https://doi.org/10.1590/1678-4499.20240047

CROP BREEDING
Article

Genotype × environment interaction in yellow melon hybrids in different locations and growing seasons

José Galdino Cavalcante Neto[1], Elaíne Welk Lopes Pereira Nunes[1], Edicleide Macedo da Silva[1]*, Adriano Ferreira Martins[1], Luiz José Pitombeira Diógenes[1], Stefeson Bezerra de Melo[2], José Hamilton Costa Filho[3], Glauber Henrique de Sousa Nunes[1]

1. Universidade Federal Rural do Semi-Árido – Departamento de Ciências Agronômicas e Florestais – Mossoró (RN), Brazil.
2. Universidade Federal Rural do Semi-Árido – Departamento de Ciências Exatas e da Informação – Angicos (RN), Brazil.
3. Universidade Federal do Rio Grande do Norte – Unidade Acadêmica Especializada em Ciências Agrárias - Macaíba (RN), Brazil.

Received: Feb. 12, 2024 | **Accepted:** Oct. 29, 2024

Section Editor: Luciana Carlini-Garcia

***Corresponding author:** edicleide.c.c@gmail.com

How to cite: Cavalcante Neto, J. G., Nunes, E. W. L. P., Silva, E. M., Martins, A. F., Diógenes, L. J. P., Melo, S. B., Costa Filho, J. H. and Nunes, G. H. S. (2025). