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Multi-trait selection and genetic progress in tiger melon (*Cucumis melo* L.) lines

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Abstract: *Melon is the most economically important cucurbit in the Brazilian Semiarid region, where recent efforts have focused on product diversification through the development of new melon types. This study aimed evaluate Tiger melon lines using the FAI-BLUP and MGIDI indices to identify genotypes combining high yield and quality for advancement in the breeding program. Twenty-four lines were evaluated in two trials conducted in a randomized block design with three replications. The following traits were evaluated: fruit yield, number of fruits per plant, mean fruit weight, pulp thickness, pulp firmness, and soluble solids. Genetic gains were observed for all traits. For the MGIDI index, gains ranged from 14.9% for pulp thickness to 72.5% for fruit weight. For the FAI-BLUP index, gains ranged from 0.39% for fruit yield to 26.36% for fruit weight. Based on both indices, lines TC-02, TC-03, TC-14, and TC-22 were identified as promising for breeding.*

Keywords: *Plant breeding, MGIDI index, FAI-BLUP index, Tiger melon lines*

INTRODUCTION

Brazilian melon production is concentrated in the states of Rio Grande do Norte and Bahia, which together account for more than 99% of the country's output and nearly all of its exports. In Brazil, the most widely cultivated melon types are 'Yellow' and 'Piel de Sapo', both classified in the *Inodorus* horticultural group, as well as cantaloupe, which belongs to the *Cantalupensis* group. The success of melon cultivation in the Semiarid region is attributed to favorable environmental conditions combined with advanced crop management practices and intensive use of technology by producing companies. The integration of all these factors has enabled fruit yields exceeding 25 Mg ha^{-1} (Nunes et al. 2016, Kist and Beling 2023).

Therefore, a trend toward diversification in the melon market is evident in the coming years. In this context, breeding programs capable of generating new melon types are necessary and relevant. At the Federal Rural University of the Semi-Arid Region (UFERSA), several parallel breeding programs have been conducted to develop different melon types for various market niches. Tiger melon lines, exhibiting bicolor Tiger exocarps, derived from the cross between 'Timeless' and I-180 have shown potential for the development of new cultivars.

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In plant breeding programs, the simultaneous evaluation of multiple traits is common to guide selection. Methods for multi-trait selection are generally classified into three categories: i) tandem selection; ii) independent culling levels; and iii) selection indices, which combine information from multiple traits into a single value to facilitate selection decisions (Ramalho et al. 2012). Selection indices allow balanced genetic gains across multiple traits, thereby enabling more efficient and accurate decision-making (Michel et al. 2019, Céron-Rojas and Crossa 2020). Reliable genetic gains require methodologies that allow inference of genotypic values, thereby enhancing the precision of genotype selection (Candido et al. 2020).

In this context, the restricted maximum likelihood/best linear unbiased prediction (REML/BLUP) procedure provides accurate estimates of genetic parameters and predicted genotypic values (Resende 2016). Two recent indices that incorporate REML/BLUP predictions with the ideotype concept are the FAI-BLUP index (Factor Analysis and Ideotype-Design Best Linear Unbiased Prediction) (Rocha et al. 2018) and the MGIDI index (Multi-Trait Genotype–Ideotype Distance Index) (Olivoto and Nardino 2021). The FAI-BLUP method enables multi-criteria ranking of genotypes while accounting for multicollinearity, whereas the MGIDI index calculates the distance between a genotype and a defined ideotype using factor analysis, thereby combining multiple traits into a single metric.

Both indices have been successfully applied in crops such as wheat, elephant grass, tomato, durum wheat (*Triticum turgidum*), barley, and mustard (Rocha et al. 2018, Akram et al. 2024, Silva et al. 2024, Kumar et al. 2025, Pour-Aboughadareh et al. 2025). The objective of this study was to evaluate Tiger melon lines using the FAI-BLUP and MGIDI indices and to identify genotypes combining high fruit yield and quality for advancement in the breeding program.

