

## ORIGINAL ARTICLE

## Crop Breeding &amp; Genetics

# Multitrait selection in seedless grape hybrids in semiarid regions of Brazil

Jullyanna Nair de Carvalho<sup>1</sup>  | Pollyanna Aparecida de Carvalho<sup>2</sup> | Rafael Pio<sup>1</sup> | Maria Angélica Guimarães Barbosa<sup>3</sup> | Patrícia Coelho de Souza Leão<sup>3</sup>

<sup>1</sup>Department of Agriculture, Federal University of Lavras (UFLA), Lavras, Minas Gerais, Brazil

<sup>2</sup>Research and Development, Sugarcane Technology Center (CTC), Piracicaba, Sao Paulo, Brazil

<sup>3</sup>Irrigated Agriculture Department, Embrapa Semiárido, CP23, Petrolina, Pernambuco, Brazil

## Correspondence

Jullyanna Nair de Carvalho, Department of Agriculture, Federal University of Lavras (UFLA), CEP: 37200-900, Lavras, MG, Brazil.

Email: [jullyannacarvalho@gmail.com](mailto:jullyannacarvalho@gmail.com)

Assigned to Associate Editor Lori Hinze.

## Funding information

Coordenação de Aperfeiçoamento de Pessoal de Nível Superior; The Brazilian Agricultural Research Corporation (Embrapa)

## Abstract

The absence of seeds has been one of the most valued traits in grapes (*Vitis* spp.) for fresh consumption. However, the simultaneous selection of superior genotypes for multiple traits is complex. The objective of this study was to select genotypes of superior seedless table grapes in semiarid regions of Brazil. Multiple traits were considered by using the factor analysis and genotype–ideotype best linear unbiased prediction (FAI-BLUP) selection index. A total of 110 grape progenies from 24 crosses were evaluated for traits of agronomic interest. Each hybrid was represented by a single vine plant, without experimental design or repetition. The mixed-model methodology was used to predict the breeding values. The FAI-BLUP index was used to select superior genotypes based on factor analysis and the genotype–ideotype distance. Four factors explained the 11 characteristics studied, with a variability of 81.84%. Desirable gains were observed for 10 of the 11 traits evaluated. The FAI-BLUP index allowed the selection of superior seedless table grape hybrids, which can be used in the genetic improvement of grapevines. In conclusion, we report the selection of seedless table grape hybrids for our study to advance in the table grape breeding program in Brazilian semiarid regions.

## 1 | INTRODUCTION

Throughout the history of grapevine domestication, the vegetative propagation method used for reproduction has allowed spontaneous seedless somatic varieties to be propagated and cultivated (Royo et al., 2018). However, the global demand

for seedless table grape cultivars (*Vitis* spp.) is increasing, and winegrowers are increasingly interested in new apyrenic cultivars to remain competitive in the market (Akkurt et al., 2019). Therefore, the absence of seeds or apyrenia has been one of the most valued traits in grapes for fresh consumption.

The Submédio São Francisco Valley, located in a semiarid region of Brazil, is the main producer of seedless table grapes in the tropical axis. However, despite the increase and the economic importance of cultivars introduced in the region, the susceptibility to diseases and lack of adaptation to environmental conditions of some old and traditional cultivars have increased the demand for new seedless table grape cultivars

**Abbreviations:** BeD, berry diameter; BeL, berry length; BeW, berry weight; BuL, bunch length; BuW, bunch weight; BuWi, bunch width; FAI-BLUP, factor analysis and ideotype design—best linear unbiased prediction; LRT, likelihood ratio test; NB, number of bunches per plant; REML/BLUP, restricted maximum likelihood/best linear unbiased prediction; SS, soluble solids content; TA, titratable acidity; *Y*, yield per plant.

adapted to the environmental conditions in semiarid regions of Brazil (Leão, 2021).

In genetic breeding of perennial plants, such as grapevines, one of the most important steps is the selection of superior genotypes. In selection, breeders must deal with the difficulties of choosing the best statistical model to predict genetic values, in addition to the set of characteristics of economic expressiveness that, when used simultaneously, increase the chance of success in selection. However, simultaneously selecting high-performance grape genotypes for multiple traits can be a difficult task.

Some selection indices, such as the classic Smith–Hazel index (Hazel, 1943; Smith, 1936) and the additive genetic index (Resende, 2016), have been proposed for the simultaneous selection of multiple traits. However, there are several limitations regarding the determination of the economic weights of multicollinearity traits and problems (Rocha et al., 2018).

On the other hand, the factor analysis and genotype–ideotype best linear unbiased prediction (FAI-BLUP) index allows genotypes to be ranked based on multiple traits, free of multicollinearity, and does not require weight assignment for traits of economic interest. In addition, this index considers factor analysis and the genetic correlation structure within each factor, preserving the relationship between traits and guiding the selection of genotypes closer to the assumptions by the breeder (Rocha et al., 2018).

The efficiency of this selection index has been reported for the improvement of different crops (Almeida et al., 2021; Meier et al., 2021; Oliveira et al., 2019, 2021; Peixoto et al., 2021; Rocha et al., 2019; Silva et al., 2018; Volpato et al., 2021; Woyann et al., 2020). However, no references were found for the use of the FAI-BLUP index in the genetic improvement of grapevines. Its use in grapevine breeding programs should facilitate and increase selection efficiency. Thus, the objective of this study was to select superior seedless table grape genotypes in a semiarid region of Brazil for multiple traits using the FAI-BLUP selection index.

## 2 | MATERIALS AND METHODS

### 2.1 | Growth conditions

The study was conducted in the Mandacaru Experimental Field of Embrapa Semiárido in Juazeiro, Bahia, Brazil (09°24'S, 40°26'W, at 375 m altitude), in soil classified as vertisol (Cunha et al., 2008). Grapevines were grafted into IAC 572 rootstock and placed in a trellis system with a spacing of 3 × 1 m. Irrigation was performed daily in a drip system. Fertilization was performed according to the soil analysis. The management practices recommended for the crop were performed. Hydrogen cyanamide (5%) was applied after prun-

### Core Ideas

- The absence of seeds is one of the most valued traits in grapes for fresh consumption.
- Simultaneous selection of superior genotypes of seedless table grapes for multiple traits is complex.
- It was possible to select seedless table grape hybrids with desirable agronomic characteristics.
- The use of the genotype–ideotype index allowed the selection of 10 superior seedless table grape hybrids.

ing to break bud dormancy and standardize sprouting. Six harvests from 2018 to 2021 were evaluated.

The climatic information was collected from the Agrometeorological Station of the Campo Experimental de Mandacaru (Figure S1). The monthly average values corresponding to the period of each production cycle (from the date of pruning to the final date of harvest) are presented in the Table 1. Variations were observed in all climatic variables between the six production cycles carried out with the 1st, 3rd, 4th, and 6th production cycles standing out with milder temperatures, while the 2nd and 5th cycles carried out between November to March were characterized by higher temperatures. Average relative humidity and global solar radiation showed smaller variations between production cycles, except for the 3rd cycle with the highest average relative humidity (89%) and lowest global solar radiation (15.14 MJ). In turn, the accumulated rainfall during the period varied from 26.5 mm in the 1st production cycle to 196 mm in the 2nd cycle, demonstrating the temporal irregularity of rainfall, which is typical of the semiarid tropical climate in the Northeast region of Brazil.

