

Estimations of genetic gains using different selection indices in hybrid table grape populations

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ABSTRACT: This study estimated genetic gains obtained with different selection indices to select superior genotypes for multiple traits in table grape progenies from controlled hybridizations using the REML/BLUP methodology. Seventy-six table grape hybrids (F1) were evaluated for yield, number of clusters, cluster weight, berry length, berry diameter, and berry weight in Juazeiro, Bahia, Brazil, over four to nine growing seasons. Repeatability coefficients ranged from 0.12 to 0.53, with accuracy estimates higher than 79% for all evaluated variables. The factor analysis and genotype-ideotype and multi-trait genotype-ideotype distance indices showed more balanced genetic gains across traits, which were proportional to the gains obtained through direct selection. Multi-trait selection led to selection of nine promising table grape genotypes exhibiting favorable performance for traits related to yield, cluster, and berry physical traits. These genotypes should advance to subsequent evaluation and selection stages for development of new table grape cultivars adapted to the semi-arid conditions of the São Francisco Valley in Brazil.

Key words: *Vitis* spp., REML/BLUP, grape breeding, multi-trait selection.

INTRODUCTION

In the São Francisco Valley in the northeast region of Brazil, grape growing is of considerable economic and social importance. In 2023, around 554 thousand tons of grapes were harvested, generating a production value of BRL 2.21 billion, accounting for nearly two-thirds of the total grape production value in Brazil (Embrapa 2025). The technologies used and the possibility of two and a half crop seasons per year have enabled mean yields of 51.7 t·ha⁻¹ in the municipality of Petrolina, Pernambuco, Brazil, representing an increase of 83% compared to the Brazilian average (Embrapa 2025). In 2024, grape exports totaled 58,865 tons, generating revenues of USD 151.359 million (Brasil 2025).

Among the technological advances that have supported expansion in grape growing in this region, the use of cultivars better adapted to the semi-arid tropical conditions in the northeast region of Brazil stands out. In recent decades, new cultivars for public use developed by the Brazilian Agricultural Research Corporation (Embrapa) and cultivars from private and international breeding programs have been introduced, which have expanded the number of available cultivars and the genetic base. This has contributed to an increase in the competitiveness, sustainability, and strength of regional grape growing (Leão and Carvalho 2024).

Currently, new technological challenges have required the development of table grape cultivars with an increasingly complex combination of traits to meet producer and consumer demands (Alonso et al. 2024). In addition, the globalized market has become increasingly competitive, and consumers are now concerned with aspects that extend far beyond fruit appearance, size, color, and flavor. These additional factors include plant health, food safety, health benefits, the social system of production, and environmental sustainability (Hsu et al. 2024).

In plant breeding, the selection of superior genotypes based on a single trait or on only a few traits is considered inadequate, as that approach may result in genotypes with unfavorable performance in other traits that are not under specifically under consideration but are also of interest to breeders (Cruz and Carneiro 2006). Therefore, the use of methods that enable simultaneous selection of a set of economically important traits is recommended (Rocha et al. 2018). This is possible by selection indices, which allow identification of genotypes with superior performance for multiple traits of interest (Rocha et al. 2018, Olivoto and Nardino 2021). Several selection indices have been proposed, which can be classified as linear or parametric indices and non-linear or non-parametric indices.

The first selection index was proposed by Smith (1936) and is based on genotypic and phenotypic variance and covariance matrices, assigning economic weights to each trait. The rank-sum index, proposed by Mulamba and Mock (1978), consists of ranking genotypes for each trait in an order favorable to plant breeding, assigning higher absolute values to those of better performance. The values assigned to each trait are then added together to obtain the rank sum, which determines the final classification of the genotypes (Cruz and Carneiro 2006).

The factor analysis and genotype-ideotype index (FAIBLUP) is based on adjusted phenotypic mean values and the Euclidean distances between each individual genotype and an ideal genotype. The resulting indices are subsequently standardized and ranked according to weights assigned to each trait. This approach also allows the definition of optimal and minimum desirable values for each trait for purposes of selection (Cruz and Carneiro 2006).

