred table grape hybrids were evaluated during six harvests at the Mandacaru Experimental Field in Embrapa Semiárido, Juazeiro, Bahia, Brazil. The experiment was implemented in the absence of an experimental design, with a single individual of each genotype. Twelve quantitative morphoagronomic variables were evaluated. The repeatability coefficients were as follows: 0.20 (yield), 0.18 (number of bunches), 0.37 (bunch length), 0.30 (bunch width), 0.47 (bunch weight), 0.60 (berry length), 0.68 (bunch diameter), 0.70 (berry weight), 0.14 (soluble solids content) and 0.13 (*ratio*). The accuracies obtained by performing *m* repeated measurements revealed that for berry characteristics, only one measurement was sufficient; two measurements were required for the length and weight of the bunch; three measurements were required for the bunch width; four measurements were required for the yield and five measurements for the number of bunches; for the soluble solids content and *ratio*, seven and six measurements were needed, respectively. Individual genotypic selection allows high genetic gains for bunch and berry traits and satisfactory gains for quality traits. In addition, three superior genotypes ('BRS Tainá', CPATSA 05.168 and CPATSA 79.100) were identified for eight traits simultaneously, with 'BRS Tainá' being identified as an apyrenic cultivar.

Keywords *Vitis* spp · REML/BLUP · Grapevine breeding · Repeatability coefficient · Selective accuracy

Introduction

Given its great economic importance, the superior quality of its existing cultivars and its high morphological and genetic diversity, constituting the basis of world viticulture, the species *Vitis vinifera* has attracted attention (Grassi and Lorenzis 2021). In Brazil, the main producing region of *Vitis vinifera* grapes is the Submédio São Francisco Valley, with a cultivated area of 9,990 hectares and production of 457 thousand tons (IBGE 2022).

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Published online: 13 February 2023

The breeding of perennial plants, such as grapes, has specific characteristics, such as the use of selected genetic material for several years, the use of repeated evaluations in each individual over time and the reduction in the survival rate of the experiments during its useful life, which tend to generate unbalanced data for use in the estimation of variance components (genetic parameters) and in the prediction of breeding values (Rodrigues et al. 2020).

Currently, the standard analytical procedure used for quantitative genetic approaches and the selection of perennial plants is restricted maximum likelihood/best unbiased linear prediction (REML/BLUP) (Sanchéz et al. 2017), an important tool for selecting superior genotypes. Mixed model methods (REML/BLUP) make it possible to analyze unbalanced data, in addition to estimating genetic parameters and accurately and unbiasedly predicting genotypic values, leading to the maximization of accuracy and genetic gain in the selection process (Viana and Resende 2014).

Thus, this methodology has been widely used in the context of plant breeding, especially for perennial plants. In fruit species, there are studies on peach (Della Bruna et al. 2012), passion fruit (Silva et al. 2017), mango (Maia et al. 2017), soursop (Sanchéz et al. 2017), and lemon (Malikouski et al. 2021), among others. In grapevines, its use has been described in studies conducted by Embrapa in the Submédio São Francisco Valley; these studies were related to the selection of vine progenies for table grapes (Leão et al. 2018; Sales et al. 2019) and the selection of grape hybrids resistant to the nematode *Pratylenchus brachyurus* (Santos et al. 2018; Santos et al. 2019).

The objective of this study was to estimate the repeatability coefficients, optimal number of harvests and genetic gains, select superior table grape hybrids and develop cultivars adapted to Brazilian semiarid conditions.

Materials and methods

This study was conducted at the Mandacaru Experimental Field of Embrapa Semiárido in Juazeiro, Bahia, Brazil, located at 09°24″S and 40°26″W at an altitude of approximately 375 m above sea level. According to Köppen, the climate of the region is classified as BSwh, which corresponds to a hot and dry tropical climate, and vertisol soil (Cunha et al. 2008).

Plant material

The vine plants used in this study were grafted onto IAC 572 rootstock and carried out in a overhead trellis system with a spacing of 3 × 1 m. Irrigation was performed daily in a drip system, and the volume of water applied was calculated based on the evapotranspiration of the crop.

The fertilization of the vines was based on foliar and soil analyses, following the recommendations for the crop, via fertigation. The management practices consisted of mowing, mixed pruning with canes and spurs, thinning, tying and weekly phytosanitary control. Hydrogen cyanamide (5%) was applied after pruning to break bud dormancy and to promote uniform sprouting. There was no application of gibberellic acid, selection or thinning of bunches. Six crops season were evaluated in the period from 2018 to 2021. The pruning and harvest dates are shown in Table 1.

The evaluated genotypes were 200 hybrids (F1) originating from 39 crosses between cultivars of *Vitis vinifera*, between interspecific hybrids and between *V. vinifera* and interspecific hybrids (Table 2). The

Table 1 Pruning and harvest dates of the evaluated cycles

Pruning	Harvest dates	Evaluated cycles
1	April 30, 2018	August 17, 2018 to a September 15, 2019
2	November 06, 2019	February 17, 2019 to March 17, 2019
3	March 04, 2020	June 02, 2020 to June 30, 2020
4	July 15, 2020	October 23, 2020 to November 20, 2020
5	December 16, 2020	March 08, 2021 to April 16, 2021
6	June 30, 2021	September 28, 2021 to October 29, 2021

Table 2 Male and female parents, cross code and number of genotypes evaluated per cross

Cross	Code	Number of genotypes evaluated
Thompson × Moscatel Nazareno	1	2
Maroo × BRS Isis	2	1
Maroo × Ferlongo	5	1
CG351 × A Dona	10	1
CG351 × CNPUV24	12	1
Thompson × Moscatel Alexandria	13	1
Thompson × Superior	14	4
Maroo × Superior	15	2
Superior × Moscatel Alexandria	19	2
Crimson × Moscato Noir	21	4
Crimson × Ferlongo	22	3
Maroo × Burdin	23	1
BRS Linda × Maroo	24	3
BRS Vitória × Maroo	26	1
A1581 × Maroo	28	24
CG351 × CG102295	31	7
BRS Linda × CG351	32	1
Maroo × Itália Melhorada	38	6
Catalunha × Feal	40	2
Catalunha × Superior	42	5
Feal × A1581	45	1
Feal × Princess	47	2
Júpiter × Maroo	49	60
Thompson × Sulfok Red Seedless	51	1
CG38049 × Superior	53	1
Grenache × Júpiter	60	1
Feal × Maroo	62	8
CG351 × Maroo	63	9
A1105 × Maroo	64	2
BRS Clara × Maroo	65	7
CG33716 × A Dona	67	8
Grenache × Superior	69	2
Ferlongo × Thompson	70	1
CNPUV8 × CG351	74	1
BRS Linda × Seyve Villard 12375	75	1
A Dona × CG351	76	6
BRS Isis × Maroo	79	16
Grenache × Thompson	89	1

parents used in crosses had one or more superior characteristics related to grape production or quality, such as bud fertility, yield, bunch size, berry size, soluble solids content and absence of seeds. Each hybrid was represented by a single grapevine, without experimental design or repetitions.

Evaluated characteristics

Twelve agronomic traits were evaluated for the 200 genotypes: yield—Y (kg/vine), number of bunches—NB (bunches/vine), bunch length—BuL (cm), bunch width—BuWi (cm), bunch weight—BuW (g), berry length—BeL (mm), berry diameter—BeD (mm), berry weight—BeW (g), soluble solids content—SS (%), titratable acidity—TA (%), *ratio*—SS/TA (dimensional), and seed dry weight—DW (mg).

The yield was obtained through the weight of all the bunches harvested per vine. For the number of bunches per vine, the bunches on the plant at the time of harvest were counted. The bunch characteristics were determined from the average of a sample composed of 5 bunches per plant. Berry characteristics were obtained by averaging a random sample of 10 berries from each of the five bunches previously evaluated. The soluble solids content (g 100 g^{-1}) was measured in a wort (AOAC 2010) using a portable digital refractometer. The titratable acidity (100 g tartaric acid mL^{-1}) was determined by titration with 0.1 N NaOH to the neutral point (AOAC 2010) using a manual titrator. The *ratio* was calculated as the ratio of soluble solids to titratable acidity.

The dry mass of the seeds was determined from a sample of 100 seeds that were kept in a forced circulation oven at 60 °C for 24 h and subsequently weighed on a precision analytical balance. The genotypes were classified according to the presence or absence of seeds according to the descriptors of the International Plant Genetic Resources Institute (IPGRI 1997): trace seed (≤ 10 mg), small seed (10–25 mg), medium seed (25–40 mg), large seed (40 to 55 mg) and very large seed (≥ 55 mg). Only those genotypes that presented a seed mass less than or equal to 10 mg were considered apyrenic genotypes.

Statistical analysis

The significance of the random effects of the model (permanent phenotypic effects) was assessed using deviance analysis (ANADEV) via the likelihood ratio test (LRT), as recommended by Viana and Resende (2014). Mathematically, $LRT = (-2LogL)_{p-1} - (-2LogL)_p$, where $LogL$ is

the logarithm of the maximum point of the residual likelihood function (L) associated with the reduced ($_{p-1}$) and complete ($_p$) models, and ($-2LogL$) is the deviance. The LTR was compared with the value of the probability density function (χ^2) with one degree of freedom at 1% and 5% probability.