MATERIAL AND METHODS

Field location

Two field trials were conducted, one in 2021 and the other in 2022, both from September to December. Both trials were conducted at Rafael Fernandes Farm, located in Alagoinha, approximately 20 km from Mossoró, Rio Grande do Norte, Brazil (lat 5° 03′ 40.3″ S, long 37° 23′ 52.3″ W, alt 79 m asl). The climate of the region is classified as BSh (hot semi-arid), according to the Köppen-Geiger climate classification system, with well-defined rainy (February to May) and dry (June to January) seasons (Alvares et al. 2013). Mean temperature, relative humidity, and total precipitation were 28 °C, 68%, and 3.1 mm, respectively, during the first trial and 27.22 °C, 66%, and 0.0 mm, respectively, during the second trial.

Experimental design

A randomized complete block design with three replications was used in both trials, with 10 plants per plot and spacing of 2.0 m between rows and 0.3 m between plants.

Plant material and field management

Twenty-four Tiger melon lines, exhibiting bicolor Tiger exocarps, developed within the Melon Breeding Program of the Federal Rural University of the Semi-Arid (UFERSA) were evaluated together with their parental genotypes: the cantaloupe hybrid ‘Timeless’ from the Cantalupensis horticultural group and the accession I-180 from the Dudaim group (Supplementary Figure 1). These inbred lines have salmon-colored pulp, yellow rind with orange stripes, sweet aroma, fruit weight ranging from 0.7 to 1 kg, and high soluble solids content.

Seeds were sown in 200-cell polyethylene trays filled with a commercial substrate (Basaplant®) composed of limestone, vermiculite, charcoal, phosphate rock, and pine bark. Seedlings were transplanted to the field 12 days after sowing into raised beds covered with white plastic mulch. After transplanting, non-woven fabric (NWF) was placed over the beds and removed at the onset of anthesis to allow pollination. Crop management followed regional commercial melon production practices, including pest and disease control.

The soil in the experimental area was classified as a Typic Haplustalf (Argissolo Vermelho-Amarelo Eutrófico típico) (Soil Survey Staff 2022, Santos et al. 2025). Soil chemical analysis showed the following results: pH (H_2O) of 6.04; electrical conductivity of 37.7 µS cm^{-1}; 10.7 mg dm^{-3} P; 49.3 mg dm^{-3} K^+; 6.4 mg dm^{-3} Na^+; 0.77 cmol$_c$ dm^{-3} Ca^{2+}; 0.26 cmol$_c$ dm^{-3} Mg^{2+}; and 0.0 cmol$_c$ dm^{-3} Al^{3+}. Basal fertilization consisted of single superphosphate applied at 250 kg ha^{-1}.

Topdressing fertilization was applied via fertigation, with amounts adjusted according to crop phenological stages. The total fertilizer quantities and sources applied were 6.87 kg of urea (NH_2CONH_2), 7.43 kg of monoammonium phosphate (MAP; $NH_4H_2PO_4$), 13.03 kg of potassium chloride (KCl), 7.41 kg of potassium nitrate (KNO_3), 7.01 kg of calcium nitrate [$Ca(NO_3)_2$], 2.67 kg of magnesium sulfate ($MgSO_4$), 0.52 kg of boric acid [$B(OH)_3$], and 1.11 kg of zinc sulfate ($ZnSO_4$).

Fruit harvest and evaluation

Two fruit harvests were conducted based on ripeness, the first at 60 days and the second at 65 days after transplanting. The following traits were evaluated using a sample of 5 fruits per plot: fruit yield (Mg ha^{-1}), calculated by weighing all fruits from the plot; mean fruit weight (kg), calculated as the total weight of sampled fruits divided by the number of fruits; pulp thickness (cm), defined as the mean mesocarp thickness measured twice per fruit using a ruler; pulp firmness (kgf), measured as pulp resistance with two measurements per fruit using a Wagner® penetrometer equipped with an 8.0-mm-diameter conical plunger (Fruit Tester FDK 30); and soluble solids (°Brix). Soluble solids were determined in two samples collected from the equatorial region of each fruit toward the locule, at approximately two-thirds of the longitudinal axis; juice was extracted by cutting and manual pressing and analyzed using a digital refractometer (1-877-ATAGO PAL-1).