The final selection index considered in this study, the multi-trait genotype-ideotype distance index (MGIDI), is based on four main steps: rescaling traits to a 0–100 range; carrying out factor analysis for consideration of correlation structure and dimensionality reduction; defining a desired ideotype for the traits; and calculating the distance between each genotype and the defined ideotype (Olivoto and Nardino 2021).

Considering the global economic importance of grape production, several studies have used genetic gain estimates and selection indices to identify superior genotypes, contributing to the efficiency of grapevine breeding programs (Leão et al. 2018, Sales et al. 2019, Carvalho et al. 2023a, Carvalho et al. 2023b, Rodrigues et al. 2024). However, few studies have compared different selection indices with the aim of maximizing efficiency and genetic gains in table grape breeding. Therefore, the objective of the present study was to compare the effectiveness of different selection indices based on estimated genetic gains, aiming to identify promising genotypes and to develop table grape cultivars adapted to the Brazilian semi-arid region.

MATERIALS AND METHODS

Location and characterization of the experiment

The experiment was conducted at the Mandacaru Experimental Field of Embrapa Semiárido in Juazeiro, Bahia, in the northeast region of Brazil (9°24'S, 40°26'W, and 375 m). The climate in the region is tropical semi-arid, hot and dry, according to the Köppen's classification (Alvares et al. 2013). Historical climate data over 59 years (1965–2024), obtained from the Mandacaru agricultural meteorological station, indicate mean annual rainfall of 491 mm, and mean, minimum, and maximum air temperatures of 27, 21, and 32°C, respectively (Embrapa 2025).

The grapevines were grafted onto IAC 572 rootstock and trained using a vertical shoot position trellis system. Plant spacing was 3 m × 1 m within a drip irrigation system. Plants were irrigated daily, and irrigation volumes were determined based on crop evapotranspiration. Plant nutrition and fertilization were managed using a fertigation system based on leaf and soil analysis, following the recommendations of Silva et al. (2010). Shoot growth was managed through pruning and vine tying. No growth regulators were applied, and clusters were not selected or thinned.

Plant material

The evaluated genotypes consisted of 76 hybrids (F1) derived from crosses between *Vitis vinifera* cultivars, between interspecific hybrids, and between *V. vinifera* and interspecific hybrids (Table 1). These genotypes are part of a progeny field (F1) in which each

hybrid is represented by a single plant; therefore, the experiment was not arranged in an experimental design with replicates. The evaluated genotypes had been previously selected for absence of seeds. Despite the lack of replicates, several production cycles were evaluated and considered as repetitions over time. A minimum of four production cycles were required in this study. However, due to differences in vine age, the number of evaluated production cycles per genotype ranged from four to nine.

Table 1. Hybrids evaluated, derived from crosses between *Vitis vinifera* cultivars and interspecific hybrids or between two hybrid cultivars.