### 2.2 | Plant material

A total of 110 genotypes of apyrenic grape hybrids (F1) originating from 24 crosses between cultivars of *Vitis vinifera* and interspecific hybrids were evaluated (Table S1). In this study, the genotypes considered apyrenic, presented seed weights less than or equal to 10 mg, which are classified as trace seeds according to the International Plant Genetic Resources Institute (IPGRI, 1997). Each hybrid was represented by a single vine plant, without experimental design or repetition. However, the multiple harvests would give an estimate of phenotypic trait means along with error estimates. Thus, there were six harvests (“sub-samples”) that provided a form of replication in the experiment even though each hybrid plant itself was not replicated.

**TABLE 1** Pruning and harvesting dates and averages for main climatic variables during six growing seasons, Juazeiro, BA, Brazil.

Growing season	Pruning date	Harvestdate	$T_a$ (med) (°C)	$T_a$ (max) (°C)	$T_a$ (min) (°C)	$H_r$ (med) (%)	$R_G$ (MJ)	$P$ (mm)
1st	Apr. 30, 2018	Aug. 17 to Sept. 15, 2018	25.47	32.42	19.38	71.15	21.86	26.52
2nd	Nov. 6, 2018	Feb. 12 to Mar. 17, 2019	27.59	34.34	22.06	71.12	21.42	196.10
3rd	Mar. 4, 2020	June 2 to June 30, 2020	25.38	31.49	20.91	89.02	15.14	147.57
4th	July 15, 2020	Oct. 23 to Nov. 20, 2020	25.71	32.69	19.60	72.36	20.79	81.79
5th	Dec. 16, 2020	Mar. 8 to Apr 16, 2021	27.18	33.71	21.67	71.69	21.68	97.28
6th	June 30, 2021	Sept. 28 to Oct. 29, 2021	25.30	32.11	19.56	72.68	20.27	62.22

Abbreviations:  $T_a$ , temperature;  $H_r$ , relative humidity;  $R_G$ , global radiation;  $P$ , precipitation.

## 2.3 | Evaluated traits

The following traits were evaluated: yield (kg plant<sup>-1</sup>), obtained through the weight of all bunches harvested from each plant; number of bunches (bunches plant<sup>-1</sup>), counting the bunches on the plant at the time of harvest; bunch length (cm), bunch width (cm) and bunch weight (g), obtained from the average of a sample composed of five bunches per plant; berry length (mm), diameter (mm) and weight (g), obtained as the average of a sample of 10 berries randomly collected from each of the five bunches evaluated above; soluble solids content (%) and titratable acidity (%), obtained from the juice of a sample of 50 berries using a digital refractometer and digital titrator, respectively; *ratio* (soluble solids content/titratable acidity) (dimensionless); berry consistency (crunchy, fleshy, and melty), which was considered a restrictive trait in the selection index; and berry flavor (special, muscatel, foxado, and neutral) and berry color (green, red, and black), for characterization purposes.

## 2.4 | 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,  $LRT = (-2\text{Log}L)_{p-1} - (-2\text{Log}L)_p$ , where  $\text{Log}L$  is the logarithm of the maximum point of the residual likelihood function ( $L$ ) associated with the reduced ( $p-1$ ) and complete ( $p$ ) models, and  $(-2\text{Log}L)$  is the deviance. The  $LRT$  was compared with the value of the probability density function ( $\chi^2$ ) with one degree of freedom at 1% and 5% probability.

The variance components were estimated by restricted maximum residual likelihood (REML), while the genotypic values were predicted by the best unbiased linear predictor (BLUP) (Henderson, 1975; Patterson & Thompson, 1971).

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 equation:

$$y = X_m + Z_p + e, \quad (1)$$

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.

The genotypic values (BLUP mean values) were predicted for each of the 110 genotypes based on the 11 quantitative traits evaluated. The BLUP mean values were used for the simultaneous selection of the best genotypes of apyrenic hybrids using the FAI-BLUP index.

This index is based on structural equation models combining the technique of factor analysis (exploratory factor analysis) with the ideotype design (confirmatory factor analysis) of multiple characteristics in addition to exploring the correlations between the evaluated characteristics.

The factor analysis has the objective of resuming the various variables in a smaller set of dimensions with a minimum loss of information. Thus, it seeks to define, in a study with many variables, sets of highly correlated variables, known as factors (Rocha et al., 2018).

The proportion of variability of each variable explained by the factors is called commonality. The higher the commonality, the more informative the variable is for the factor and, therefore, the factor in which it is inserted represents it. The average commonality is equivalent to the accumulated variance for the factors (Cruz et al., 2014; Peixoto et al., 2021; Rocha et al., 2018).

The predicted gain with selection (GS%) was calculated considering 25% as the selective intensity and was obtained by

$$GS\% = \left[ \frac{\bar{X}_m - \bar{X}_0}{\bar{X}_0} \right] \times 100, \quad (2)$$

where GS% is the gain in the selection of the best genotypes for the variable,  $\bar{X}_m$  is the mean BLUP of the genotype selected for the variable, and  $\bar{X}_0$  is the overall BLUP mean of all genotypes for the variable.

In the FAI-BLUP index, the ideotype was defined based on the combination of desirable and undesirable quantitative traits according to the selection objective. After determining the ideotype, the distances of each genotype according to the ideotype (genotype–ideotype distance) were estimated and converted into spatial probabilities, allowing the ranking of genotypes based on the adaptation by Rocha et al. (2018):

$$P_{ij} = \frac{\frac{1}{d_{ij}}}{\sum_{i=1:n; j=1:m} \frac{1}{d_{ij}}} c_{ij}, \quad (3)$$

$$c_{ij} \begin{cases} 1 & \text{if } C = \text{crunchor fleshy} \\ 0 & \text{if } C = \text{melty} \end{cases}, \quad (4)$$

where  $P_{ij}$  is the probability that the  $i$ th genotype ( $i = 1, 2, \dots, n$ ) is similar to the  $j$ th ideotype ( $j = 1, 2, \dots, m$ ),  $d_{ij}$  is the genotype–ideotype distance from the  $i$ th genotype to the  $j$ th ideotype based on the standardized mean Euclidean distance, and  $c_{ij}$  is the restriction imposed in the selection considering the consistency of the berry ( $C$ ).

The restriction on the selection index for  $C$  was imposed by a dummy variable (1 and 0), which multiplies the index, penalizing progenies with a score of 0, i.e., grapes that have melty berries were not selected.

The software Selegen-REML/BLUP, version 1.0.0.0 (Resende, 2016) was used for deviance analysis, estimative of variance components, and the prediction of breeding values. The software R, version 4.1.2 (R Development Core Team, 2019) was used to apply the FAI-BLUP index for the selection of hybrids, according to the script described by Rocha et al. (2018). The software GENES, version 1990.2023.3 (Cruz, 2016) was used to estimate the correlation with Pearson's coefficient.