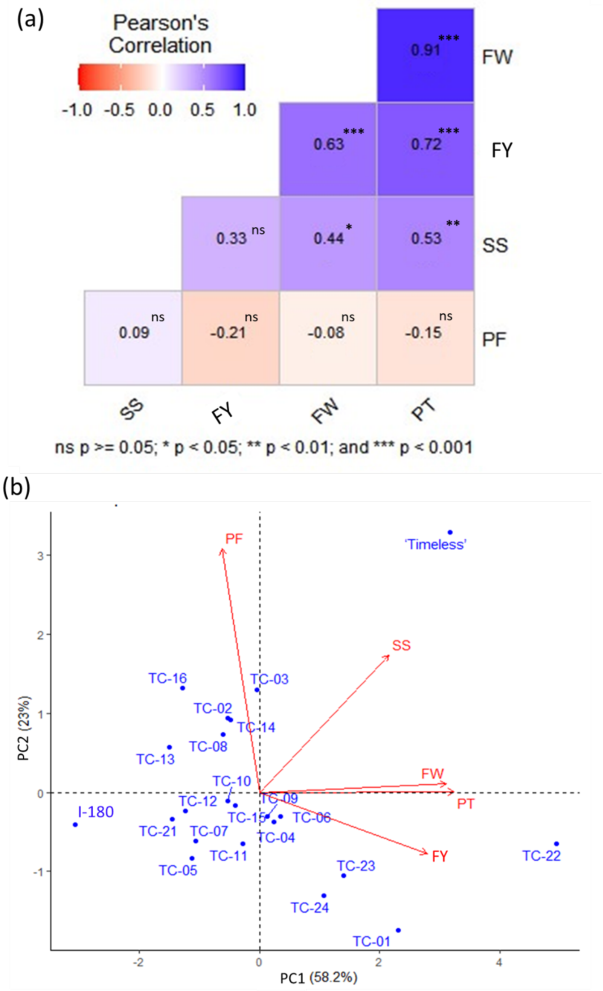

Figure 1. a) Genotypic correlations among yield and fruit quality traits in Tiger melon lines evaluated in two trials. b) Biplot of the first two principal components showing genotype dispersion. Traits: FY, fruit yield (Mg ha^{-1}); FW, mean fruit weight (kg); PT, pulp thickness (cm); PF, pulp firmness (kgf); SS, soluble solids (°Brix).

Statistical analysis

The dataset was subjected to deviance analysis, in which the effects of genotypes and genotype-by-environment interactions were modeled as random, whereas all other sources of variation were treated as fixed. Subsequently, variance components were estimated, and genotypic means were predicted using the restricted maximum likelihood/best linear unbiased prediction (REML/BLUP) approach, according to Equation 1:

$$y = Xb + Zg + Wc + e \qquad (1)$$

where *y* is the data vector corresponding to block means across environments; *b* is the vector of fixed-effect coefficients; *g* represents genotype effects, treated as random; *c* represents genotype–environment interaction effects, treated as random; and *e* represents the random error term in the model. The matrices *X*, *Z*, and *W* serve as incidence matrices for the fixed effects (*b*), genotype effects (*g*), and genotype–environment interaction effects (*c*), respectively.

In addition, two multivariate selection indices were computed: FAI-BLUP (Factor Analysis and Ideotype-Design Best Linear Unbiased Prediction) (Rocha et al. 2018) and MGIDI (Multi-Trait Genotype–Ideotype Distance Index) (Olivoto and Nardino 2021). The FAI-BLUP index was calculated using the fai_blup() function, and the MGIDI index was calculated using the mgidi() function.

The FAI-BLUP index was calculated according to Equation 2:

$$p_{i\bar{j}} = \frac{\frac{1}{d_{ij}}}{\sum_{i=1;j=1}^{i=n;\bar{j}=m} \frac{1}{d_{ij}}} \qquad (2)$$

where *Pij* is the probability that genotype *i* (*i* = 1, 2, ..., n) is similar to ideotype *j* (*j* = 1, 2, ..., m), and *dij* is the standardized mean Euclidean distance between genotype *i* and ideotype *j*.