	Hybrid code	Crosses		Hybrid code	Crosses
1	CPATSA 24_04	Marroo × BRS Linda	39	CPATSA 49_266	Marroo × Jupter
2	CPATSA 24_61	Marroo × BRS Linda	40	CPATSA 49_27	Marroo × Jupter
3	CPATSA 24_79	Marroo × BRS Linda	41	CPATSA 49_29	Marroo × Jupter
4	CPATSA 26_18	Marroo × BRS Vitória	42	CPATSA 49_30	Marroo × Jupter
5	CPATSA 28_03	Marroo × A1581	43	CPATSA 49_32	Marroo × Jupter
6	CPATSA 28_08	Marroo × A1582	44	CPATSA 49_86	Marroo × Jupter
7	CPATSA 28_13	Marroo × A1583	45	CPATSA 49_93	Marroo × Jupter
8	CPATSA 28_14	Marroo × A1584	46	CPATSA 49_97	Marroo × Jupter
9	CPATSA 28_17	Marroo × A1585	47	CPATSA 62_03	Marroo × Feal
10	CPATSA 28_22	Marroo × A1586	48	CPATSA 62_19	Marroo × Feal
11	CPATSA 28_26	Marroo × A1587	49	CPATSA 62_56	Marroo × Feal
12	CPATSA 28_29	Marroo × A1588	50	CPATSA 63_01	Marroo × CG 351
13	CPATSA 31_01	CG 102295 × CG 351	51	CPATSA 63_02	Marroo × CG 352
14	CPATSA 31_06	CG 102295 × CG 352	52	CPATSA 63_29	Marroo × CG 353
15	CPATSA 31_09	CG 102295 × CG 353	53	CPATSA 63_57	Marroo × CG 354
16	CPATSA 31_11	CG 102295 × CG 354	54	CPATSA 64_03	Marroo × A1105
17	CPATSA 31_13	CG 102295 × CG 355	55	CPATSA 64_61	Marroo × A1106
18	CPATSA 38_113	Italia melhorada × Marroo	56	CPATSA 64_83	Marroo × A1107
19	CPATSA 38_121	Italia melhorada × Marroo	57	CPATSA 65_16	Marroo × BRS Clara
20	CPATSA 38_122	Italia melhorada × Marroo	58	CPATSA 67_13	A Dona × CG 33716
21	CPATSA 49_01	Marroo × Jupter	59	CPATSA 67_22	A Dona × CG 33717
22	CPATSA 49_06	Marroo × Jupter	60	CPATSA 74_10	CG 351 × CNPUV 8
23	CPATSA 49_12	Marroo × Jupter	61	CPATSA 74_11	CG 351 × CNPUV 9
24	CPATSA 49_129	Marroo × Jupter	62	CPATSA 76_25	CG 351 × A Dona
25	CPATSA 49_148	Marroo × Jupter	63	CPATSA 79_04	Marroo × BRS Isis
26	CPATSA 49_155	Marroo × Jupter	64	CPATSA 79_100	Marroo × BRS Isis
27	CPATSA 49_156	Marroo × Jupter	65	CPATSA 79_104	Marroo × BRS Isis
28	CPATSA 49_162	Marroo × Jupter	66	CPATSA 79_107	Marroo × BRS Isis
29	CPATSA 49_165	Marroo × Jupter	67	CPATSA 79_21	Marroo × BRS Isis
30	CPATSA 49_167	Marroo × Jupter	68	CPATSA 79_27	Marroo × BRS Isis
31	CPATSA 49_171	Marroo × Jupter	69	CPATSA 79_28	Marroo × BRS Isis
32	CPATSA 49_172	Marroo × Jupter	70	CPATSA 79_29	Marroo × BRS Isis
33	CPATSA 49_173	Marroo × Jupter	71	CPATSA 79_33	Marroo × BRS Isis
34	CPATSA 49_187	Marroo × Jupter	72	CPATSA 79_34	Marroo × BRS Isis
35	CPATSA 49_20	Marroo × Jupter	73	CPATSA 79_42	Marroo × BRS Isis
36	CPATSA 49_22	Marroo × Jupter	74	CPATSA 79_49	Marroo × BRS Isis
37	CPATSA 49_236	Marroo × Jupter	75	CPATSA 79_57	Marroo × BRS Isis
38	CPATSA 49_239	Marroo × Jupter	76	CPATSA 79_78	Marroo × BRS Isis

Variables evaluated

Production components and physical traits of the clusters and berries were evaluated according to grapevine descriptors proposed by the International Plant Genetic Resources Institute (IPGRI 1997), including yield ($\text{kg}\cdot\text{plant}^{-1}$), number of clusters per plant, cluster weight (g), berry length (mm), berry diameter (mm), and berry weight (g). For cluster traits, five clusters were sampled per plant. For berry traits, 50 berries were randomly collected from the sampled clusters, with 10 berries taken from each cluster.

Statistical analyses

The mixed model methodology was adopted using restricted maximum likelihood (REML) to estimate variance components and best linear unbiased prediction (BLUP) to calculate genotypic values. Considering that genotypes were evaluated over multiple production cycles and that each genotype is represented by a single plant, the basic repeatability model (model 63) of the Selegen-REML/BLUP software (Resende 2016) was adopted. This model is recommended for perennial crops with longitudinal evaluations and unbalanced data.

In this model, random genotypic effects, permanent environmental effects associated with plants, and residual effects are considered, allowing the separation of permanent and temporary sources of variations over time. In matrix form, the model is represented by Eq. 1:

$$y = Xm + Zp + \theta \quad (1)$$

where: y : the data vector (of the variable to be analyzed); m : the vector of the measurement effects, assumed to be fixed, added to the overall mean; p : the vector of permanent phenotypic effects of plants (genotypic effects + permanent environmental effects), assumed to be random; θ : the vector of random residual errors; X : the incidence matrices for fixed effects; Z : the incidence matrices for random effects (Viana and Resende 2014).