### 3 | RESULTS

#### 3.1 | Deviance analysis

The deviance analysis for the 11 quantitative traits revealed that genotypes conferred significant effects ( $p < 0.01$ ) for phenotypic variations. The deviance analysis indicated variability among hybrids for all traits evaluated, and therefore all of them were used for genotypic selection.

#### 3.2 | Variance components (REML) and genotypic values (BLUP)

The estimation of the genetic and phenotypic parameters for the variables considered in this study are presented in Table 2.

The general average production was 2.14 kg per plant, corresponding to an estimated yield of 10 t ha<sup>-1</sup> per crop. In addition, the average number of bunches per plant was reduced to approximately 14 bunches, a characteristic 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, titratable acidity, and *ratio* were 13.62 cm, 7.95 cm, 174.02 g, 17.30 mm, 14.83 mm, 2.34 g, 16.41%, 0.52%, and 36.51%, respectively.

The estimated temporary environmental variance ( $V_{te}$ ) was higher than the permanent phenotypic variance between plants ( $V_{pp}$ ) for all traits evaluated, representing most of the phenotypic variance ( $V_p$ ) (Table 2).

The estimates of the repeatability coefficient ( $r$ ) ranged from 0.14 to 0.54 (Table 2) and were considered intermediate berry weight (0.54), berry diameter (0.49), berry length (0.37), bunch length (0.29), bunch width (0.22), bunch weight (0.40), yield (0.25) and number of bunches (0.24). In contrast, the estimates for the soluble solids content (0.13) and titratable acidity (0.15) were considered low.

The selective accuracy ( $A_{cm}$ ) predicted by REML for the evaluated parameters ranged from 0.69 (soluble solids content) to 0.94 (berry weight). Selective accuracy values were higher than 0.70 for 10 of the 11 variables analyzed (Table 2), indicating accuracy and a medium to high degree of certainty in the inferences, with selection gains for all variables.

The genotypic values (BLUP) and genetic gains of the 110 genotypes for each of the traits are presented in Tables S2 to S5. The genotypic values were used in the FAI-BLUP for ranking the genotypes. Without practicing selection, the greatest gains obtained for the evaluated traits were 4.77 kg (yield), 11.87 bunches (number of bunches), 2.65 cm (bunch length), 2.33 cm (bunch width), 128 g (bunch weight), 3.67 mm (berry length), 2.86 mm (berry diameter), 150 g (berry weight), 0.99% (soluble solids content), 0.11% (titratable acidity) and 8.76 (*ratio*).

#### 3.3 | Factor analysis

Regarding the factor analysis, the eigenvalues and cumulative variance were estimated for the 11 principal components obtained by the genetic correlation matrix between traits (Table 3). The accumulated variance for the first four principal components indicates that these components are sufficient

**TABLE 2** Variance components (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 110 hybrid genotypes of *Vitis* spp.

Traits evaluated	General average	$V_{pp}$	$V_{te}$	$V_p$	$r = h^2$	$r_m$	$A_{cm}$
Yield (kg)	2.14 ± 0.74	1.12	3.36	4.48	0.25 ± 0.07	0.67	0.82
Number of bunches	13.78 ± 3.49	25.29	81.94	107.24	0.24 ± 0.07	0.65	0.81
Bunch length (cm)	13.62 ± 1.16	2.45	5.95	8.40	0.29 ± 0.08	0.71	0.84
Bunch width (cm)	7.95 ± 0.64	0.80	3.15	4.05	0.22 ± 0.07	0.63	0.79
Bunch weight (g)	174.01 ± 46.02	3164.84	4628.10	7792.95	0.40 ± 0.09	0.80	0.90
Berry length (mm)	17.30 ± 1.29	2.64	4.42	7.05	0.37 ± 0.09	0.78	0.88
Berry diameter (mm)	14.83 ± 1.05	1.49	1.52	3.02	0.49 ± 0.11	0.85	0.92
Berry weight (g)	2.34 ± 0.47	0.24	0.29	0.52	0.54 ± 0.11	0.88	0.94
Soluble solids content (%)	16.41 ± 0.49	0.79	5.27	6.06	0.13 ± 0.05	0.47	0.69
Titrate acidity (%)	0.52 ± 0.05	0.01	0.02	0.03	0.22 ± 0.07	0.63	0.79
Ratio	36.51 ± 3.20	31.71	190.53	222.25	0.14 ± 0.06	0.50	0.70

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

**TABLE 3** Eigenvalue estimates using principal component analysis and the proportion of variance explained by them for eleven apyrenic grape hybrid traits.

Main component	Eigenvalue	Eigenvalue (%)	Cumulative variance (%)
PC1	3.74	34.00	34.00
PC2	2.35	21.45	55.45
PC3	1.66	15.14	70.59
PC4	1.22	11.18	81.77
PC5	0.89	8.11	89.88
PC6	0.39	3.59	93.47
PC7	0.27	2.50	95.97
PC8	0.21	1.99	97.96
PC9	0.08	0.74	98.70
PC10	0.07	0.70	99.40
PC11	0.06	0.60	100.00

to represent 81% of all the variability existing among the hybrids.

The variables that most correlated with each factor were identified based on the magnitude of the factor loadings, which indicate the correlation of each variable with a given factor (Table 4).

For the first factor, which explained 34.00% of the variance (Table 3), there was a high genetic correlation between the bunch length, bunch width and bunch weight, and this factor was referred to as the bunch factor. For the second factor, responsible for 21.45% of the variance (Table 3), there was a high genetic correlation between the soluble solids content, titrate acidity, and *ratio*, and this factor was referred to as the quality factor. For the third factor, a high genetic

correlation was observed between the berry length, berry diameter and berry weight, and this factor, which explained 15.14% of the variance (Table 3), was referred to as the berry factor. Finally, the fourth factor, which represented 11.18% of the variance (Table 3), was referred to as the yield factor, where the yield and number of bunches per plant were strongly correlated.

For the second factor, there was a negative correlation between the titrate acidity and soluble solids, as expected. Regarding the first, third, and fourth factors, correlations in the same direction were observed between the characteristics within each factor (Table 4).

The commonality values ranged from 0.48 to 0.95 (Table 4). The commonalities of all variables were high, indicating a good association between the variables and factors, with the exception of the soluble solids content (0.48), which indicates a minimal relationship between this variable and the factor in which it is inserted.

The estimates of Pearson's linear correlation between the evaluated traits ranged from 0.001 to 0.84 (Table S6). 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 weight; titrate acidity, and the *ratio* showed high positive correlations.

The characterization of the genotypes regarding the trait's consistency, flavor, and berry color is presented in Table S7. Regarding the berry consistency, 61% of the genotypes had melty berries, 31% had fleshy berries and 8% had crunchy berries. Thus, only 38% (43 genotypes) were suitable for selection. The pulp flavor was neutral (85.5%), special (9%), and muscatel (5.5%). Finally, 58% of the genotypes had green berries, 40% had red berries and 2% had black berries.