The variance components were estimated by restricted maximum likelihood (REML), while the genotypic values were predicted by the best unbiased linear predictor (BLUP) using Selegen-REML/BLUP software (Resende 2016). The statistical model used was the basic repeatability model, in which the absence of an experimental design is assumed (Model 63). It can be represented in matrix form through the following equation: $y = Xm + Zp + e$, where y is the data vector (variable to be analyzed); m is the vector of the measurement effects, assumed to be fixed, added to the general mean; p is the vector of permanent phenotypic effects of plants (genotypic effects + permanent environmental effects), assumed to be random; e is the vector of errors or random effects residues; and X and Z are the incidence matrices for fixed effects and random effects, respectively (Viana and Resende 2014).

The mixed model equations were expressed by (Eq. 1)

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + I\left(\sigma_e^2/\sigma_g^2\right) \end{bmatrix} \begin{bmatrix} \hat{m} \\ \hat{p} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix},$$

where I is the identity matrix, σ_g^2 is the genotypic variance and σ_e^2 is the residual variance. The estimators to obtain σ_g^2 and σ_e^2 are (Eq. 2)

$$\hat{\sigma}_g^2 = \left[\hat{g}'\hat{g} + \sigma_e^2 trC^{22}\right]/N_g \text{ and } \hat{\sigma}_e^2 = \left[y'y - \hat{b}'X'y - \hat{g}'Z'y\right]/[N - r(X)]$$

where N_g is the number of random elements (individuals), tr is the matrix trace operator, which is given by the sum of the diagonal elements of the matrix; N is the total number of data, $r(X)$ is the number of linearly independent columns of X, and C^{22} is given by the formula $\begin{bmatrix} C^{11} & C^{12} \\ C^{21} & C^{22} \end{bmatrix} = \begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + A^{-1}\left(\sigma_e^2/\sigma_g^2\right) \end{bmatrix}^{-1}$. A^{-1} is the matrix of additive genetic correlation and dominance among the individuals evaluated.

The repeatability coefficient (r) was calculated from Eq. 3.

$$r = \left(\sigma_g^2 + \sigma_{ep}^2\right)/\sigma_f^2$$

where σ_g^2 is the genetic variance, σ_{ep}^2 is the permanent environmental variance and σ_f^2 is the estimate of the individual phenotypic variance. The accuracy of the use of m measures in each plant compared to the use of only one measure in terms of the genetic gain of selection A_{cm} was obtained by using Eq. 4.

$$A_{cm} = \sqrt{[(mr)/(mr) + 1 - r]}$$

where m is the number of repeated measurements and r is the repeatability coefficient. The efficiency of the use of m measures in each plant compared to only one measure (E) was obtained by $E = \{m/[1 + (m-1)r_m]\}^{0,5}$ (Viana and Resende 2014). The correlation was estimated by Pearson's coefficient using GENES statistical software (Cruz 2016).

A selection intensity of 25% was applied to each trait analyzed, which corresponds to the 50 best individuals in a sample of 200 hybrids at the individual level.

Results

The analysis of deviance via the likelihood ratio test is presented in Table 3. All traits evaluated exhibited significant genetic effects ($p < 0.01$).

The estimates of Pearson's linear correlation between the evaluated traits ranged from 0.01 to 0.89 (Table 4). Genetic correlations were of low magnitude for most traits. However, the yield and number of bunches, the bunch length, bunch width and bunch weight, the berry length, berry diameter and berry mass showed high positive correlations. The soluble solids content and *ratio* showed negative correlations with most traits, but they were nonsignificant or were of low magnitude.

The estimation of the genetic and phenotypic parameters for the variables considered in this study are presented in Table 5.

Table 3 Analysis of deviance for the yield, number of bunches, bunch length, bunch width, bunch weight, berry length, berry diameter, berry weight, soluble solids content, and *ratio* for the 200 hybrid genotypes of *Vitis* spp

Traits evaluated		Effect	
		Genotype	Full model
Yield	DEV	1985.97	1952.22
	LRT	33.75*	
Number of bunches	DEV	3874.81	3852.68
	LRT	22.13*	
Bunch length	DEV	2109.69	2014.50
	LRT	95.19*	
Bunch width	DEV	1626.52	1576.76
	LRT	49.76*	
Bunch weight	DEV	6931.05	6776.20
	LTR	154.85*	
Berry length	DEV	2148.94	1895.46
	LRT	253.48*	
Berry diameter	DEV	1701.03	1342.46
	LRT	358.57*	
Berry weight	DEV	799.12	415.71
	LRT	383.41*	
Soluble solids content	DEV	1921.42	1906.82
	LRT	14.60*	
Ratio (SS/AT)	DEV	4324.31	4306.74
	LRT	17.57*	

^{ns} not significant; $*p<0.01$; $**p<0.05$ by the X^2 test ($p<0.01=6.63$; $p<0.05=3.84$)

LRT—likelihood ratio test, distribution with 1 degree of freedom; DEV—deviance

The general average production was 3.03 kg per vine, corresponding to an estimated yield of 10 t ha^{-1} per vine. In addition, the average number of bunches per plant was reduced to approximately 15 bunches, a characteristic that is directly correlated with productivity.

The general mean values of the bunch length, bunch width, bunch weight, berry length, berry diameter, berry weight, soluble solids content and *ratio* were 14.13 cm, 8.20 cm, 211.02 g, 18.51 mm, 15.97 mm, 2.95 g, 16.50% and 36.36%, respectively.

The estimated permanent phenotypic variance between vines (V_{pp}) was higher than the temporary environmental variance (V_{te}) for the berry-related traits, representing most of the phenotypic variance (V_p). For the yield, number of bunches, bunch length, bunch width, bunch weight, soluble solids content and *ratio*, the values of V_{te} were higher than the values of $V_{pp.}$

The individual repeatability coefficients ($r=h^2$) ranged from 0.14 to 0.70 (Table 5). The individual repeatability values were as follows: berry weight was 0.70, berry width was 0.68, berry length was 0.60, bunch length was 0.37, bunch width was 0.30, bunch weight was 0.47, yield was 0.20, number of bunches was 0.18, soluble solids content was 0.14 and *ratio* was 0.15 (Fig. 1).

The selective accuracies, coefficients of determination and selective efficiencies increased as the number of measurements increased, as expected (Fig. 2).

Table 4 Pearson's linear correlation between the yield (Y), number of bunches (NB), bunch length (BuL), bunch width (BuWi), bunch weight (BuW), berry length (BeL), berry diameter (BeD), berry weight (BeW) and soluble solids content (SS) for the 200 hybrid genotypes of *Vitis* spp

	Y	NB	CC	BuWi	BuW	BeL	BeD	BeW	SS
Y		**0.66****	0.44**	0.28**	0.55**	0.28**	0.31**	0.36**	−0.14**
NB			0.14**	−0.02 ^{ns}	0.03 ^{ns}	0.01 ^{ns}	−0.01 ^{ns}	0.03 ^{ns}	−0.19**
BuL				**0.64****	**0.73****	0.31**	0.32**	0.35**	−0.09*
BuWi					**0.66****	0.31**	0.37**	0.36**	−0.06 ^{ns}
BuW						0.46**	0.52**	0.57**	−0.06 ^{ns}
BeL							**0.79****	**0.81****	0.07 ^{ns}
BeD								**0.89****	0.04 ^{ns}
BeW									0.05 ^{ns}
SS									

^{ns} not significant; * $p<0.01$; ** $p<0.05$

Table 5 Components of variance (individual REML) for the yield, number of bunches, bunch length, bunch width, bunch weight, berry length, berry diameter, berry weight, soluble solids content, and *ratio* for the 200 hybrid genotypes of *Vitis* spp

Traits evaluated	General average	Vfp	Vet	Vf	$r = h^2$	r_m	A_{cm}
Yield (kg)	3.03	1.32	5.31	6.63	0.20 ± 0.05	0.60	0.77
Number of buches	15.13	19.96	89.51	109.47	0.18 ± 0.05	0.57	0.76
Bunch length (cm)	14.13	2.96	5.06	8.03	0.37 ± 0.06	0.78	0.88
Bunch width (cm)	8.20	1.00	2.91	3.91	0.30 ± 0.05	0.70	0.82
Bunch weight (g)	211.02	4753.84	5319.13	10072.97	0.47 ± 0.07	0.84	0.92
Berry length (mm)	18.51	4.97	3.50	8.47	0.60 ± 0.08	0.90	0.95
Berry diameter (mm)	15.97	2.97	1.40	4.36	0.68 ± 0.09	0.93	0.96
Berry weight (g)	2.95	0.80	0.35	1.15	0.70 ± 0.09	0.93	0.97
Soluble solids content (%)	16.50	0.84	5.22	6.06	0.14 ± 0.04	0.49	0.70
Ratio	36.39	31.63	180.14	211.77	0.15 ± 0.04	0.51	0.72