This approach makes it possible to use information from multiple production cycles as a form of repetition over time, increasing the efficiency of genotypic value prediction even in the absence of replications in the field (Viana and Resende 2014). Consequently, this model has been widely used in breeding programs for perennial and fruit species to assist in identification of promising genotypes.

The significance of the model effects was evaluated through analysis of deviance using the likelihood ratio test, as recommended by Viana and Resende (2014). Mathematically, it is expressed as Eq. 2:

$$LTR = (-2 \text{Log}L)_{p-1} - (-2 \text{Log}L)_p \quad (2)$$

where: $(\text{Log}L)$: the logarithm of the maximum value of the residual likelihood function (L) associated with the reduced $(p-1)$ and full (p) models; $(-2 \text{Log}L)$: the deviance.

The likelihood ratio test was compared with the value of the probability density function (χ^2) with one degree of freedom at 1 and 5% probability.

The genetic values (BLUP means) for each of the 76 genotypes were predicted based on the six quantitative traits evaluated. The BLUPs were then used for simultaneous selection of the best seedless hybrid genotypes through four different selection indices: the classic Smith-Hazel index (SH) (Smith 1936, Hazel 1943), the Mulamba and Mock rank-sum index (MM) (Mulamba and Mock 1978), the factor analysis and genotype-ideotype design index (FAIBLUP) (Rocha et al. 2018), and the multi-trait genotype-ideotype distance index (MGIDI) (Olivoto and Nardino 2021). For all indices, equal economic weights were assigned to each trait evaluated.

The predicted gain from selection (GS%) was calculated considering a 33% selection intensity using Eq. 3:

$$GS\% = [X_m - X_0] \times 100 \quad (3)$$

where: GS%: the gain from selecting the best genotypes for the variable; X_m : the BLUP mean of the genotype selected for the variable; X_0 : the overall BLUP mean of all the genotypes for the variable.

Coincidence among the grapevine genotypes selected pairwise through the indices was quantified using the equation by Hamblin and Zimmermann (1986) (Eq. 4):

$$CI (\%) = \frac{A - C}{B - C} \times 100 \quad (4)$$

where: $CI (\%)$: the coincidence index; A : the number of grapevine genotypes that coincide between two selection indices; B : the total number of genotypes selected ($n = 25$); C : the number of coincidences attributed to randomness (standardized to $n = 2$).

Statistical analyses were performed using the software Selegen-REML/BLUP, version 1.0.0.0 (Resende 2016); GENES, version 1990.2023.3 (Cruz 2016); and R, version 4.1.2 (R Development Core Team 2019).

RESULTS AND DISCUSSION

In this study, each genotype was represented by a single plant, without replication, which imposes limitations on statistical robustness and restricts accurate separation of genotypic and environmental effects. However, this approach is compatible with the initial selection phase of the genetic breeding program of Embrapa Semiárido. Despite the inherent limitations of the design, the data obtained provide relevant preliminary information for identification and selection of promising genotypes under field conditions in the Brazilian semi-arid region.

In experiments without replication analyzed using the basic repeatability model, it is not possible to separate genetic variance into its additive and non-additive components or to estimate heritability; instead, only the repeatability coefficient can be obtained, which expresses the proportion of phenotypic variance associated with permanent differences between individuals. Furthermore, in this approach, it is not possible to evaluate the genotype $\times$ environment interaction, perform classic mean comparison tests, or infer stability and adaptability. Thus, inferences are restricted to the preliminary ranking and selection of genotypes, which should be further evaluated in trials with replicates across multiple environments.

The yield traits of grape genotypes are of utmost importance for good agronomic performance and market acceptance of new cultivars. Traits such as number of clusters (NC), cluster weight (CW), berry length (BL), berry diameter (BD), and berry weight (BW) are among the grapevine descriptors proposed by the IPGRI (1997), which highlights traits of economic importance to growers and consumers.