**TABLE 4** Factor loadings after varimax rotation and commonalities for the evaluated apyrenic grape hybrid traits.

Traits	Factor				
	Bunch	Quality	Berry	Production	Commonality
Yield	-0.5421	-0.0117	0.1846	0.6910	0.8056
Number of bunches	0.0129	-0.0930	-0.0137	0.9245	0.8638
Bunch length	-0.8580	0.1297	-0.0177	0.1257	0.7692
Bunch width	-0.8709	0.0159	0.2156	-0.0226	0.8059
Bunch weight	-0.8923	0.1162	0.2602	0.0453	0.8797
Berry length	-0.1264	-0.0741	0.9139	0.0226	0.8573
Berry diameter	-0.1517	-0.0428	0.9318	0.0029	0.8931
Berry weight	-0.1567	-0.0200	0.9554	0.0757	0.9436
Soluble solids content	-0.0320	-0.5838	0.0026	-0.3765	0.4837
Titrateable acidity	-0.1229	0.8240	-0.0430	-0.2045	0.7378
Ratio	0.1363	-0.9589	0.0876	0.0945	0.9548
Average	–	–	–	–	0.8177

### 3.4 | Genetic gains

The predicted genetic gains obtained with the selection of the 10 genotypes (23% selection intensity) for all traits evaluated simultaneously by means of direct selection and the FAI-BLUP index are presented in Table 5.

### 3.5 | Obtaining genetic gains in the desirable direction for the bunch factor, quality factor, berry factor, and production factor using the FAI-BLUP index

The gains obtained using the FAI-BLUP index in relation to those obtained using direct selection were approximately 56% for the traits to be increased and approximately 68% for the traits to be decreased.

Considering the selection intensity of 23% (10 genotypes) used in this study, we can identify in which traits the hybrids selected by the index would also be selected applying direct selection. The “BRS Tainá” cultivar, the first hybrid selected using the FAI-BLUP index, is on the list of 10 cultivars selected using direct selection for all traits, except for the soluble solids content. The second hybrid selected by using the FAI-BLUP index, the CPATSA 79.04, was present on the list of the 10 cultivars selected using direct selection for nine of the 11 traits evaluated; there was only disagreement in the results for number of bunches and soluble solids content. CPATSA 49.171, the third hybrid selected using the FAI-BLUP index, was absent on the list of the 10 cultivars selected using direct selection only for traits for soluble solids content and ratio, for example.

In addition, the percentage of genotypes that coincided between the FAI-BLUP selection index and direct selection

**TABLE 5** Predicted genetic gains based on direct selection and the FAI-BLUP index.

Factor	Traits	Predicted genetic gain (%)	
		Direct selection	FAI-BLUP
Bunch	BuL	8.24	2.52
	BuWi	11.32	6.07
	BuW	24.30	10.58
Quality	SS	3.21	0.91
	TA	-12.13	-8.30
	Ratio	12.66	9.01
Berry	BeL	10.45	5.70
	BeD	11.85	6.44
	BeW	36.68	19.04
Production	Y	45.41	31.81
	NB	34.79	20.08
Total desirable gains (%) <sup>a</sup>		56.39	
Total undesirable gains (%) <sup>b</sup>		68.24	

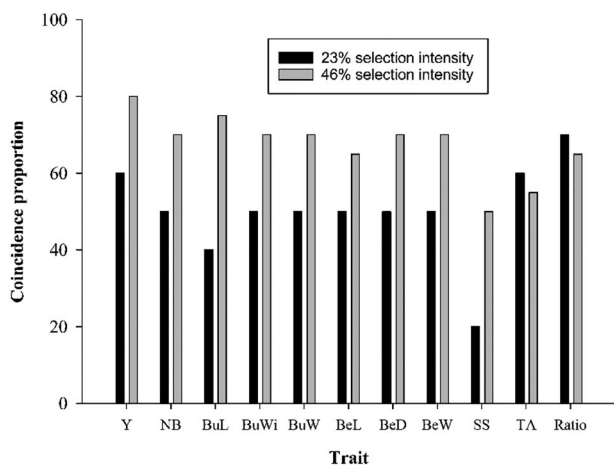
Note: Genotypes selected using the FAI-BLUP index: 5, 98, 38, 103, 85, 31, 4, 77, 30 e 52.

Abbreviations: BeD, berry diameter (mm); BeL, berry length (mm); BeW, berry weight (g); BuL, bunch length (cm); BuWi, bunch width (cm); BuW, bunch weight (g); ratio SS/AT (dimensionless); SS, soluble solids content (%); TA, titrateable acidity (%); Y, yield per plant (kg); NB, number of bunches per plant.

<sup>a</sup>Proportion of the predicted gain for traits to be increased (BuL, BuWi, BuW, SS, ratio, BeL, BeD, BeW, Y, NB) in relation to the predicted gain for direct selection.

<sup>b</sup>Proportion of the predicted gain for traits to be decreased (TA) in relation to the predicted gain for direct selection.

was greater than or equal to 50% for most traits, except for the soluble solids content and bunch length. Using a selection intensity of 23% (10 genotypes), the proportions of the



**FIGURE 1** Proportion of the best hybrids that were selected by the index, with selection intensities of 23% and 46%. Traits: yield per plant (Y), number of bunches per plant (NB), bunch length (BuL), bunch width (BuWi), bunch weight (BuW), berry length (BeL), berry diameter (BeD), berry weight (BeW), soluble solids content (SS), titratable acidity (TA), *ratio*.

agreement were 70% for the *ratio*; 60% for the yield and titratable acidity; 50% for number of bunches, bunch width, bunch weight, berry length, berry diameter, and berry weight; 40% for bunch length, and 20% for the soluble solids content.

The percentage of agreement between the selection index and the direct selection increased as the proportion of the selected hybrids increased. The proportion increased as the intensity of selection also increased, reaching 80% (yield), 75% (bunch length), 70% (number of bunches, bunch width, bunch weight, berry diameter and berry weight), 65% (berry length), 60% (*ratio*), 55% (titratable acidity), 50% (soluble solids content), and less than 46% selection intensity. These results demonstrate that the index was efficient in selecting the best hybrids (Figure 1).

The classification of the 43 genotypes of seedless grapes, with crunchy and fleshy consistency, according to direct selection, for each of the characteristics (yield, number of bunches, bunch length, bunch width, bunch weight, berry length, diameter length, berry weight, soluble solids content, titratable acidity, and *ratio*) is presented in Table S8.

### 3.6 | Ranking of genotypes by the FAI-BLUP index

Figure 2 shows the classification of the 43 genotypes of seedless grapes with firm texture (consistency of the crunchy or fleshy pulp) according to the FAI-BLUP index and its associated spatial probability.

Ten genotypes were selected at a selection intensity of 23% over the 43 genotypes of seedless grapes with firm tex-

ture. According to the index, the first 10 genotypes selected were BRS Tainá, CPATSA 79.04, CPATSA 49.171, CPATSA 79.28, CPATSA 65.112, CPATSA 49.104, CPATSA 63.108, CPATSA 49.06, CPATSA 15.04, CPATSA 49.234.