The MGIDI index was calculated according to Equation 3:

$$MGIDI_i = \sum_{\bar{j}=1}^{f} (F_{ij} - F_j)^2 \qquad (3)$$

where *MGIDIi* is the multi-trait genotype–ideotype distance index for the *i*-th genotype; *Fij* is the score of the *i*-th genotype in the *j*-th factor (*i* = 1, 2, ..., g; *j* = 1, 2, ..., f, where g and f are the numbers of genotypes and factors, respectively); and *Fj* is the score of the ideotype on the *j*-th factor. The genotype with the lowest MGIDI value is closest to the ideotype and thus exhibits the desired values for all analyzed traits.

Pearson correlation analysis, principal component analysis, and factor analysis were performed on the predicted genotypic values to examine relationships among traits. Analyses were conducted using the metan package (version 1.19.0) in R software (R Core Team 2025).

RESULTS AND DISCUSSION

Mixed model

Deviance analysis of the combined data from the two trials revealed significant genotypic effects for all traits, confirming genetic variability among the lines and the potential for selection of superior Tiger melon genotypes (Table 1). This result supports the potential for genetic progress through selection, consistent with previous reports of high variability for fruit traits in other melon populations (Cavalcante et al. 2020, Chikh-Rouhou et al. 2024).

Genotype × environment (G × E) interaction was significant for pulp firmness (PF) and fruit yield (FY), indicating differential line performance across trials. This interaction was primarily simple, resulting from differences in magnitude of genetic variances between trials. No significant genotype × environment (G × E) interaction was detected for mean fruit weight (FW), pulp thickness (PT), or soluble solids (SS), indicating consistent performance across trials and supporting selection based on data combined across trials.

Table 1. Deviance analysis estimates of variance components, heritability, selective accuracy, genotype × environment (G × E) interaction coefficient of determination, genetic correlation across trials, experimental coefficient of variation, and means of yield and fruit quality traits in Tiger melon lines evaluated in two trials (2021 and 2022)

Effect	Traits				
	FY	FW	PT	PF	SS
Complete	793.400	-332.640	-140.090	52.490	203.070
Genotype	809.540**	-262.980**	-81.540**	57.950*	238.190**
G × E	803.750**	-332.630	-140.080	61.930**	203.180
$\hat{\sigma}^2_g$	66.765	0.127	0.296	0.188	1.863
$\hat{\sigma}^2_{gxe}$	18.245	0.019	0.001	0.140	0.029
$\hat{\sigma}^2_e$	35.319	0.127	0.074	0.289	0.779
$\hat{h}^2_m$ (%)	0.816	0.975	0.959	0.614	0.928
SA (%)	0.904	0.988	0.979	0.784	0.963
r^2_{gxe}	0.152	0.001	0.002	0.227	0.011
r_g	0.785	0.998	0.998	0.573	0.985
$\widehat{CV}_e$ (%)	22.179	18.880	9.490	21.588	13.000
Mean	26.796	0.730	2.868	2.494	6.787

$\hat{\sigma}^2_g$: genotypic variance; $\hat{\sigma}^2_{gxe}$: G × E interaction variance; $\hat{\sigma}^2_e$: residual variance; $\hat{h}^2_m$(%) : broad-sense heritability; *SA* (%): selective accuracy; r^2_{gxe} coefficient of determination for G × E interaction; r_g: genetic correlation across trials; $\widehat{CV}_e$: experimental coefficient of variation. Traits: FY, fruit yield (Mg ha^{-1}); FW, mean fruit weight (kg); PT, pulp thickness (cm); PF, pulp firmness (kgf); SS, soluble solids (°Brix). *,** Significant for a 5% and 1% of probability, respectively.