V_{pp}—permanent phenotypic variance among vines; V_{te}—temporary environmental variance; V_p—individual phenotypic variance; $r = h^2$—individual repeatability and its confidence interval; r_m—mean repeatability of crops or repeated measures; and A_{cm} the selection accuracy based on the mean of the seasons or repeated measures

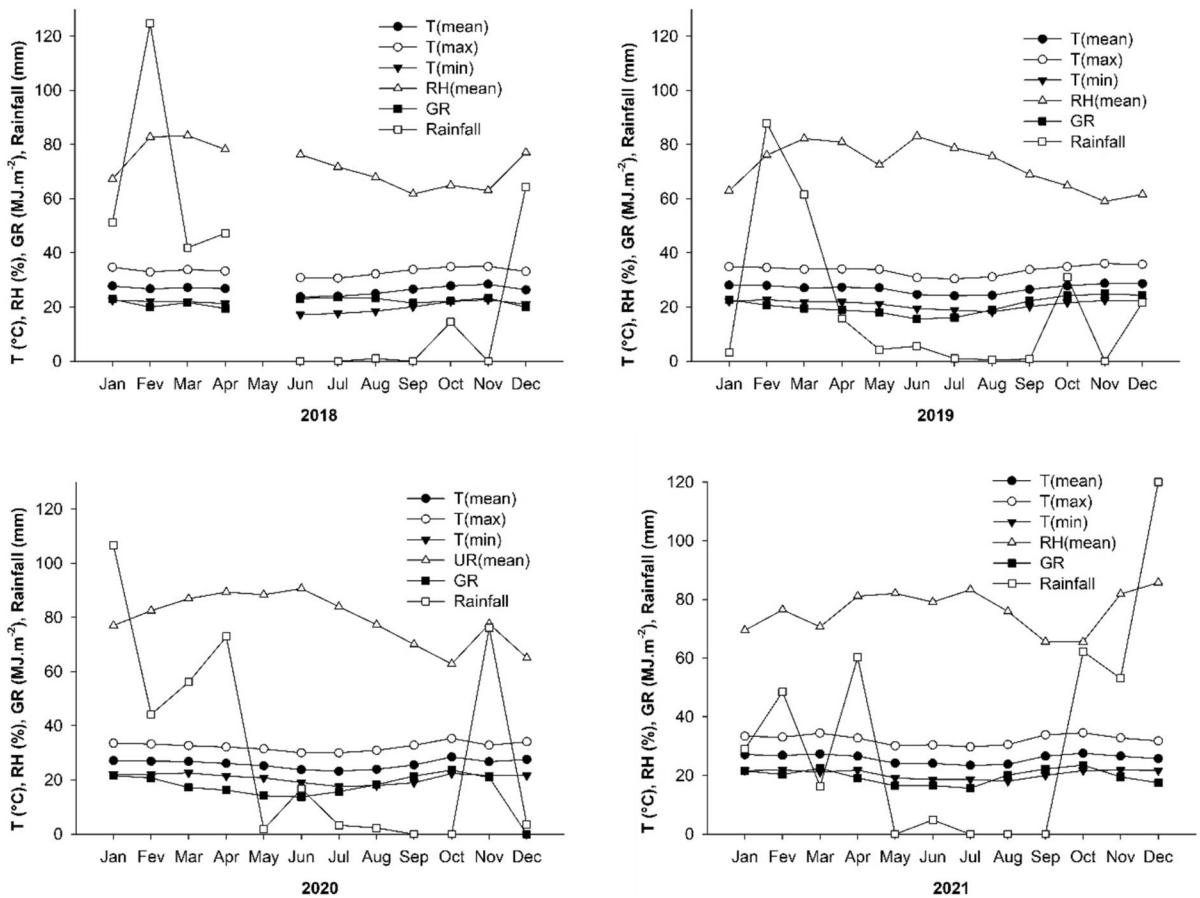

Fig. 1 Meteorological data on precipitation (mm), average, minimum and maximum air temperature (°C), relative humidity (%) and global radiation (MJ m^{-2}) for the years 2018, 2019, 2020 and 2021

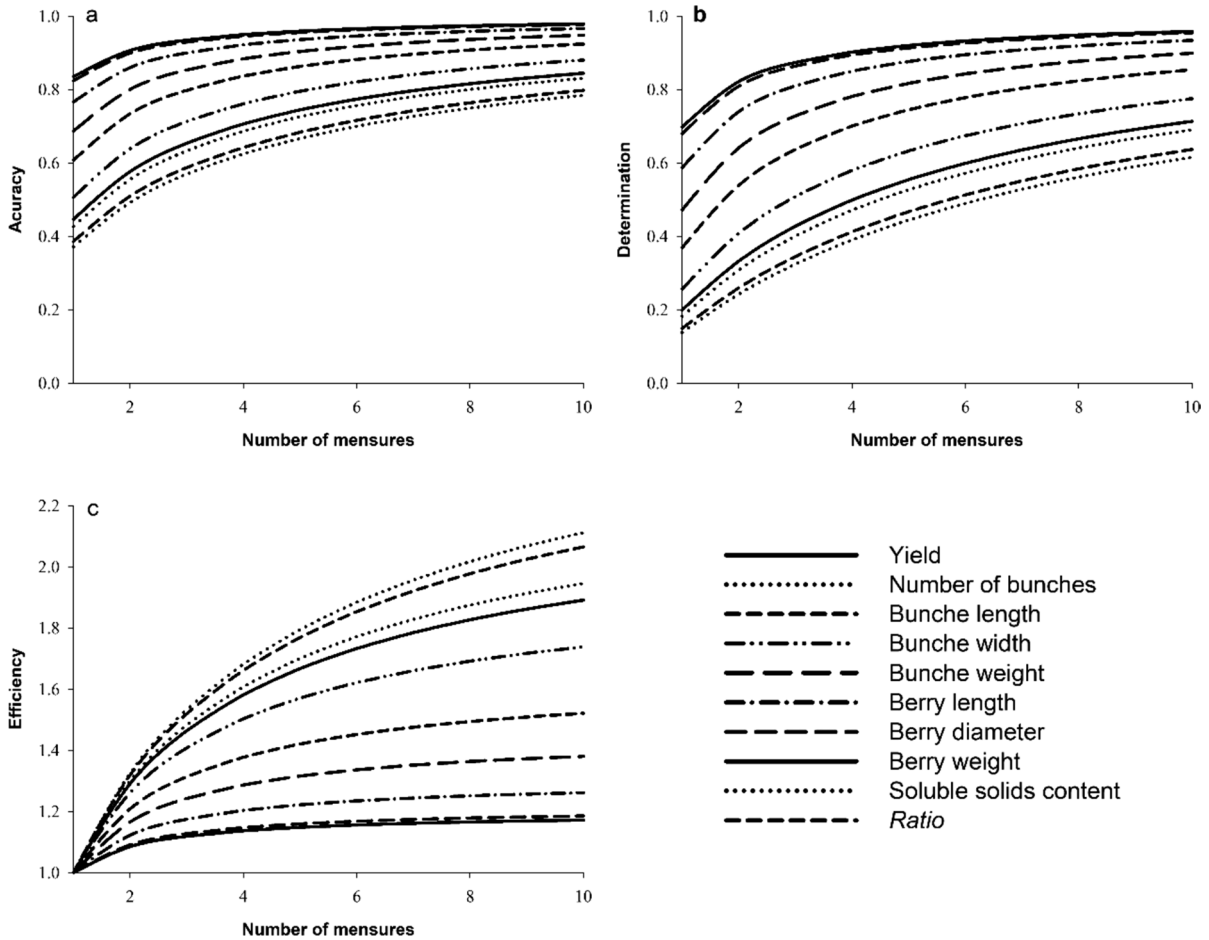

Fig. 2 Selective accuracy of the permanent phenotypic effects (**a**), determination (**b**) and efficiency (**c**) of performing m repeated measures for all evaluated traits for the 200 hybrid genotypes of *Vitis* spp

The accuracy estimates obtained by performing *m* repeated measurements revealed that for berry length, diameter and weight, only one measurement was sufficient; two measurements were required for the length and weight of the bunch and for the width of the bunch; three measurements were required for bunch width; four measurements were required for production and five measurements for the number of bunches; for the soluble solids content and *ratio*, 7 and 6 measurements were needed, respectively, to achieve an accuracy equal to or greater than 70% (Fig. 2). It is noteworthy that the characteristics of the berry have high heritability, requiring only one harvest for an accuracy greater than 70% to be obtained.

It was found that to obtain a determination above 80%, 7 measurements were required for bunch length, 5 measurements for bunch mass, 3 measurements for berry length and only 2 measurements for diameter and berry weight. The minimum desired values were not obtained for the yield, number of bunches, bunch width, soluble solids content and *ratio*, even with the maximum number of estimated measurements (ten). For the soluble solids content and *ratio*, the very low individual repeatability values obtained correspond to the need to evaluate 10 harvests to reach the desired values.

In addition, the use of four harvests for selection allowed obtaining accuracy equal to or greater than 70% for all traits evaluated, with the exception of soluble solids content and *ratio*. Thus, in general, four consecutive harvests are recommended to

select superior genotypes of table grape hybrids for Brazilian semiarid regions.

The components of the mean values (individual BLUP), genetic gains and new estimated mean values for the yield, bunch traits, berry traits and quality are presented in Tables 6, 7, 8 and 9, respectively. The 50 best individuals were selected for all variables analyzed, representing 25% of the evaluated hybrids.

The estimates of the genetic gain with selection ranged from 1.00 to 3.64 kg for yield and from 4.08 to 7.84 bunches per vine. The new mean values ranged from 4.03 to 6.68 kg for yield and from 19.21 to 22.97 berries per plant (Table 6).

For bunch traits, the gains ranged from 1.83 to 4.82 cm for bunch length, 0.93 to 2.86 cm for bunch width and 81.14 to 262.74 g for bunch weight. The new mean values ranged from 15.96 to 18.95 cm for bunch length, 9.13 to 11.06 cm for bunch width and 292.17 to 473.76 g for bunch weight (Table 7).

Regarding the berry traits, the genetic gains ranged from 2.50 to 6.17 mm for length, 2.02 to 4.00 mm for diameter and 1.13 to 2.82 g for berry weight. The new mean values for berry length, diameter and weight ranged from 21.02 to 24.68 mm, 17.99 to 19.96 mm and 4.08 to 5.78 g, respectively (Table 8).

The quality traits showed gains ranging from 0.69 to 1.42% for soluble solids, which presented a new average of 17.19 to 19.92%, and earnings ranged from 4.73 to 11.88, with an overall mean between 41.13 and 48.28 for the *ratio* (Table 9).

Among the 50 best hybrids selected by direct selection for each trait, three matched eight of the ten traits evaluated (CPATSA 28.09, CPATSA 05.168, CPATSA 79.100), ten matched seven (CPATSA 15.05, CPATSA 28.12, CPATSA 28.03, CPATSA 21.60, CPATSA 28.19, CPATSA 79.24, CPATSA 01.02, CPATSA 38.135, CPATSA 69.09 e CPATSA 69.07) and ten matched six (CPATSA 28.17, CPATSA 49.100, CPATSA 28.08, CPATSA 38.121, CPATSA 28.25, CPATSA 49.171, CPATSA 49.122, CPATSA 28.22, CPATSA 45.09 and CPATSA 21.09). The soluble solids content and *ratio* were the least present in the hybrids selected for six or more traits. The cultivars 'BRS Tainá' and CPATSA 49,171 did not contain seeds.

Regarding seed weight, 110 genotypes had a seed weight below 10 mg (Table 10). Considering only the hybrids classified as apyrenic, nine hybrids were considered superior for at least four traits. High mean values were obtained for the yield, number of bunches, bunch length, bunch width, berry length, berry weight and *ratio* for the 'BRS Tainá' grape developed by Embrapa (Leão et al., 2021). High average values were obtained for the yield, number of bunches, bunch length, bunch width, berry length and berry weight for the CPATSA 49.171 cultivar. Excellent results in terms of the bunch width, bunch weight, berry length, berry diameter, berry weight and *ratio*, were obtained for CPATSA 79.04. Higher yield, bunch length, bunch width and bunch weight values were obtained for CPATSA 31.11 and CPATSA 01.06. Good results in terms of bunch length, bunch width, bunch weight and berry length were obtained for CPATSA 23.09 and CPATSA 21.114. Superior yield, bunch number, berry length and *ratio* values were obtained for CPATSA 42.157. Finally, high mean values for yield, number of bunches, soluble solids content and *ratio* were obtained for CPATSA 79.28.

Discussion

The stages of a genetic improvement program for perennial species are time-consuming due to the prolonged production cycles of these crops, which require time and resources (Azevedo et al. 2020). The mixed model methodology (REML/BLUP) allows the optimization of these steps, as selection is achieved without the need for experimental designs, predicting permanent phenotypic values through repeated measures, weighted by the coefficient of temporal repeatability of the trait (Resende 2009).

The basic premise for selection is the presence and knowledge of genetic variability (Malikouski et al. 2021). Furthermore, models with significant genetic parameters are the most suitable for estimating variance components and predicting genotypic values for each trait. The deviance analysis using the likelihood ratio test to evaluate the significance of the genotypic effects is indicated for the analysis of mixed models with unbalanced data. In this study, this analysis revealed the existence of variability among the evaluated hybrids; that is, its effects explain part of the total variation, which demonstrates the possibility of obtaining genetic gains through direct selection in all evaluated traits and, therefore, the recommendation of superior genotypes.

Table 6 Components of the average (individual BLUP), genetic gain and new average, with the selection of 50 superior genotypes for the yield (kg) and number of bunches per plant

Rk	Yield			Number of bunches		
	Genotype	Gain	New average	Genotype	Gain	New average
1	CPATSA 01.06	3.64	6.68	CPATSA 15.05	7.84	22.97
2	CPATSA 14.00G	3.38	6.41	CPATSA 28.01	7.51	22.65
3	CPATSA 28.09	3.06	6.09	CPATSA 49.20	7.35	22.48
4	CPATSA 15.05	2.86	5.89	CPATSA 49.197	7.20	22.33
5	CPATSA 28.12	2.70	5.74	CPATSA 49.221	6.97	22.11
6	CPATSA 28.18	2.59	5.62	CPATSA 67.02	6.81	21.94
7	CPATSA 28.17	2.50	5.54	CPATSA 79.28	6.65	21.78
8	CPATSA 28.03	2.42	5.45	CPATSA 28.09	6.51	21.65
9	CPATSA 67.02	2.36	5.39	CPATSA 49.191	6.40	21.54
10	CPATSA 28.05	2.27	5.30	CPATSA 49.28	6.32	21.45
11	CPATSA 05.168	2.19	5.22	CPATSA 42.157	6.24	21.37
12	CPATSA 49.100	2.10	5.14	CPATSA 28.18	6.16	21.30
13	CPATSA 42.157	2.03	5.07	CPATSA 67.03	6.09	21.22
14	CPATSA 28.08	1.97	5.00	CPATSA 49.246	6.02	21.15
15	CPATSA 38.121	1.91	4.94	CPATSA 49.100	5.94	21.08
16	CPATSA 49.43	1.84	4.88	CPATSA 49.171	5.87	21.00
17	CPATSA 21.60	1.79	4.82	CPATSA 49.234	5.80	20.94
18	CPATSA 28.25	1.73	4.77	CPATSA 49.235	5.74	20.87
19	CPATSA 28.19	1.69	4.72	CPATSA 79.47	5.67	20.80
20	CPATSA 62.19	1.65	4.68	CPATSA 62.19	5.60	20.74
21	CPATSA 79.24	1.61	4.64	CPATSA 49.49	5.54	20.68
22	CPATSA 49.171	1.57	4.61	CPATSA 49.31	5.48	20.62
23	CPATSA 67.03	1.54	4.57	CPATSA 49.30	5.43	20.56
24	CPATSA 01.02	1.51	4.54	CPATSA 28.03	5.38	20.51
25	CPATSA 49.31	1.48	4.51	CPATSA 28.12	5.31	20.45
26	CPATSA 49.122	1.45	4.48	CPATSA 65.64	5.26	20.39
27	CPATSA 28.22	1.42	4.45	CPATSA 49.42	5.20	20.33
28	CPATSA 28.35	1.39	4.43	CPATSA 49.90	5.14	20.28
29	CPATSA 79.17	1.37	4.40	CPATSA 62.04	5.09	20.22
30	CPATSA 79.100	1.34	4.38	CPATSA 28.25	5.04	20.17
31	CPATSA 79.28	1.32	4.35	CPATSA 49.43	4.99	20.13
32	CPATSA 38.135	1.30	4.33	CPATSA 42.316G	4.95	20.08
33	CPATSA 45.09	1.28	4.31	CPATSA 28.16	4.90	20.03
34	CPATSA 69.09	1.26	4.29	CPATSA 49.156	4.86	19.99
35	CPATSA 69.07	1.24	4.28	CPATSA 28.17	4.81	19.95
36	CPATSA 28.23	1.22	4.26	CPATSA 49.215	4.77	19.90
37	CPATSA 28.01	1.20	4.24	CPATSA 65.112	4.72	19.86
38	CPATSA 62.13	1.19	4.22	CPATSA 49.114	4.67	19.81
39	CPATSA 22.09	1.17	4.20	CPATSA 62.80	4.62	19.76
40	CPATSA 28.29	1.15	4.18	CPATSA 49.122	4.58	19.71
41	CPATSA 21.09	1.13	4.17	CPATSA 31.10	4.53	19.66
42	CPATSA 38.50	1.12	4.15	CPATSA 49.22	4.48	19.62
43	CPATSA 64.83	1.10	4.13	CPATSA 49.37	4.43	19.56
44	CPATSA 49.30	1.08	4.12	CPATSA 05.168	4.38	19.51
45	CPATSA 31.11	1.07	4.10	CPATSA 49.25	4.32	19.46

Table 6 (continued)

Rk	Yield			Number of bunches		
	Genotype	Gain	New average	Genotype	Gain	New average
46	CPATSA 49.221	1.05	4.09	CPATSA 31.12	4.27	19.41
47	CPATSA 79.47	1.04	4.07	CPATSA 22.09	4.22	19.35
48	CPATSA 67.04	1.02	4.06	CPATSA 63.29	4.17	19.31
49	CPATSA 28	1.01	4.04	CPATSA 49.192	4.12	19.26
50	CPATSA 28.16	1.00	4.03	CPATSA 65.132	4.08	19.21

Genetic correlations measure the level of association between two traits and can be positive or negative. Results similar to those in the present study were found by Maia et al (2017) for pink mango. In contrast, Wei et al. (2002) found a low correlation between soluble solids content and titratable acidity (0.04); however, the correlations were high for berry weight, length and diameter. Nikolic et al. (2018) observed a correlation of 0.45 between bunch weight and berry weight and −0.21 between soluble solids content and titratable acidity.