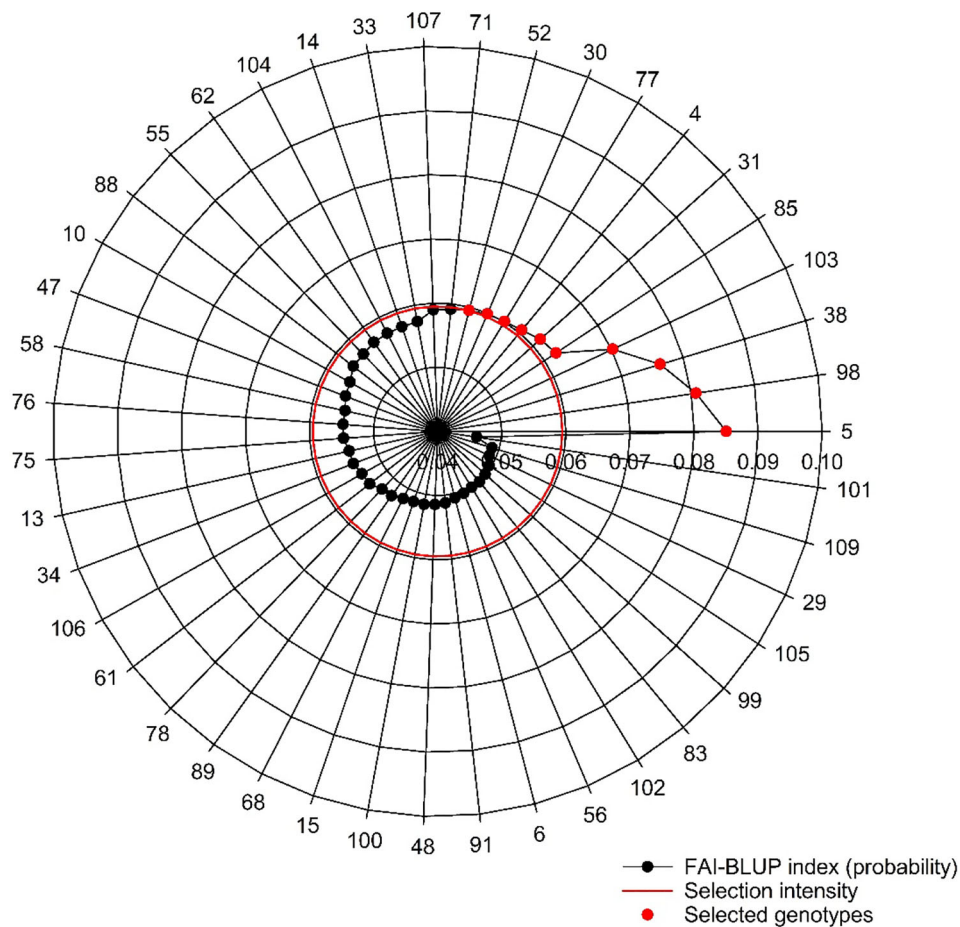
The hybrids BRS Tainá, CPATSA 79.04, and CPATSA 49.171 showed good performance for production, bunch, berry, and quality factors. CPATSA 79.28 stood out more in terms of production and quality. CPATSA 65.112 showed good production, bunch, and quality traits, but in relation to the berry factor, it was average. CPATSA 49.104 had good performance in bunch, berry, and quality factors, but in relation to production, the performance was unsatisfactory. CPATSA 63.108 did not show good bunch characteristics, but for production, berry, and quality factors, it performed well. The strong point of the CPATSA 49.06 hybrid was the quality factor. CPATSA 15.04 presented production, bunch, and berry factors as strengths. The hybrid CPATSA 49.234, on the other hand, presented the quality factor as a weak point.

## 4 | DISCUSSION

The basic premise for selection is the presence and knowledge of genetic variability. 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 (Malikouski et al., 2021). 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.

The analysis via mixed models (REML/BLUP) allows reducing this time by performing selection without requiring experimental designs using different measures per plant and predicting permanent phenotypic values through the mean of repeated measures weighted by the temporal repeatability coefficient of the trait (Resende, 2016).

The superiority of the temporary environmental variance ( $V_{te}$ ) in relation to the permanent phenotypic variance estimated between plants ( $V_{pp}$ ) (Table 2) indicate that these characteristics are highly influenced by environmental conditions. Results similar to these were reported by Carvalho et al. (2023) for yield, number of bunches, bunch traits, soluble solids content, titratable acidity and *ratio*; Sánchez et al. (2017) for fruit production; 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  $V_{pp}$



**FIGURE 2** Classification of seedless table grape genotypes, and the 10 genotypes selected using the factor analysis and genotype-ideotype distance (FAI-BLUP). The numbers on the outer circle correspond to the hybrid number in Table S7, making it possible to identify the selected genotype.

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 in the 1st and 2nd semester crops in the Submédio São Francisco Valley, together with the alternations common in consecutive seasons.  $V_{te}$  values higher than  $V_{pp}$  values hamper the selection of promising genotypes based on simple plant breeding methods, such as clone selection, which takes into account only the individual phenotype (Leão et al., 2018).

According to the Kaiser criterion (Kaiser, 1958), the number of principal components is determined by the number of eigenvalues greater than 1. In this study, the first four principal components had eigenvalues greater than 1, and thus, the data could be condensed into four factors, which explained 81% of the variance. In a study on genetic divergence among grapevine cultivars from the Active Germplasm Bank of Embrapa Semiárido, considering 11 fruit quality traits, it was found that two main components explained 79.45% of the total

variance contained in the set of traits analyzed (Batista et al., 2015). At the same Germplasm Bank of Embrapa Semiárido, the genetic diversity and performance of grape cultivars were evaluated based on nine morphoagronomic traits (cycle duration, production, number of bunches, length, width and weight of the bunch, soluble solids content, titratable acidity, and *ratio*) and four factors explained 84.12% of the variance (Leão et al., 2011). Pereira et al. (2008), evaluating the quality characteristics of wine grapes, found that the variables evaluated were reduced to four main components, which explained 67.36% of the total variation.

Traits grouped into the same factor exhibit greater correlation with each other than with variables from different factors. This means that characteristics belonging to the same factor can be grouped into a “macrocharacteristic” (factors) with a biological meaning. In this study, the “macrocharacteristics” formed were production, bunch, berry, and quality. Therefore, each factor has biological significance based on the genetic correlation between the traits (Cruz et al., 2014; Rocha et al., 2018). Genetic correlations between traits within a factor can be given in the same direction and/or in the opposite direction



and are given by the signs of the factor loadings. In this study, the direction of correlations between characteristics within the same factor occurred as expected, with most correlations being positive (Table 4). In the selection by FAI-BLUP index, it is important that the correlations between the characteristics are high and that they have biological sense, since the selection of genotypes for multiple characteristics is based on the analysis of factors.