Variability among grape genotypes for production traits was assessed through analysis of deviance using the likelihood ratio test. The results indicated significant genotypic effects ($p \leq 0.001$) for all the yield traits evaluated: yield, NC, CW, BL, BD, and BW (Table 2). According to Malikouski et al. (2021), the fundamental condition for selecting superior genotypes is the existence of genetic variability. Thus, the results obtained here show potential for genetic gains through selection in all these traits and for recommendation of superior genotypes.

Table 2. Analysis of deviance for yield, number of clusters, cluster weight, berry length, berry diameter, and berry weight of grapevine genotypes.

Variable	Deviance reduced model	Deviance full model	Likelihood ratio test
Yield (kg)	1,044.42	1,032.52	11.90*
Number of clusters	2,474.11	2,456.24	17.87*
Cluster weight (g)	3,937.47	3,898.98	38.49*
Berry length (mm)	1,443.95	1,351.87	92.08*
Berry diameter (mm)	1,138.71	1,048.26	90.45*
Berry weight (g)	573.78	387.29	186.49*

Yield per plant exhibited an overall mean of 2.74 kg, which corresponds to an estimated yield of 10 t·ha⁻¹. The NC was 12 per plant. CW ranged from 63 to 317.4 g, with a mean of 192.2 g. Berry traits ranged from 13.4 to 25.9 mm for length (mean of 18.9 mm), from 12.5 to 21.2 mm for diameter (mean of 16.3 mm), and from 1.5 to 6.3 g for weight (mean of 3.2 g).

The mean values of the traits evaluated in this study were lower than those reported by Leão et al. (2018), Sales et al. (2019), and Carvalho et al. (2023b), who also evaluated these and other traits in grape hybrids in the same experimental field. These differences are attributable to the use of different populations, the polygenic nature of the evaluated traits, and the strong effect of environment (Carvalho et al. 2023b).

Similarly, in this experiment, a strong environmental effect was observed on the evaluated traits, as the temporary environmental variance exceeded the permanent phenotypic variance among plants, constituting most of the phenotypic variance for all the traits. The estimated variance components, including genetic and phenotypic parameters, are shown in Table 3.

Table 3. Variance components for yield, number of clusters, cluster weight, berry length, berry diameter, and berry weight of grape genotypes.

Trait	Overall mean	VFP	VET	VF	$r = h^2 \pm SE$	ACM
Yield (kg)	2.74	0.53	3.85	4.38	0.12 ± 0.05	0.79
Number of clusters	11.91	20.01	106.31	126.32	0.16 ± 0.05	0.81
Cluster weight (g)	192.2	1913.85	5648.96	7562.81	0.25 ± 0.07	0.89
Berry length (mm)	18.97	3.89	6.51	10.39	0.37 ± 0.08	0.93
Berry diameter (mm)	16.26	1.85	3.12	4.98	0.37 ± 0.08	0.93
Berry weight (g)	3.16	0.68	0.59	1.27	0.53 ± 0.09	0.96

VFP: permanent phenotypic variance; VET: temporary environmental variance; VF: phenotypic variance; $r = h^2$: estimated individual repeatability; SE: standard error; ACM: selective accuracy.

Repeatability is important in plant breeding, because it measures the ability of individuals to maintain expression of a trait over various crop seasons. Thus, it allows selection of genotypes that maintain their genetic superiority over successive crop seasons, thereby minimizing the effects of environmental conditions in the selection process (Ferreira et al. 2020).

The estimated individual repeatability (r), which expresses the proportion of phenotypic variance associated with permanent effects (genetic + permanent environmental effects), ranged from 0.12 to 0.53 for the evaluated traits and can thus be classified as low. This result indicates low stability in individual performance throughout the evaluated cycles, which may be related to seasonal climatic variations that occur in the two annual harvests in the (Lower Middle) São Francisco Valley, as well as to common alternations in consecutive harvests.

Selective accuracy (ACM) ranged from 0.79 to 0.96, indicating high reliability in the ranking of genotypes within this dataset. According to Resende and Alves (2020), accuracy values above 0.70 are classified as high precision; therefore, the ACM estimates obtained in this study were high. ACM is the main component of genetic progress, because it reflects accuracy in selection; that is, it corresponds to the correlation between predicted genetic values and true genetic values of individuals (Resende and Duarte 2007, Resende and Alves 2020). The greater the accuracy in evaluation of an individual, the greater the reliability of both the evaluation process and the predicted genetic value of the individual (Maia et al. 2017).