Estimates of the genetic correlation between traits are important for the success of breeding programs because they allow the breeder to evaluate the selective response and obtain indirect gains in other variables. Thus, some polygenic traits strongly influenced by the environment can be indirectly selected from other variables measured more easily and accurately.

The mean values of the yield and bunch mass found in this study (Table 5) were lower than those found by Leão et al. (2018) (13 t ha^{-1} and 334 g) and Sales et al. (2019) (19 t ha^{-1} and 314 g) when evaluating grape hybrids in a trellis management system. However, this yield is related to the trellis management system as well as the management adopted in the vineyard. Thus, the yield can be improved with the trellis management system and cultural practices recommended in the commercial cultivation of the vine. In addition, yield is a quantitative trait, and the evaluation was performed based on a single plant. The bunch weight of the 'BRS Vitória', 'BRS Isis' and 'BRS Melodia' cultivars ranged from 290 to 375 g (Maia et al. 2012, 2019; Zilio et al. 2019).

Regarding the berry diameter and soluble solids content (Table 5), similar results were observed by Leão et al. (2018) and Sales et al. (2019). In addition, the values are close to those of the 'BRS Vitória', 'BRS Ísis' and 'BRS Melodia' table grape cultivars (Maia et al. 2012, 2019; Zilio et al. 2019). For 'Chardonnay' and 'Cabernet Sauvignon' wine grapes, Cargnin (2016) found soluble solids contents of 22% and a berry weight of approximately 1 g. In general, with the exception of bunch weight, the other characteristics are within the values expected for table grapes.

The superiority of the permanent phenotypic variance estimated between plants (V_{pp}) in relation to the temporary environmental variance (V_{te}) (Table 5) for the berry-related traits reflects the possibility of successful genotype selection by vegetative propagation, preserving traits of superior genotypes. Leão et al. (2018) also found V_{pp} values greater than V_{te} values for the berry diameter. However, the higher values of V_{te} in relation to the values of V_{pp} for the other variables indicate that these characteristics are highly influenced by environmental conditions. Results similar to these were found by Sanchéz et al. (2017) for fruit production, Maia et al. (2017) for fruit characteristics and Sales et al. (2019) for all the variables evaluated by them (yield, bunch weight, soluble solids content and *ratio,* with the exception of the number of bunches, in which the V_{pp} values were greater than the V_{te} values. In contrast, Leão et al. (2018) detected higher V_{pp} values than V_{te} values for the yield and number of bunches but observed higher V_{te} values than V_{pp} values for the bunch mass and soluble solids content.

The environmental influence on the yield, bunch characteristics, soluble solids content and *ratio* can be explained by seasonal climatic variations and multiple crop seasons a year in the Submédio São Francisco Valley, together with the alternations common in consecutive seasons (Leão et al. 2018). Higher V_{te} values than V_{pp} values hampers the selection of promising genotypes based on simple plant breeding methods, such as clone selection, which only take into account the individual phenotype (Leão et al. 2018).

Table 7 Components of the average (individual BLUP), genetic gain and new average, with the selection of 50 superior genotypes for bunch traits

Rk	Bunch length			Bunch width			Bunch weight		
	Genotype	Gain	New average	Genotyoe	Gain	New average	Genotype	Gain	New average
1	CPATSA 01.02	4.82	18.95	CPATSA 38.121	2.86	11.06	CPATSA 01.06	262.74	473.76
2	CPATSA 14.00G	4.72	18.85	CPATSA 65.90	2.60	10.80	CPATSA 14.00G	253.31	464.33
3	CPATSA 69.09	4.46	18.59	CPATSA 69.09	2.50	10.70	CPATSA 69.09	228.69	439.71
4	CPATSA 38.135	4.23	18.36	CPATSA 01.06	2.44	10.63	CPATSA 69.07	212.07	423.09
5	CPATSA 69.07	4.01	18.14	CPATSA 38.135	2.35	10.54	CPATSA 38.135	200.70	411.72
6	CPATSA 31.11	3.85	17.98	CPATSA 38.113	2.21	10.41	CPATSA 38.167	189.29	400.31
7	CPATSA 60.29	3.68	17.81	CPATSA 23.09	2.11	10.30	CPATSA 23.09	178.12	389.14
8	CPATSA 23.09	3.54	17.67	CPATSA 14.00G	2.02	10.21	CPATSA 38.121	169.47	380.49
9	CPATSA 38.121	3.43	17.56	CPATSA 79.100	1.94	10.14	CPATSA 01.02	162.01	373.04
10	CPATSA 31.10	3.34	17.47	CPATSA 70.04	1.87	10.06	CPATSA 31.11	155.97	366.99
11	CPATSA 49.171	3.26	17.39	CPATSA 21.114	1.81	10.00	CPATSA 28.09	150.91	361.93
12	CPATSA 76.22	3.19	17.32	CPATSA 62	1.76	9.95	CPATSA 28.19	146.42	357.44
13	CPATSA 79.100	3.12	17.25	CPATSA 69.07	1.71	9.91	CPATSA 60.29	142.38	353.40
14	CPATSA 01.06	3.07	17.19	CPATSA 49.172	1.67	9.86	CPATSA 70.04	138.85	349.87
15	CPATSA 31.P1	3.01	17.14	CPATSA 31.11	1.63	9.83	CPATSA 38.50	135.74	346.76
16	CPATSA 28.09	2.96	17.09	CPATSA 49.171	1.59	9.79	CPATSA 67.15	132.95	343.97
17	CPATSA 63.47	2.92	17.05	CPATSA 79.04	1.56	9.75	CPATSA 21.09	130.46	341.48
18	CPATSA 28.22	2.87	17.00	CPATSA 49.63	1.52	9.72	CPATSA 79.100	128.21	339.23
19	CPATSA 28.19	2.83	16.96	CPATSA 63.01	1.49	9.69	CPATSA 28.03	125.65	336.67
20	CPATSA 49.70	2.79	16.91	CPATSA 01.02	1.46	9.66	CPATSA 79.24	123.28	334.30
21	CPATSA 31.12	2.74	16.86	CPATSA 63.47	1.43	9.63	CPATSA 21.114	121.09	332.11
22	CPATSA 76.20	2.69	16.82	CPATSA 60.29	1.41	9.61	CPATSA 49.10	118.96	329.98
23	CPATSA 49.22	2.64	16.77	CPATSA 63.108	1.38	9.58	CPATSA 05.168	116.85	327.87
24	CPATSA 28.29	2.60	16.72	CPATSA 28.19	1.36	9.55	CPATSA 28.35	114.83	325.85
25	CPATSA 49.197	2.56	16.68	CPATSA 49.40	1.33	9.53	CPATSA 31.07	112.93	323.95
26	CPATSA 49.100	2.52	16.65	CPATSA 21.09	1.31	9.51	CPATSA 47.01	111.17	322.20
27	CPATSA 31.07	2.48	16.60	CPATSA 62.13	1.29	9.48	CPATSA 21.60	109.49	320.51
28	CPATSA 79.24	2.43	16.56	CPATSA 49.166	1.26	9.46	CPATSA 28.22	107.83	318.85
29	CPATSA 28.35	2.39	16.52	CPATSA 28.09	1.24	9.44	106.28	317.31	
30	CPATSA 38.50	2.35	16.48	CPATSA 42.72T	1.22	9.42	104.75	315.77	
31	CPATSA 38.113	2.32	16.45	CPATSA 79.24	1.20	9.40	103.30	314.32	
32	CPATSA 28.17	2.28	16.41	CPATSA 49.70	1.19	9.38	101.93	312.95	
33	CPATSA 38.167	2.25	16.38	CPATSA 31P1	1.17	9.36	100.63	311.65	
34	CPATSA 79.38	2.22	16.35	CPATSA 14.25G	1.15	9.35	99.39	310.41	
35	CPATSA 26.18	2.19	16.32	CPATSA 05.168	1.13	9.33	98.22	309.24	
36	CPATSA 76.27	2.16	16.29	CPATSA 21.60	1.12	9.31	97.02	308.04	
37	CPATSA 28.12	2.13	16.26	CPATSA 49.06	1.10	9.30	95.71	306.73	
38	CPATSA 21.114	2.10	16.23	CPATSA 67.15	1.09	9.28	94.38	305.40	
39	CPATSA 53.38	2.08	16.21	CPATSA 49.122	1.07	9.27	93.11	304.13	
39	CPATSA 53.38	2.08	16.21	CPATSA 49.122	1.07	9.27	93.11	304.13	
40	CPATSA 28.08	2.05	16.18	CPATSA 76.22	1.06	9.25	91.90	302.92	
41	CPATSA 76.06	2.03	16.15	CPATSA 38.167	1.04	9.24	90.71	301.73	
42	CPATSA 75.09	2.00	16.13	CPATSA 28.22	1.03	9.22	89.54	300.56	
43	CPATSA 21.60	1.98	16.11	CPATSA 28.38	1.02	9.21	88.41	299.43	