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.

Nikolic et al. (2018), evaluating the phenotypic correlations between agronomic traits in grapevines, identified a significant and negative correlation between the soluble solids content and titratable acidity but also observed a positive correlation between the bunch mass and berry mass. Wei et al. (2002) also found a strong positive correlation between the berry mass, length, and diameter and a strong negative correlation between the soluble solids content and titratable acidity, in addition to a high positive correlation between the soluble solids content and *ratio*. Cargnin (2019) evaluated the magnitude of association between traits of clones of two cultivars of *Vitis vinifera* using canonical correlation, obtaining correlations  $r = -0.71$  and  $r = 0.55$  between the yield and number of bunches,  $r = 0.98$  and  $r = 0.90$  between the bunch weight and yield,  $r = -0.82$  and  $r = 0.16$  between the number of bunches and bunch weight,  $r = -0.18$  and  $r = -0.77$  between the number of berries and berry weight and  $r = 0.13$  and  $r = -0.05$  between the soluble solid content and titratable acidity for “Cabernet Sauvignon” and “Chardonnay,” respectively.

The genetic correlation coefficients estimated by Pearson’s linear correlation (Table 6) confirm that the traits grouped in the factors present high genetic correlation and are in the desirable direction, contributing to the efficiency of the selection by FAI-BLUP.

The commonalities of all variables were high, indicating a good association between the variables and the factors, with the exception of the soluble solids content, which indicates a minimal relationship between this variable and the factor in which it is inserted (Table 4). Commonality is the proportion of variability of each variable explained by the factors. The higher the commonality is, the more informative the variable is for the factor and, therefore, the factor in which it is inserted represents it. The average commonality is equivalent to the accumulated variance for the factors (Cruz et al., 2014; Peixoto et al., 2021; Rocha et al., 2018). The good association between the characteristics of the factors associated with high correlation and in the desirable sense, already mentioned, once again signal the efficiency in the selection by the FAI-BLUP.

An ideotype-based breeding program focuses on multiple traits simultaneously. The ideotype in the FAI-BLUP index is determined from the genetic correlations of each factor (Meier et al., 2021). The ideal agronomic and commercial ideotype of seedless table grapes was designed using the maximum breeding values for the yield, number of bunches, bunch length, bunch width, bunch weight, berry length, berry diameter, bunch weight, and soluble solids content and *ratio*, and the minimum breeding value for titratable acidity. Berry consistency was considered an eliminatory qualitative trait in the selection process, since the ideotype must have a berry with a firm texture, according to consumer market requirements.

Thus, based on the restriction applied, only grapes with a crunchy or fleshy consistency were selected. Fernandes Filho et al. (2021), seeking potato clones suitable for industry, and Melo et al. (2020), aiming to select superior common bean progenies to mitigate the effects of genotype-environment interactions, incorporated a restriction on the selection index for multiple traits based on the genotype-ideotype distance.)

By using the FAI-BLUP selection index, the genotypes were ranked based on multiple traits simultaneously. Considering the seedless table grape ideotype in this study, a total of 10 genotypes with the highest potential were selected using this index.

In addition, the use of the FAI-BLUP index allowed desirable genetic gains to be obtained for all traits evaluated (Table 5), demonstrating the efficiency of the index used to provide balanced gains. Similar results were found by Volpato et al. (2021), who obtained desired gains for all traits evaluated for soybean using the FAI-BLUP selection index. When using other indices, gains in the undesirable direction were obtained for some variables. Almeida et al. (2021), selecting mangaba genotypes using the FAI-BLUP index, also found desirable gains for most of the variables considered in the study. In the selection of superior wheat genotypes, it was also possible to obtain desirable genetic gains for yield traits (Meier et al., 2021).

When using direct selection, the maximum predicted gain can be obtained by considering one trait at a time. The selection of several combined traits often results in reduced selection gains for all traits evaluated when compared to gains obtained using direct selection (Cruz et al., 2014). Gains with multitrait selection represented more than 50% of gains obtained with direct selection. This reveals efficiency in multitrait selection for the 11 traits considered in this study, knowing that the greater the number of traits to be selected, the smaller the gain compared to direct selection. Thus, even if greater gains were obtained using direct selection in relation to the FAI-BLUP index, the latter should be preferred in the process of selecting superior hybrids considering the set of traits.

In addition, the percentage of genotypes that coincided between the FAI-BLUP selection index and direct selection

was greater than or equal to 50% for most traits evaluated in this study. Fernandes Filho et al. (2021) observed that the proportion of agreement between direct selection and the FAI-BLUP index increased as the intensity of selection also increased, reaching between 59% and 73% when applying a selection intensity of 50%. These results demonstrate that the index was efficient in the selection of the best seedless table grape hybrids.

According to the FAI-BLUP index, the first 10 genotypes selected (Figure 2) have greater potential to pass to the next stage as advanced selections in table grape breeding because they have characteristics closer to the ideotype in terms of the yield, number of bunches, bunch length, bunch width, bunch weight, berry length, berry diameter, berry weight, soluble solids content, and *ratio*.

Among the selected genotypes, the use of total genetic variance (additive and dominance) by vegetative multiplication is expected to maximize genetic gains in selection.

This index constitutes a new tool for applications in genetic improvement programs of any crop (Rocha et al., 2018). Its use allows the ranking of genotypes based on spatial probability. Moreover, it does not require weight assignment to different traits and does not present multicollinearity problems. In addition, the procedure allows the selection of genotypes through predicted breeding values, which excludes environmental effects (Almeida et al., 2021). Studies have compared indices of multitrait selection and observed that the best gains were obtained with the use of the FAI-BLUP index (Rocha et al., 2018; Volpato et al., 2021).

Although proposed only recently, the FAI-BLUP index has already been used efficiently in (i) the evaluation and selection of sorghum hybrids for biomass increase and energy cogeneration (Oliveira et al., 2019; Silva et al., 2018); (ii) soybean selection for biodiesel production (Woyann et al., 2020); (iii) selection of superior common bean progenies (Rocha et al., 2019); (iv) selection of *Jatropha curcas* L. genotypes for bioenergetic purposes (Rodrigues et al., 2020); (v) selection of superior pumpkin genotypes with smaller size and higher seed yield for oil production (Oliveira et al., 2020); (vi) combined selection in maize (Peixoto et al., 2021); (vii) simultaneous selection of mangaba based on eleven agronomic traits (Almeida et al., 2021); (viii) selection of early soybean progenies that are more erect and have higher grain yield potential (Volpato et al., 2021); (ix) and selection of superior wheat genotypes for grain yield, tiller number and grain weight per plant (Meier et al., 2021).

In this study, the FAI-BLUP index was efficient in the selection of grapevine hybrids, simultaneously presenting balanced genetic gains for all desirable traits. The methodology successfully identified genotypes similar to materials already launched on the market, such as the “BRS Tainá” cultivar, confirming the efficiency of selection via the FAI-BLUP index in generating selection gains for multiple traits. The 10

hybrids selected in this study met the minimum requirements for the table grape market: berry length greater than 17 mm, berry diameter greater than 15 mm, soluble solids content greater than 16%, and ratio higher than 20. The mass of the bunch was around 250 g, a little below what is required by the market (300 g). But this trait, as well as the traits production and number of bunches, can be improved with plant management. In addition, 10 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. Therefore, it is a suitable tool for the simultaneous selection of important traits in table grape breeding, contributing to the success and speed in the development of apyrenic table grape cultivars.