The significant G × E interaction for PF and FY suggests greater environmental influence on these traits, necessitating multi-year or multi-location trials to select stable genotypes (Aragão et al. 2015). However, the high genetic correlations across trials for most traits, combined with low coefficients of determination for the interaction, indicate that the G × E interaction was predominantly simple. Thus, although genotypic effects differed in magnitude between trials, the relative ranking of the lines remained stable, facilitating consistent selection across trials (Nunes et al. 2011, Cavalcante et al. 2025). Despite similar climatic conditions between trials, minor environmental differences likely contributed to the differential expression of PF and FY, as evidenced by the detected G × E interaction. Therefore, even moderate environmental variations can induce G × E interaction (Silva et al. 2019, Cavalcante et al. 2025, Lima et al. 2025).

Heritability estimates indicated a substantial genotypic variance contribution to phenotypic variance, suggesting high selection efficiency. Selective accuracy was consistently above 0.90 for all traits, except PF, indicating high experimental precision and strong agreement between predicted and observed genotypic values. These high heritability and selective accuracy values support the reliability of the inferences and the potential for substantial genetic gains through selection (Aragão et al. 2015). High values of these parameters are indicative of well-conducted trials with good precision and close agreement between predicted and observed genotypic values (Resende and Duarte 2007, Lima et al. 2022).

Genetic correlations across trials were high for most traits, supporting the predominance of simple G × E interaction and relative stability in line ranking across trials. Only PF showed a moderate correlation, indicating greater environmental sensitivity. These results indicate efficient selection potential for fruit quality traits, whereas PF and FY require particular attention in multi-trial evaluations.

The lower heritability and selective accuracy observed for PF, combined with moderate genetic correlation across trials, suggest stronger environmental influence and reduced predictability of selection response (Aragão et al. 2015). PF has been reported as particularly sensitive to environmental variation in melon, potentially requiring targeted strategies such as multi-location or multi-year trials or the use of multi-trait selection indices (Gomes et al. 2021, Bayoumy et al. 2021).

Variance component estimates showed that genotypic variance predominated for FW, PT, SS, and FY, whereas residual variance predominated for PF (Table 1). The G × E interaction variance component was larger for PF than for FY. Substantial genotypic variance for agronomically important traits such as SS, PT, and FY supports direct selection for superior genotypes combining high fruit yield and fruit quality (Aragão et al. 2015, Cavalcante et al. 2025). Overall, fruit quality traits such as SS and PT exhibited greater stability and stronger genetic control, making them more suitable for direct selection. In contrast, PF requires greater consideration of environmental effects, highlighting the value of multi-trial evaluations in melon breeding programs (Lima et al. 2025).

Correlation and principal component analysis for yield and quality traits

Genotypic correlations among yield and fruit quality traits were positive and significant, ranging from 0.44 to 0.91 (Figure 1a). PT showed high correlations with FW and FY, and a moderate correlation with SS. FW was moderately and positively correlated with FY and SS (Figure 1a).

Given the presence of genetic variability, understanding covariation among agronomically important traits is critical for developing effective selection strategies to identify superior genotypes. The observed genotypic correlations revealed strong positive associations between PT and both FW and FY, moderate association with SS, and moderate positive associations of FW with FY and SS. These favorable associations enable indirect selection using easily measured traits (Cavalcante et al. 2025). Selection for one trait is expected to improve both fruit yield and fruit quality because all correlations were positive, and larger fruits contribute directly to higher fruit yield (Chikh-Rouhou et al. 2021).

Principal component analysis (PCA) showed that the first principal component (PC1) explained 58.2% of the total variation and the second principal component (PC2) 23.0%, with the first two accounting for 81.2% of the total variation (Figure 1b). PT, FW, and FY were the primary contributors to the PC1, whereas PF and SS were primarily associated with PC2.

The distribution of genotypes along the first principal component (PC1) highlights that genotypes TC-01, TC-22, TC-23, and TC-24 exhibited the highest positive PC1 scores, with TC-22 showing the strongest association with higher FY, PT, and fruit size. In contrast, the four genotypes with the most negative PC1 scores (GW-180, TC-13, TC-21, and TC-16) were positioned on the opposite side of this axis, suggesting a lower contribution of these traits. The second principal component (PC2) was mainly associated with PF, with an additional contribution from SS, indicating its relevance for fruit quality attributes. The genotype 'Timeless', together with TC-16 and TC-03, showed the highest positive PC2 scores, demonstrating, mainly, a strong association with increased pulp firmness. Conversely, the genotypes with the most negative PC2 scores (TC-01, TC-24, and TC-23) exhibited lower association with the quality traits represented by this component. Overall, the PCA revealed complementary patterns of variation, allowing the identification of genotypes with contrasting profiles for productivity and fruit quality, which is particularly useful for defining selection strategies in breeding programs.

Factorial analysis and selection gains

Factor analysis for the MGIDI and FAI-BLUP indices showed that the first factor (eigenvalue $\lambda_1 = 2.85$) explained 56.9% of the variation and the second ($\lambda_2 = 1.09$) explained 21.8%, for a cumulative explained variance of 78.7%. This result indicates that most genotypic variability could be represented in two dimensions, providing stability and confidence in the multi-trait indices. A cumulative explained variance ≥ 70% is generally considered satisfactory in multi-trait selection studies; similar values have been reported for MGIDI and FAI-BLUP applications in various crops, with first factors explaining 60-80% of the variance (Olivoto and Nardino 2021). The proportion of variance explained in this study falls within the expected range, supporting the appropriateness of these methods and the reliability of genotype rankings.

Factorial analysis results for the MGIDI and FAI-BLUP indices grouped traits into two factors, with a mean communality of 0.79 (Table 2), indicating that a high proportion of trait variation was explained by the factors. Factor 1 comprised FW, PF, SS, and FY, whereas Factor 2 consisted solely of PT. Factor 1 grouped strongly intercorrelated traits related to yield and fruit quality, whereas Factor 2 represented pulp thickness, a trait with weaker correlations with the others. Original means, selection means, and percentage selection gains for the MGIDI and FAI-BLUP indices across traits are presented in Table 2. Selection means for FW, PF, SS, and FY were higher with MGIDI than with FAI-BLUP. Consequently, selection gains for these traits were greater with MGIDI. Positive gains were achieved for all traits at a selection intensity of 15%. Selection gains ranged from 14.9% for PT to 72.5% for FW with MGIDI, and from 0.39% for FY to 26.36% for FW with FAI-BLUP.

The MGIDI index selected the parental hybrid 'Timeless' and lines TC-22, TC-2, and TC-3, whereas the FAI-BLUP index selected 'Timeless', TC-3, TC-2, and TC-14 (Table 3; Supplementary Figure 2a, b). At this selection intensity, 75% of the selected genotypes coincided between methods (three of four genotypes common to both). The number of coincidence genotypes was highly correlated with selection intensity ($\rho = 0.996$; $p < 0.01$). Thus, the application of both indices allows a more reliable and comprehensive assessment of multi-trait genotype performance (Supplementary Figure 2c). Selection gains were higher with MGIDI than with FAI-BLUP for all traits, except pulp thickness. In a wheat study using five indices at a 20% selection intensity, Casagrande et al. (2020) reported that FAI-BLUP resulted in the lowest total selection gains, consistent with the present results. The ranking discrepancy for TC-22 between indices is likely attributable to methodological differences: MGIDI assesses genotype proximity to the ideotype using factor analysis to reduce multicollinearity while integrating all traits simultaneously, whereas FAI-BLUP applies more independent trait weighting.

Table 2. Factor loadings after varimax rotation, communalities from factor analysis (C), original means (X_o), selected means (X_{sMGIDI}; $X_{sFAI\text{-}BLUP}$), and percentage selection gains (G_S) for the MGIDI and FAI-BLUP indices of yield traits and fruit quality in Tiger melon lines evaluated in two trials (2021 and 2022)

Traits[1]	Factors		C	Factor	X_o	$X_{s\,(MGIDI)}$	$X_{s\,(FAI\text{-}BLUP)}$	$G_{S\,(MGIDI)}$ (%)	$G_{S\,(FAI)}$ (%)
	1	2							
FY	-0.80	0.26	0.71	1st	26.87	31.60	26.89	18.10	0.39
FW	-0.91	0.03	0.83	1st	0.72	1.25	0.92	72.50	26.36
PF	-0.96	0.08	0.92	1st	2.87	3.45	3.06	20.50	6.86
PT	0.11	-0.93	0.87	2nd	2.50	2.87	3.05	14.90	22.12
SS	-0.66	-0.41	0.61	1st	6.79	8.00	7.56	17.80	11.37
Mean			0.79						