Table 7 (continued)

Rk	Bunch length			Bunch width			Bunch weight		
	Genotype	Gain	New average	Genotyoe	Gain	New average	Genotype	Gain	New average
44	CPATSA 79.47	1.96	16.08	CPATSA 38.50	1.00	9.20	87.30	298.32	
45	CPATSA 28.03	1.93	16.06	CPATSA 79.49	0.99	9.19	86.21	297.23	
46	CPATSA 49.172	1.91	16.04	CPATSA 67.18	0.98	9.17	85.15	296.17	
47	CPATSA 28.05	1.89	16.02	CPATSA 64.83	0.97	9.16	84.12	295.15	
48	CPATSA 15.05	1.87	16.00	CPATSA 28.12	0.95	9.15	83.12	294.14	
49	CPATSA 70.04	1.85	15.98	CPATSA 15.05	0.94	9.14	82.11	293.13	
50	CPATSA 28.11	1.83	15.96	CPATSA 79.38	0.93	9.13	81.14	292.17	

Knowledge of the coefficient of repeatability of the traits of interest allows us to evaluate the time expenditure required for the selection of genetically superior individuals to be performed with the accuracy desired by the researcher (Della Bruna et al. 2012). The higher the coefficient of the individual repeatability is, the lower the number of repeated measures to predict the true value of the individual. On the other hand, when the repeatability of the trait is low, several repetitions are required to reach a satisfactory determination value (Resende 2009). When selecting a genotype, it is expected that its initial superiority will persist, high repeatability values are desired.

Repeatability is important for plant breeding because it provides the maximum value that can be achieved with respect to broad-sense heritability (Cargnin 2016). Thus, according to the repeatability coefficient, the heritability of the traits evaluated in this study tends to be low, except for the berry attributes.

The repeatability coefficient is a measure of the ability of individuals to maintain the expression of the trait over several harvests. Thus, it allows the selection of genotypes that maintain their genetic superiority in successive harvests, minimizing the environmental effects on selection (Ferreira et al. 2020). According to Resende (2009), repeatability can be classified as high ($r > 0.60$), medium ($0.30 < r < 0.60$), and low ($r < 0.30$). Therefore, the individual repeatability values for berry characteristics was considered high, for bunch characteristics was considered medium and for the yield, number of bunches, soluble solids content and *ratio* was considered low (Table 5). These results demonstrate greater genetic control and greater stability in terms of similarity of values for the berry traits in successive evaluation cycles, which aids in the better prediction of genotypic values.

The individual repeatability estimates observed in this study are higher than those mentioned for fruits such as mango (Maia et al. 2017), similar to those observed for lemon (Malikouski et al. 2021) and peach (Della Bruna et al. 2012), and lower than those found for soursop (Sanchéz et al. 2017) and Brazil nut (Pedrozo et al. 2015). These results are in agreement with Sales et al. (2019), who found low repeatability coefficients for the soluble solids content and *ratio*, and Leão et al. (2018), who also found similar repeatability for the bunch weight, berry diameter and soluble solids content. Finally, Cargnin (2016) found higher repeatability than those obtained in this study for the yield, number of bunches, bunch weight and soluble solids content of grapes, with similar results obtained only the for repeatability coefficient of the berry weight.

The increase in the number of measurements reduces the values of environmental variance, which represents a gain in precision (Ferreira et al. 2020). However, it is important to optimize the perennial plant selection process, estimating the ideal number of phenotypic observations necessary to obtain significant accuracy and determination values, thus saving resources.

Selective accuracy demonstrates the regularity of superiority of individuals from one crop to another and that the expression of this trait has good genetic control (Della Bruna et al. 2012). The estimates of accuracy in this study obtained by performing *m* repeated measurements revealed that it is possible to achieve accuracy values of greater than 70% for all characteristics (Fig. 2). Accuracy values above 70% are considered high and therefore sufficient for the

Table 8 Components of the average (individual BLUP), genetic gain and new average, with the selection of 50 superior genotypes for berry traits

Rk	Berry length			Berry diameter			Berry weight		
	Genotype	Gain	New average	Genotype	Gain	New average	Genotype	Gain	New average
1	CPATSA 49.172	6.17	24.68	CPATSA 47.01	4.00	19.96	CPATSA 47.02	2.82	5.78
2	CPATSA 47.02	6.12	24.64	CPATSA 21.09	3.86	19.82	CPATSA 47.01	2.58	5.53
3	CPATSA 79.24	6.06	24.58	CPATSA 47.02	3.80	19.77	CPATSA 21.09	2.48	5.43
4	CPATSA 47.01	5.99	24.50	CPATSA 45.09	3.75	19.72	CPATSA 45.09	2.38	5.33
5	CPATSA 79.100	5.93	24.44	CPATSA 05.168	3.65	19.62	CPATSA 49.22	2.30	5.25
6	CPATSA 49.22	5.69	24.21	CPATSA 49	3.58	19.54	CPATSA 05.168	2.23	5.18
7	CPATSA 23.09	5.50	24.01	CPATSA 49.10	3.52	19.49	CPATSA 49	2.18	5.13
8	CPATSA 21.09	5.29	23.81	CPATSA 21.60	3.43	19.40	CPATSA 49.10	2.12	5.08
9	CPATSA 70.04	5.09	23.60	CPATSA 28.25	3.35	19.32	CPATSA 70.04	2.07	5.02
10	CPATSA 79.17	4.92	23.43	CPATSA 28.23	3.29	19.25	CPATSA 28.23	2.02	4.97
11	CPATSA 45.09	4.76	23.27	CPATSA 70.04	3.23	19.20	CPATSA 67.15	1.97	4.92
12	CPATSA 05.168	4.60	23.12	CPATSA 49.22	3.18	19.15	CPATSA 49.43	1.92	4.87
13	CPATSA 49.10	4.46	22.97	CPATSA 67.15	3.14	19.10	CPATSA 79.24	1.88	4.83
14	CPATSA 49.240	4.33	22.84	CPATSA 28.08	3.08	19.05	CPATSA 28.25	1.84	4.79
15	CPATSA 49	4.22	22.73	CPATSA 49.43	3.02	18.98	CPATSA 21.60	1.81	4.76
16	CPATSA 28.23	4.11	22.62	CPATSA 79.38	2.96	18.93	CPATSA 28.32	1.77	4.72
17	CPATSA 21.60	3.99	22.51	CPATSA 28.32	2.91	18.88	CPATSA 65.132	1.74	4.69
18	CPATSA 28.08	3.90	22.41	CPATSA 42.10 T	2.87	18.83	CPATSA 79.38	1.70	4.66
19	CPATSA 79.04	3.81	22.32	CPATSA 28.19	2.82	18.79	CPATSA 79.100	1.67	4.62
20	CPATSA 49.24	3.72	22.24	CPATSA 79.04	2.79	18.75	CPATSA 69.09	1.65	4.60
21	CPATSA 38.135	3.65	22.16	CPATSA 38.121	2.74	18.71	CPATSA 28.08	1.62	4.57
22	CPATSA 28.25	3.57	22.09	CPATSA 28.03	2.70	18.67	CPATSA 38.135	1.59	4.54
23	CPATSA 28.19	3.51	22.02	CPATSA 28.18	2.67	18.63	CPATSA 28.19	1.57	4.52
24	CPATSA 01.02	3.44	21.96	CPATSA 65.132	2.63	18.60	CPATSA 49.172	1.54	4.49
25	CPATSA 65.132	3.38	21.90	CPATSA 28.12	2.60	18.57	CPATSA 28.03	1.52	4.47
26	CPATSA 49.237	3.33	21.84	CPATSA 01.02	2.57	18.53	CPATSA 79.04	1.50	4.45
27	CPATSA 49.43	3.27	21.79	CPATSA 28	2.54	18.50	CPATSA 28	1.48	4.43
28	CPATSA 28.32	3.22	21.74	CPATSA 28.09	2.51	18.47	CPATSA 28.09	1.46	4.41
29	CPATSA 28.18	3.18	21.69	CPATSA 28.27	2.48	18.44	CPATSA 38.113	1.43	4.39
30	CPATSA 79.38	3.13	21.64	CPATSA 38.113	2.45	18.42	CPATSA 01.02	1.41	4.37
31	CPATSA 49.21	3.09	21.60	CPATSA 28.35	2.42	18.39	CPATSA 28.12	1.40	4.35
32	CPATSA 28.09	3.05	21.56	CPATSA 28.14	2.40	18.36	CPATSA 49.31	1.38	4.33
33	CPATSA 42.10 T	3.01	21.52	CPATSA 38.167	2.37	18.34	CPATSA 28.16	1.36	4.31
34	CPATSA 49.100	2.97	21.48	CPATSA 28.17	2.35	18.31	CPATSA 28.27	1.34	4.29
35	CPATSA 28.03	2.93	21.45	CPATSA 49.49	2.32	18.29	CPATSA 69.07	1.33	4.28
36	CPATSA 49.167	2.90	21.41	CPATSA 69.09	2.30	18.26	CPATSA 79.175	1.31	4.26
37	CPATSA 28.16	2.86	21.38	CPATSA 28.38	2.27	18.24	CPATSA 42.10 T	1.29	4.24
38	CPATSA 69.07	2.83	21.34	CPATSA 28.28	2.25	18.22	CPATSA 38.121	1.28	4.23
39	CPATSA 49.213	2.80	21.31	CPATSA 79.24	2.23	18.20	CPATSA 28.18	1.26	4.21
40	CPATSA 67.15	2.77	21.28	CPATSA 79.100	2.21	18.18	CPATSA 49.240	1.25	4.20
41	CPATSA 49.171	2.74	21.25	CPATSA 28.22	2.19	18.16	CPATSA 28.14	1.23	4.19
42	CPATSA 49.122	2.71	21.22	CPATSA 28.05	2.17	18.14	CPATSA 28.05	1.22	4.17
43	CPATSA 15.05	2.68	21.19	CPATSA 69.07	2.15	18.12	CPATSA 28.17	1.21	4.16
44	CPATSA 28.27	2.65	21.17	CPATSA 28.29	2.13	18.10	CPATSA 28.28	1.19	4.15