## 5 | CONCLUSION

In the present study, we selected seedless grape hybrids with desirable agronomic characteristics. “BRS Tainá,” CPATSA 79.04, CPATSA 49.171, CPATSA 79.28, CPATSA 65.112, CPATSA 49.104, CPATSA 63.108, CPATSA 49.06, CPATSA 15.04, CPATSA 49.234 stood out as promising hybrids to advance in the table grape breeding program for Brazilian semiarid regions.

### AUTHOR CONTRIBUTIONS

**Jullyanna Nair de Carvalho:** Data curation; formal analysis; investigation; methodology; software; validation; visualization; writing – original draft; writing – review and editing.

**Pollyanna Aparecida de Carvalho:** Data curation; formal analysis; writing – review and editing. **Rafael Pio:** Supervision; writing – review and editing. **Maria Angélica Guimarães Barbosa:** Supervision; writing – review and editing. **Patrícia Coelho de Souza Leão:** Conceptualization; methodology; project administration; resources; supervision; validation; writing – review and editing.

### ACKNOWLEDGMENTS

The authors thank Coordination of Superior Level Staff Improvement (CAPES) for financial support and Brazilian Agricultural Research Corporation (Embrapa Semiárido) for financial support and their partnership.

### CONFLICT OF INTEREST STATEMENT

The authors declare to have no conflict of interest associated with this research.

### DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available from the corresponding author (Carvalho, J. N) upon reasonable request.

## ORCID

Jullyanna Nair de Carvalho  <https://orcid.org/0000-0003-1228-6731>

## REFERENCES

- Akkurt, M., Tahmaz, H., & Veziroğlu, S. (2019). Recent developments in seedless grapevine breeding. *South African Journal of Enology and Viticulture*, *40*, 260–265. <https://doi.org/10.21548/42-2-3342>
- Almeida, G. Q., Rocha, J. R. A. S. C., Pessoa, H. P., Alves, F. M., & Chaves, L. J. (2021). Selection of *Hancornia speciosa* germplasm accessions based on the FAI-BLUP index. *Pesquisa Agropecuária Tropical*, *51*, e67226. <https://doi.org/10.1590/1983-40632021v5167226>
- Batista, P. F., Lima, M. A. C., Leão, P. C. S., Souza, F. F., & Alves, E. R. (2015). Genetic divergence among grapevine varieties from the Active Germplasm Bank of Embrapa Semiárido. *Revista Ciência Agronômica*, *46*, 800–808. <https://doi.org/10.5935/1806-6690.20150068>
- Cargnin, A. (2019). Canonical correlations among grapevine agronomic and processing characteristics. *Acta Scientiarum Agronomy*, *41*, e42619. <https://doi.org/10.4025/actasciagron.v41i1.42619>
- Carvalho, J. N., Pio, R., Carvalho, P. A., Barbosa, M. A. G., & Leão, P. C. S. (2023). Estimates of genetic parameters and the selection of table grape hybrids in semi-arid regions of Brazil. *Euphytica*, *35*, 1–18. <https://doi.org/10.1007/s10681-023-03163-8>
- Cruz, C. D. (2016). Genes Software – Extended and integrated with the R, Matlab and Selegen. *Acta Scientiarum Agronomy*, *38*, 547–552. <https://doi.org/10.4025/actasciagron.v38i4.32629>
- Cruz, C. D., Carneiro, P. C. S., & Regazzi, A. J. (2014). *Biometric models applied to genetic breeding*. (4th ed.): UFV.
- Cunha, T. J. F., Silva, F. H. B. B. D., Silva, M. S. L. D., Giongo, V., Sa, I. B., Oliveira Neto, M. B. D., & Cavalcanti, A. C. (2008). *Solos do Submédio do Vale do São Francisco: Potencialidades e limitações para o uso agrícola*. Embrapa Semiárido.
- Fernandes Filho, C. C., Andrade, M. H. M. L., de Souza Marçal, T., Fernandes, M. O., Bastos, A. J. R., Guedes, M. L., de Paula Ribeiro, S. R. R., Pinto, C. A. B. P., & Nunes, J. A. R. (2021). Selection of potato (*Solanum tuberosum* L.) clones for heat tolerance and resistance to viruses X and Y for processing purposes. *Crop Science*, *61*, 552–565. <https://doi.org/10.1002/csc2.20361>
- Hazel, L. N. (1943). The genetic basis for constructing selection indexes. *Genetics*, *28*, 476–490. <https://doi.org/10.1093/genetics/28.6.476>
- Henderson, C. R. (1975). Best linear unbiased estimation and prediction under a selection model. *Biometrics*, *31*, 423–447. <https://doi.org/10.2307/2529430>
- International Plant Genetic Resources Institute (IPGRI). (1997). *Descriptors for grapevine: Vitis spp.* IPGRI.
- Kaiser, H. (1958). The varimax criterion for analytic rotation in factor analysis. *Psychometrika*, *23*, 187–200. <https://doi.org/10.1007/BF02289233>
- Leão, P. C. S. (2021). BRS Tainá: New white seedless grape cultivar for the Brazilian semi-arid region. *Crop Breeding and Applied and Biotechnology*, *21*, 1–6. <https://doi.org/10.1590/1984-70332021v21n3c49>
- Leão, P. C. S., Cruz, C. D., & Motoike, S. Y. (2011). Genetic diversity of table grape based on morphoagronomic traits. *Scientia Agrícola*, *68*, 42–49. <https://doi.org/10.1590/S0103-90162011000100007>
- Leão, P. C. S., Nunes, B. T. G., & Souza, E. M. C. (2018). Repeatability coefficients and genetic gains in table grape progenies for the Brazilian semi-arid region. *Scientia Agriculture*, *75*, 387–392. <https://doi.org/10.1590/1678-992X-2017-0046>
- Malikowski, 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*, 1–10. <https://doi.org/10.4025/actasciagron.v43i1.51740>
- Meier, C., Marchioro, V. S., Meira, D., Olivoto, T., & Klein, L. A. (2021). Genetic parameters and multiple-trait selection in wheat genotypes. *Pesquisa Agropecuária Tropical*, *51*, e67996. <https://doi.org/10.1590/1983-40632021v5167996>
- Melo, V. L. d., Marçal, T. D. S., Rocha, J. R. A. S. D. C., Anjos, D., R, S. R., Carneiro, P. C. S., & Carneiro, J. E. D. S. (2020). Modeling (co)variance structures for genetic and non-genetic effects in the selection of common bean progenies. *Euphytica*, *216*, 1–13. <https://doi.org/10.1007/s10681-020-02607-9>
- Nikolić, D., Miljković, J., Rakonjac, V., Radojević, I., & Vasic, Z. R. (2018). Inheritance and phenotypic correlations of agronomic traits in grapevine offsprings. *Acta Scientiarum Polonorum Hortorum Cultus*, *17*, 87–99. <https://doi.org/10.24326/asphc.2018.5.8>
- Oliveira, I. C. M., Marçal, T. D. S., Bernardino, K. D. C., Ribeiro, P. C. D. O., Parrella, R. A. D. C., Carneiro, P. C. S., Schaffer, R. E., & Carneiro, J. E. D. S. (2019). Combining ability of biomass sorghum lines for agroindustrial characters and multitrait selection of photosensitive hybrids for energy cogeneration. *Crop Science*, *59*, 1554–1566. <https://doi.org/10.24326/asphc.2018.5.8>
- Oliveira, R. L., Gomes, R. S. G., Almeida, C. F. A., Júnior, R. M., Rocha, J. R. A. S. C., Silva, D. J. H., & Carneiro, P. C. S. (2020). Multitrait selection of pumpkin genotypes aimed at reducing the growth habit and improving seed production. *Crop Science*, *61*, 1–10. <https://doi.org/10.1002/csc2.20386>
- Patterson, H. D., & Thompson, R. (1971). Recovery of inter-block information when block sizes are unequal. *Biometrika*, *58*, 545–554. <https://doi.org/10.2307/2334389>
- Peixoto, M. A., Coelho, I. F., Evangelista, J. S. P. C., Santos, S. S. de O., Alves, R. S., Pinto, J. F. N., dos Reis, E. F., & Bhering, L. L. (2021). Selection of maize hybrids: an approach with multi-trait, multi-environment, and ideotype-design. *Crop Breeding and Applied Biotechnology*, *21*(2). <https://doi.org/10.1590/1984-70332021v21n2a31>
- Pereira, G. E., Lima, L. C. O., Regina, M. A., Rosier, J. P., Ferraz, V., & Mourão, Junior, M. (2008). Potential evaluation of five American cultivars for grape juices in the south of Minas Gerais state. *Ciência e Agrotecnologia*, *32*, 1531–1537. <https://doi.org/10.1590/S1413-70542008000500026>
- R Development Core Team. (2019). *R: A language and environment for statistical computing*. R foundation for statistical computing. <http://www.R-project.org>
- Resende, M. D. V. (2016). Software Selegen-REML/BLUP: A useful tool for plant breeding. *Crop Breeding and Applied and Biotechnology*, *16*, 330–339. <https://doi.org/10.1590/1984-70332016v16n4a49>
- Rocha, J. R. A. S. C., Nunes, K. V., Carneiro, A. L. N., Marçal, T. D. S., Salvador, F. V., Carneiro, P. C. S., & Carneiro, J. E. S. (2019). Selection of superior inbred progenies toward the common bean ideotype. *Agronomy Journal*, *11*, 1181–1189. <https://doi.org/10.2134/agronj2018.12.0761>
- Rocha, J. R. A. S. C., Machado, J. C., & Carneiro, P. C. S. (2018). Multi-trait index based on factor analysis and ideotype-design: Proposal and application on elephant grass breeding for bioenergy. *Global Change Biology Bioenergy*, *10*, 52–60. <https://doi.org/10.1111/gcbb.12443>