ACM was obtained as the ratio between the predicted genetic variance and the total phenotypic variance, and it is directly related to the prediction error of genotypic values (BLUPs). In repeatability models, selection accuracy increases with the number of measurements per individual, as multiple evaluations reduce the influence of temporary environmental variance on the predicted genotypic mean (Ferreira et al. 2020).

Thus, the combination of repeatability and the number of cycles evaluated explains the high accuracy values observed, reflecting greater reliability in the relative ranking of genotypes. However, these results should be interpreted considering the low repeatability coefficients found, which reinforce the preliminary nature of the selection carried out in this study.

The genotypic values (BLUPs) of the 76 grape genotypes for each trait evaluated were shown on Table 4 and used to classify them considering the four selection indices: the classic SH, the MM, the FAIBLUP, and the MGIDI. Therefore, genotypic values can provide reliable results for classification of grape genotypes considering direct selection, the classic SH, the MM, the FAIBLUP, and the MGIDI.

Table 4. Genotypic values (BLUPs) of grape genotypes as selected based on the coincidence of the Smith-Hazel, Mulamba and Mock, factor analysis and genotype-ideotype design, and multi-trait genotype-ideotype distance indices in relation to the following traits: yield (YD), number of clusters (NC), cluster weight (CW), berry length (BL), berry diameter (BD), and berry weight (BW).

Genotypes	BLUPs					
	YD	NC	CW	BL	BD	BW
CPATSA 49_22	3.9385	16.4971	190.4631	24.7562	19.3507	5.996
CPATSA 49_23	3.7212	14.8076	242.8657	20.459	17.4009	3.9121
CPATSA 49_24	3.5095	14.2395	289.2279	20.3109	17.3317	3.7803
CPATSA 49_25	3.2033	11.9001	261.039	22.6498	17.2649	4.1228
CPATSA 49_26	3.2164	13.6701	253.7581	22.7401	15.5184	2.729
CPATSA 49_27	3.5796	22.5277	213.4858	18.7584	16.3118	3.1271
CPATSA 49_28	2.9497	15.817	190.2095	20.2988	16.5303	3.4526
CPATSA 49_29	3.3243	19.9067	199.7762	17.785	15.8103	2.7641
CPATSA 49_30	2.9034	12.5094	176.3831	19.6341	16.7327	3.5972

The genetic gains obtained from selection of 25 grape genotypes (33% selection intensity) for each trait, as well as the sum of gains for all the traits evaluated simultaneously, both through direct selection and through the SH, MM, FAIBLUP, and MGIDI indices, are shown in Table 5.

Table 5. Estimates of genetic gains, means of the selected population, and means of the improved population for grape genotypes using direct selection (DS) and the Smith-Hazel (SH), Mulamba and Mock (MM), factor analysis and genotype-ideotype design (FAIBLUP), and multi-trait genotype-ideotype distance (MGIDI) indices in relation to the following traits: yield, number of clusters, cluster weight, berry length, berry diameter, and berry weight.

Trait	Predicted genetic gain (%)					Mean of the selected population					Mean of the improved population				
	DS	SH	MM	FAIBLUP	MGIDI	DS	SH	MM	FAIBLUP	MGIDI	DS	SH	MM	FAIBLUP	MGIDI
Yield (Kg)	21.10	3.47	3.44	19.25	18.84	3.39	2.02	2.11	3.33	3.31	3.58	2.88	2.87	3.47	3.48
Number of clusters	29.47	15.29	16.47	15.24	13.40	18.85	15.67	16.34	15.70	15.32	17.85	14.46	14.36	14.15	14.15
Cluster weight (g)	20.80	1.84	0.51	14.14	15.16	242.84	182.68	173.68	226.77	231.26	252.07	201.58	203.67	228.27	227.89
Berry length (mm)	10.04	1.40	1.60	6.11	6.86	21.18	19.20	19.13	20.15	20.35	21.96	19.09	19.10	21.08	21.12
Berry diameter (mm)	8.29	-0.08	-0.61	4.88	5.88	17.82	16.17	15.97	17.12	17.34	18.24	16.21	16.18	17.40	17.43
Berry weight (g)	27.85	1.50	0.36	17.44	20.93	4.09	3.21	3.13	3.69	3.83	4.49	3.21	3.21	4.05	4.07
Sum of gains	117.55	23.41	21.77	77.07	81.07										

The estimates of genetic gain were positive for yield, NC, CW, BL, and BW, regardless of the selection index used. Only the BD trait showed undesirable gains, by using the SH and MM indices.