Table 8 (continued)

Rk	Berry length			Berry diameter			Berry weight		
	Genotype	Gain	New average	Genotype	Gain	New average	Genotype	Gain	New average
45	CPATSA 69.09	2.63	21.14	CPATSA 49.167	2.11	18.08	CPATSA 28.29	1.18	4.13
46	CPATSA 89.03	2.60	21.11	CPATSA 49.13	2.09	18.06	CPATSA 22.43	1.17	4.12
47	CPATSA 28.38	2.58	21.09	CPATSA 38.135	2.07	18.04	CPATSA 38.167	1.16	4.11
48	CPATSA 28.14	2.55	21.06	CPATSA 21.114	2.06	18.02	CPATSA 49.122	1.15	4.10
49	CPATSA 42.157	2.53	21.04	CPATSA 49.240	2.04	18.00	CPATSA 28.22	1.14	4.09
50	CPATSA 28.11	2.50	21.02	CPATSA 49.171	2.02	17.99	CPATSA 15.05	1.13	4.08

selection process in breeding programs (Resende and Alves 2020), as the correct classification of genotypes is demonstrated (Resende and Duarte 2007).

Leão et al. (2018) and Sales et al. (2019) reported that accuracies of more than 80% were obtained in terms of the yield, number of bunches, bunch weight and berry diameter for vines studied in the same region. These values are higher than those found in this study. However, similar results were obtained for the soluble solids content and *ratio* when they evaluated four and three cycles, respectively. In other fruits, Alves and Resende (2008) reported that five harvests were sufficient to obtain 70% accuracy for the number of cupuassu fruits, and Malikouski et al. (2021) observed that four harvests were needed to obtain accuracy values above 90% for the yield and number of fruits per plant in 'Tahiti' acid lime.

For perennial crops, selection during the early developmental stage or at the first harvests may shorten the reproduction cycle (Ferreira et al. 2020). Thus, while additional evaluations for the yield, number of bunches, bunch width, soluble solids content and *ratio* would be necessary in this study, for bunch length, bunch weight and berry characteristics, two harvests are sufficient to achieve an accuracy equal to or greater than 70%, which saves resources. In addition, there was only a small increase in efficiency when performing more than two evaluations on these variables, while the other variables showed greater efficiency in selection, justifying the costs of additional harvests and evaluations.

The selective accuracy depends on the heritability and repeatability of the trait and on the procedures used to predict the breeding values. It is the main component of genetic progress because it is associated with selection precision, i.e., it refers to the correlation between predicted breeding values and genetic values. The greater the accuracy in the evaluation of an individual is, the greater the confidence in the evaluation and in the predicted genetic value of the individual (Maia et al. 2017).

A coefficient of determination greater than 80% is considered good for selecting superior individuals in perennial crops (Sanchéz et al. 2017). In the present study, only the bunch traits, with the exception of bunch width, and berry traits exhibited a coefficient of determination greater than 80% (Fig. 2). Thus, for the other traits, the use of indirect selection is recommended based on the study of correlations between the variable and others with better genetic control. As already demonstrated in other studies, these variables are highly influenced by the environment, so evaluations in experiments with repetition would also help to improve the results.

These results are in agreement with Malikouski et al. (2021). They found the need for eight lemon harvests to obtain 80% yield. The minimum determination was not obtained for the number of fruits and the fruit width. For soursop, eight harvests were evaluated to reach a determination of more than 80% for the number of fruits (Sanchéz et al. 2017). Maia et al. (2017) found that in mangoes, 6 and 7 evaluations were required for the *ratio* and soluble solids content, respectively, and more than 10 measurements were required for fruit traits.

In grapevine, the results found here are in agreement to those of Leão et al. (2018), who found the need to evaluate 4, 3, and 6 harvests to reach a determination greater than 80% for the yield, number of bunches and bunch weight and berry diameter, respectively. The same results were observed by Sales et al. (2019), who obtained determinations above 80% for the number of bunches and bunch weight and low values for soluble solids content and *ratio*. In contrast,

Table 9 Components of the average (individual BLUP), genetic gain and new average, with the selection of 50 superior genotypes for quality traits: soluble solids content (%) and the relationship between soluble solids content and titratable acidity (SS/TA) (dimensionless)

Rk	Soluble solids content			*Ratio*		
	Genotype	Gain	New average	Genotype	Gain	New average
1	CPATSA 38.113	1.42	17.92	CPATSA 49.235	11.88	48.28
2	CPATSA 49.14	1.38	17.88	CPATSA 49.21	10.80	47.20
3	CPATSA 28.11	1.35	17.85	CPATSA 49.24	10.17	46.57
4	CPATSA 49.44	1.30	17.80	CPATSA 79.175	9.62	46.02
5	CPATSA 49.240	1.26	17.76	CPATSA 32.02	9.29	45.69
6	CPATSA 79.175	1.23	17.73	CPATSA 49.240	9.02	45.42
7	CPATSA 32.02	1.20	17.70	CPATSA 79.28	8.79	45.19
8	CPATSA 49.90	1.17	17.67	CPATSA 49.221	8.57	44.97
9	CPATSA 74.11	1.14	17.64	CPATSA 67.15	8.37	44.77
10	CPATSA 67.15B	1.11	17.61	CPATSA 79.04	8.20	44.60
11	CPATSA 49.24	1.08	17.58	CPATSA 49.44	8.05	44.45
12	CPATSA 19.08	1.06	17.56	CPATSA 28.11	7.91	44.31
13	CPATSA 49.100	1.04	17.54	CPATSA 49.31	7.78	44.18
14	CPATSA 31.P1	1.02	17.52	CPATSA 79.17	7.63	44.03
15	CPATSA 28.16	1.01	17.50	CPATSA 49.25	7.50	43.90
16	CPATSA 49.30	0.99	17.49	CPATSA 49.30	7.38	43.78
17	CPATSA 49.21	0.98	17.48	CPATSA 63.108	7.26	43.66
18	CPATSA 22.15	0.97	17.46	CPATSA 15.04	7.14	43.54
19	CPATSA 49.233	0.95	17.45	CPATSA 49.90	7.03	43.43
20	CPATSA 63.01	0.94	17.44	CPATSA 63.01	6.92	43.32
21	CPATSA 79.28	0.93	17.43	CPATSA 49.100	6.82	43.22
22	CPATSA 49.99	0.92	17.42	CPATSA 65.104	6.73	43.13
23	CPATSA 49.93	0.91	17.41	CPATSA 24.88	6.64	43.03
24	CPATSA 49.197	0.90	17.40	CPATSA 38.113	6.54	42.94
25	CPATSA 49.235	0.89	17.39	CPATSA 49.104	6.45	42.85
26	CPATSA 49.31	0.88	17.38	CPATSA 49.197	6.36	42.76
27	CPATSA 67.24	0.87	17.37	CPATSA 49.93	6.28	42.68
28	CPATSA 65.18	0.86	17.36	CPATSA 21.99	6.20	42.60
29	CPATSA 24.88	0.85	17.35	CPATSA 79.100	6.12	42.52
30	CPATSA 63.114	0.85	17.34	CPATSA 65.112	6.04	42.44
31	CPATSA 51.01	0.84	17.34	CPATSA 49.178	5.97	42.37
32	CPATSA 28.25	0.83	17.33	CPATSA 15.05	5.90	42.30
33	CPATSA 45.09	0.82	17.32	CPATSA 74.11	5.83	42.23
34	CPATSA 49.13	0.81	17.31	CPATSA 42.157	5.75	42.15
35	CPATSA 02.04	0.80	17.30	CPATSA 63.29	5.68	42.08
36	CPATSA 05.168	0.79	17.29	CPATSA 63.114	5.61	42.01
37	CPATSA 76.27	0.79	17.28	CPATSA 14.25G	5.54	41.94
38	CPATSA 49.237	0.78	17.28	CPATSA 51.01	5.47	41.87
39	CPATSA 67.18	0.77	17.27	CPATSA 49.233	5.40	41.80
40	CPATSA 49.114	0.76	17.26	CPATSA 13.23G	5.33	41.73
41	CPATSA 76.06	0.75	17.25	CPATSA 28.32	5.26	41.66
42	CPATSA 79.23	0.75	17.24	CPATSA 49.119	5.20	41.60
43	CPATSA 63.108	0.74	17.24	CPATSA 49.14	5.14	41.54
44	CPATSA 79.42	0.73	17.23	CPATSA 49.99	5.08	41.48
45	CPATSA 49.49	0.72	17.22	CPATSA 49.13	5.03	41.43