[1] See codes in Table 1

Figure S3 presents the strengths and weaknesses of the genotypes, which are accounted for by the contribution of each factor to the MGIDI index. Regarding factor FA1, where the traits PT? and FW showed the highest factor loadings after rotation, followed by yield, the highest contribution was observed for genotype TC-22, followed by lines TC-02 and TC-03. The TC-22 line stood out with the highest values for these three traits regarding the selected genotypes (Table 3). Factor FA2, where PF was the prominent trait, showed the highest contributions, in descending order, for genotypes Timeless, TC-02, and TC-03 (Figure S3). These genotypes exhibited higher PF compared to the TC-22 line (Table 3).

Based on these results, three breeding strategies will be implemented for the selected lines TC-02, TC-03 and TC-22. First, the lines will be self-pollinated to advance to the F_7 generation and evaluated under commercial field conditions at multiple production farms to identify the most promising line. Second, intercrosses among the lines will generate a base population for selection of ridge-free fruits with high yield, fruit weight up to 1.5 kg, and superior quality, particularly SS (> 11 °Brix). Third, the lines will be used to develop experimental hybrids for evaluation under regional farm conditions.

CONCLUSION

The FAI-BLUP and the MGIDI indices identified the Tiger melon lines TC-02, TC-03, TC14, and TC-22 as the most promising for advancement to the next phase of the melon breeding program, combining high yield and superior fruit quality, traits highly valued by producers.

Table 3. Rankings according to the MGIDI and FAI-BLUP indices and predicted genotypic values for yield and fruit quality traits in Tiger melon lines and parental genotypes

Genotype	Classification		Predicted genotypic value (μ + ĝ)				
	MGIDI	FAI-BLUP	FY[1]	FW	PT	PF	SS
TC-01	21	13	35.23	1.35	3.78	1.98	7.99
TC-02	4	3	26.90	0.83	2.80	3.12	7.18
TC-03	3	2	24.29	0.87	2.89	2.99	8.90
TC-04	11	9	27.07	0.70	2.97	2.31	9.13
TC-05	25	24	20.83	0.75	2.62	2.40	6.68
TC-06	9	7	28.82	0.75	2.95	2.37	9.02
TC-07	23	22	25.67	0.65	2.61	2.56	6.58
TC-08	7	6	30.04	0.52	2.52	2.88	8.59
TC-09	12	11	19.52	0.77	3.04	2.17	9.67
TC-10	16	16	22.35	0.56	2.82	2.41	8.82
TC-11	19	19	27.33	0.67	3.00	2.45	7.38
TC-12	22	21	20.06	0.43	2.44	2.35	8.75
TC-13	18	20	19.70	0.47	2.35	2.72	8.44
TC-14	5	4	23.95	0.62	2.75	2.82	9.01
TC-15	15	15	28.37	0.50	2.73	2.49	8.61
TC-16	8	10	19.83	0.55	2.45	2.99	8.68
TC-17	6	5	31.57	0.52	3.06	2.58	9.20
TC-18	17	17	23.68	0.65	2.94	2.09	9.83
TC-19	10	8	24.99	0.68	3.04	2.27	9.49
TC-20	14	14	23.13	0.57	2.77	2.43	8.93
TC-21	24	23	20.49	0.58	2.44	2.52	7.27
TC-22	2	26	42.99	1.96	4.31	2.10	10.76
TC-23	13	12	44.41	0.68	2.96	2.19	9.39
TC-24	20	18	39.04	0.76	3.04	2.13	8.64
I-180	26	25	14.03	0.16	1.45	2.27	8.40
‘Timeless’	1	1	32.41	1.35	3.81	3.27	13.15

[1] See codes in Table 1

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DATA AVAILABILITY

The datasets generated and/or analyzed in this study, as well as the supplementary tables and figures, are available from the corresponding author upon reasonable request.

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