Direct selection of 25 genotypes resulted in selection of plants with above-average performance, with genetic gains ranging from 8.29 to 29.47% across the evaluated traits (Table 5). This selection brought about positive and above-average genetic gains for all the traits, leading to a desirable favorable shift in the means. Despite these satisfactory results, selection based on a single trait tends to be inadequate (Cruz and Carneiro 2006), because superiority may be limited to only that trait, while performance for other traits may be unfavorable. Therefore, selection methods that promote balanced gains across all the traits of interest tend to be more effective.

The SH and MM indices showed potential for greater gains only for the NC trait (gains of 15.29 and 16.47%, respectively), whereas they also showed undesirable gains for BD (-0.08 and -0.61%, respectively). For the remaining traits, the gains ranged from 0.36 to 3.47%, which are considered of low magnitude. The FAIBLUP and MGIDI indices, however, exhibited more balanced gains across the traits, and they were proportional to the gains obtained through direct selection for each trait. In the FAIBLUP index, gains ranged from 4.88 to 19.25%, while in the MGIDI index, gains ranged from 5.88 to 20.93%.

The relative gains obtained from the selection indices, compared to direct selection, were 18.52% for MM, 19.92% for SH, 65.56% for FAIBLUP, and 68.97% for MGIDI. Therefore, the MM index proved to be the least effective, whereas the MGIDI index was the most effective for selection of grape genotypes, based on the evaluated yield traits.

In summary, the SH and MM indices were not effective for selection of grape genotypes based on the yield traits, as they did not show balanced gains, and these gains were of low magnitude. In contrast, the FAIBLUP and MGIDI indices exhibited balanced gains proportional to the gains obtained through direct selection for each trait. Therefore, they proved to be more effective than the SH and MM indices.

In this study, equal economic weights were assigned to all the evaluated traits. This approach reduces subjectivity in the definition of weights and enables an exploratory evaluation, as well as a more balanced comparison among the different selection indices evaluated. Assuming equivalent importance among the traits allows the indices to be predominantly influenced by the estimated variances, covariances, and genetic associations. However, it should be noted that alternative weighting schemes may alter the results and could be explored in future studies.

The high coincidence index between FAIBLUP and MGIDI, along with the proportion of genetic gains from each of these indices compared to direct selection, shows that both indices are suitable for selection of grape genotypes based on the evaluated traits.

The highest coincidence among the selected genotypes occurred between the SH and MM indices (91.43%), as well as between the FAIBLUP and MGIDI indices (91.43%). The lowest coincidence was found between the MM and MGIDI indices (30.43%). Intermediate coincidence values (34.78%) were found for the SH and FAIBLUP, SH and MGIDI, and MM and FAIBLUP index combinations.

In practical terms, reduced coincidences among selection indices have direct implications for breeding programs, as they reveal that the choice of an index is not neutral; it can significantly influence which genotypes will be advanced to subsequent stages. This finding reinforces the importance of defining selection objectives before adopting an index. In addition, comparison of different indices can assist in identifying consistent genotypes (those selected in more than one index), while simultaneously evaluating which indices are most aligned with the goals of the breeding program.

Oliveira et al. (2008) evaluated genetic gains using different selection indices for fruit traits in 16 half-sib progenies of yellow passion fruit and reported that, although the SH index led to higher genetic gains for fruit weight and number of fruits per plant, negative gains were observed for other traits, just as occurred in this study. The authors concluded that Cruz's genotype-ideotype distance index was more effective in predicting higher and more balanced genetic gains across all the evaluated traits.

Arnhold and Silva (2009) compared the relative effectiveness of various selection indices across different plant species and observed that the SH index was not suitable in any of the scenarios analyzed, and the MM index was adequate only in some situations. In addition, they found that Pesek and Baker's genotype-ideotype distance index was suitable in all the situations analyzed. Costa et al. (2020) reported that the use of non-parametric indices, including the MM index, was effective in assisting breeding programs aimed at selecting hybrid rootstocks in citrus.