Table 9 (continued)

Rk	Soluble solids content			*Ratio*		
	Genotype	Gain	New average	Genotype	Gain	New average
46	CPATSA 49.266	0.72	17.22	CPATSA 63.77	4.97	41.37
47	CPATSA 42.316G	0.71	17.21	CPATSA 49.114	4.91	41.31
48	CPATSA 79.17	0.70	17.20	CPATSA 28.03	4.85	41.25
49	CPATSA 62.13	0.70	17.19	CPATSA 19.08	4.79	41.19
50	CPATSA 67.04	0.69	17.19	CPATSA 70.04	4.73	41.13

Cargnin (2016) evaluated two vine clones and showed that the use of three harvests is suitable for selection, with a determination above 80% for the yield, number of bunches, bunch weight, berry weight and soluble solids content.

The estimates of the new mean values of the 50 best selected individuals were higher than the overall mean for all evaluated traits (Tables 6, 7, 8 and 9). Similar results were obtained by Leão et al.

Table 10 Ranking (Rk) of table grape genotypes classified as apyrenic (seed weight ≤ 10 mg) as a function of seed dry weight

Rk	Genotype	DW	Rk	Genotype	DW	Rk	Genotype	DW	Rk	Genotype	DW
1	CPATSA 14.28G	0.00	29	CPATSA 65.04	0.00	57	CPATSA 67.18	2.37	85	CPATSA 65.64	6.39
2	CPATSA 15.04	0.00	30	CPATSA 76.06	0.00	58	CPATSA 76.05	2.51	86	CPATSA 49.192	6.47
3	'BRS Tainá'	0.00	31	CPATSA 76.23	0.00	59	CPATSA 49.06	2.55	87	CPATSA 32.02	6.58
4	CPATSA 19.08	0.00	32	CPATSA 76.27	0.00	60	CPATSA 24.88	2.60	88	CPATSA 65.104	6.75
5	CPATSA 24.30	0.00	33	CPATSA 79.18	0.00	61	CPATSA 31.11	2.77	89	CPATSA 49.40	6.92
6	CPATSA 31.01	0.00	34	CPATSA 79.23	0.00	62	CPATSA 63.01	2.78	90	CPATSA 21.99	7.10
7	CPATSA 31.10	0.00	35	CPATSA 79.25	0.00	63	CPATSA 65.90	2.78	91	CPATSA 49.63	7.18
8	CPATSA 31.13	0.00	36	CPATSA 79.27	0.00	64	CPATSA 49.05	3.15	92	CPATSA 75.09	7.85
9	CPATSA 40.05CR	0.00	37	CPATSA 79.28	0.00	65	CPATSA 49.191	3.22	93	CPATSA 28.14	8.62
10	CPATSA 40.12 T	0.00	38	CPATSA 79.42	0.00	66	CPATSA 76.20	3.29	94	CPATSA 62.04	9.20
11	CPATSA 42.72 T	0.00	39	CPATSA 79.47	0.00	67	CPATSA 31.12	3.32	95	CPATSA 23.09	9.39
12	CPATSA 49.114	0.00	40	CPATSA 79.48	0.00	68	CPATSA 49.215	3.32	96	CPATSA 49.171	9.47
13	CPATSA 49.119	0.00	41	CPATSA 79.49	0.00	69	CPATSA 49.93	3.73	97	CPATSA 21.114	9.68
14	CPATSA 49.156	0.00	42	CPATSA 89.03	0.00	70	CPATSA 63.47	3.82	98	CPATSA 14.23G	9.76
15	CPATSA 49.184	0.00	43	CPATSA 49.246	0.30	71	CPATSA 79.04	3.89	99	CPATSA 79.38	9.83
16	CPATSA 49.197	0.00	44	CPATSA 49.20	0.45	72	CPATSA 62.22	3.96	100	CPATSA 42.157	9.83
17	CPATSA 49.200	0.00	45	CPATSA 49.198	0.99	73	CPATSA 65.18	4.00	101	CPATSA 28.21	9.95
18	CPATSA 49.25	0.00	46	CPATSA 49.99	1.11	74	CPATSA 49.233	4.01	102	CPATSA 01.06	9.96
19	CPATSA 49.37	0.00	47	CPATSA 49.14	1.12	75	CPATSA 65.112	4.07	103	CPATSA 49.235	9.67
20	CPATSA 49.42	0.00	48	CPATSA 49.65	1.40	76	CPATSA 49.109	4.14	104	CPATSA 28.27	9.97
21	CPATSA 49.70	0.00	49	CPATSA 62.19	1.42	77	CPATSA 49.104	4.25	105	CPATSA 24.04	9.98
22	CPATSA 51.01	0.00	50	CPATSA 49.28	1.65	78	CPATSA 31.P1	4.53	106	CPATSA 49.221	9.98
23	CPATSA 53.38	0.00	51	CPATSA 49.178	1.77	79	CPATSA 67.24	5.05	107	CPATSA 76.22	9.99
24	CPATSA 63.108	0.00	52	CPATSA 26.18	1.81	80	CPATSA 79.50	5.11	108	CPATSA 49.90	10.00
25	CPATSA 63.114	0.00	53	CPATSA 49.266	1.86	81	CPATSA 49.166	5.14	109	CPATSA 49.188	10.00
26	CPATSA 63.15	0.00	54	CPATSA 31.07	1.89	82	CPATSA 63.02	5.27	110	CPATSA 49.234	10.00
27	CPATSA 63.29	0.00	55	CPATSA 49.213	1.92	83	CPATSA 49.58	5.45			
28	CPATSA 63.77	0.00	56	CPATSA 62.80	2.30	84	CPATSA 63.03	5.49			

DW—seed dry weight (mg seed^{-1})

(2018) in the evaluation of grape hybrids in the Submédio São Francisco Valley.

The absence of seeds is an important quality characteristic for table grapes because it is highly valued by consumers. In this study, 110 genotypes were classified as apyrenic or with small seed traits because they presented a seed dry mass less than or equal to 10 mg (Table 10), which classifies the seed as a trait, according to IPGRI (1997).

All 50 hybrids selected in this study met the minimum requirements for the table grape market: bunch mass greater than 300 g, berry length greater than 20 mm, berry diameter greater than 17 mm, soluble solids content greater than 17% and *ratio* higher than 20. In addition, ten hybrids did not have seeds. These selected hybrids have the potential to be asexually propagated and advance to the next stage of the breeding program in the semiarid region in trials with a greater number of plants per genotype.

Finally, according to these results, it can be observed that the genetic structure of a plant population can be partitioned well through estimates of variance components and predictions of components of the mean values (Maia et al. 2017). Such information is important in breeding programs because it guides the selection and supports the recommendations for launching new table grape cultivars.

Conclusion

Grape hybrids exhibit genetic variability for all traits, which allows the selection of superior genotypes for table grape breeding in Brazilian semiarid regions.

The estimates of genetic correlation for the characteristics of the berry and the bunch are of high magnitude, allowing indirect selection.

The estimates of the individual repeatability coefficient for the berry traits show high genetic control and high overall stability over successive seasons. However, with the increase in the number of cycles evaluated, it is possible to obtain high repeatability values for all the evaluated traits, except for the soluble solids content and *ratio*.

Four harvests are sufficient to evaluate the hybrids, as they correspond to a selective accuracy greater than or equal to 70% for all traits.

Individual genotypic selection allows high genetic gains for bunch and berry traits.

The fifty hybrids selected meet the minimum requirements for the table grape market, nine hybrids are apyrenic and should advance to the next stage of genetic improvement.

Acknowledgements The authors thank Coordination of Superior Level Staff Improvement (CAPES) for fnancial support. In addition, we would like to thank the Brazilian Agricultural Research Corporation (Embrapa Semiárido) for their partnership.

Declarations

Competing interest The authors declare to have no conflict of interest, whether financial or non-financial, associated with this research.

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