- Rodrigues, E. V., Rocha, J. R. do A. S. de C., Alves, R. S., Teodoro, P. E., Laviola, B. G., Resende, M. D. V. de, Carneiro, P. C. S., & Bhering, L. L. (2020). Selection of *Jatropha* genotypes for bioenergy purpose: an approach with multitrait, multiharvest and effective population size. *Bragantia*, 79(3), 346–355. <https://doi.org/10.1590/1678-4499.20200046>
- Royo, C., Pérez, R. T., Mauri, N., Diestro, N., Cabezas, J. A., Marchal, C., Lacombe, T., Ibáñez, J., Tornel, M., Carreño, J., Martínez Zapater, J. M., & Carbonell-Bejerano, P. (2018). The major origin of seedless grapes is associated with a missense mutation in the MADS-Box Gene VviAGL111. *Plant Physiology*, 177, 1234–1253. <https://doi.org/10.1104/pp.18.00259>
- Sales, W. S., Ishikawa, F. H., Souza, E. M. C., Nascimento, J. H. B., Souza, E. R., & Leão, P. C. S. (2019). Estimates of repeatability for selection of genotypes of seedless table grapes for Brazilian semiarid regions. *Scientia Horticulture*, 245, 131–136. <https://doi.org/10.1016/j.scienta.2018.10.018>
- Sánchez, C. F. B., Alves, R. S., Garcia, A. P., Teodoro, P. E., Peixoto, L. A., Silva, L. A., Bhering, L. L., & Resende, M. D. V. (2017). Estimates of repeatability coefficients and the number of the optimum measure to select superior genotypes in *Annona muricata* L. *Genetics and Molecular Research*, 16, 1–8. <https://doi.org/10.4238/gmr16039753>
- Silva, M. J., Carneiro, P. C. S., Carneiro, J. E., Damasceno, C. M. B., Parrella, N. N. L. D., Pastina, M. M., Simeone, M. L. F., Schaffert, R. E., & Parrella, R. A. (2018). Evaluation of the potential of lines and hybrids of biomass sorghum. *Industrial Crops and Products*, 125, 379–385. <https://doi.org/10.1016/j.indcrop.2018.08.022>
- Smith, H. F. (1936). A discriminant function for plant selection. *Annals of Eugenics*, 7, 240–250. <https://doi.org/10.1111/j.1469-1809.1936.tb02143.x>
- Viana, A. P., & Resende, M. D. V. (2014). *Genética quantitativa no melhoramento de fruteiras*. Interciência.
- Volpato, L., Rocha, J. R. A. S. R., Alves, R. S., Ludke, W. H., Borém, A., & Silva, F. L. (2021). Inference of population effect and progeny selection via a multi-trait index in soybean breeding. *Acta Scientiarum Agronomy*, 43, e44623. <https://doi.org/10.4025/actasciagron.v43i1.44623>
- Wei, X., Sykes, S. R., & Clingeleffer, P. R. (2002). An investigation to estimate genetic parameters in CSIRO's table grape breeding program 2. Quality characteristics. *Euphytica*, 128, 343–351. <https://doi.org/10.1023/A:1021288618316>
- Woyann, L. G., Meira, D., Matei, G., Zdziarski, A. D., Dallacorte, L. V., Madella, L. A., & Benin, G. (2020). Selection indexes based on linear-bilinear models applied to soybean breeding. *Agronomy Journal*, 112, 175–182. <https://doi.org/10.2134/agronj2019.05.0345>

## SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

**How to cite this article:** de Carvalho, J. N., de Carvalho, P. A., Pio, R., Barbosa, M. A. G., & Leão, P. C. D. S. (2023). Multitrait selection in seedless grape hybrids in semiarid regions of Brazil. *Crop Science*, 63, 2091–2102. <https://doi.org/10.1002/csc2.20990>