The present study showed that selection indices based on genotype-ideotype distance in multi-trait selection tend to be more effective. In this regard, the FAIBLUP index has shown positive results in selecting various crops, such as soybean (Woyann et al. 2020, Volpato et al. 2021), wheat (Al Ashkar et al. 2023), and maize (Yue et al. 2021). In fruit crops, Carvalho et al. (2023a) observed the effectiveness of the index in selecting multiple yield and quality traits in grape genotypes. Costa et al. (2023) also achieved good results in selecting mango genotypes for fruit quality.

Recent studies have highlighted significant advantages of the MGIDI index in increasing the yield, quality, and adaptability of numerous crops, such as yam, barley, cassava, cucumber, lentil, maize, rice, common bean, soybean, and wheat (Debnath et al. 2024). Furthermore, these studies indicated the potential of this index in breeding programs focusing on traits such as salt tolerance, stability, flood tolerance, drought-response mechanisms, tuber quality, nutritional value, yield, adaptability,

early maturity, and stress resistance. Thus, MGIDI can be considered a valuable tool for genotype selection in different crops. However, few studies have used this index on fruit species.

The FAIBLUP index provides a objective selection process, and it can be applied to any breeding program focusing on multi-trait selection (Rocha et al. 2018). The MGIDI index, in turn, is not only effective in selecting superior genotypes across multiple traits, but has also outperformed more recent selection methods, contributing to better decision making for effective multivariate selection in biological experiments (Olivoto and Nardino 2021).

The FAIBLUP index is particularly useful when breeders aim to incorporate specific goals and assign explicit weights to individual traits, whereas the MGIDI index shows advantages in situations with high correlation among traits, as it considers factor analysis and dimensionality reduction. Thus, these indices can be considered complementary, and their combined use can assist decision making in the early stages of breeding programs.

The multi-trait selection procedure, based on the results of the four indices (SH, MM, FAIBLUP, and MGIDI), enabled the initial selection of nine promising table grape genotypes with superior yield and cluster and berry physical traits: CPATSA 49_22, CPATSA 49_167, CPATSA 49_171, CPATSA 49_172, CPATSA 49_32, CPATSA 49_86, CPATSA 49_30, CPATSA 49_20, and CPATSA 49_173. These genotypes show potential for advancing the genetic improvement program for table grapes in the Brazilian semi-arid region.

Finally, multi-trait selection has been the focus of various studies that evaluate different parametric and non-parametric indices to determine their relative effectiveness for genotype selection (Arnhold and Silva 2009). When these indices are applied to key parameters such as heritability, genotypic values, and phenotypic correlation, they are effective in identifying superior genotypes (Rahimi and Debnath 2023). However, the effectiveness of each index may vary depending on the specific selection scenario. Therefore, it is important to carry out specific studies assessing the effectiveness of multi-trait selection indices in fruit species.

CONCLUSION

Positive genetic gains were observed for yield, NC, CW, BL, and BW, regardless of the selection index applied.

Multi-trait selection for yield components and physical traits of clusters and berries identified nine superior seedless table grape genotypes for advancement to subsequent stages of the breeding program.

The FAIBLUP and MGIDI indices were particularly effective for multi-trait selection and are recommended for use in grape breeding programs.

CONFLICT OF INTEREST

Nothing to declare.

AUTHORS' CONTRIBUTION

Conceptualization: Leão, P. C. S. and Carvalho, J. N.; **Methodology:** Leão, P. C. S. and Carvalho, J. N.; **Investigation:** Leão, P. C. S.; **Writing – Original Draft:** Leão, P. C. S. and Carvalho, J. N.; **Writing – Review and Editing:** Leão, P. C. S. and Carvalho, J. N.; **Funding Acquisition:** Leão, P. C. S.; **Supervision:** Leão, P. C. S.; **Final approval:** Leão, P.C.S.

DATA AVAILABILITY STATEMENT

The datasets generated and/or analyzed for this study are available from the corresponding author upon reasonable request.



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DECLARATION OF USE OF ARTIFICIAL INTELLIGENCE TOOLS

No artificial intelligence tools were used in the preparation of this manuscript.

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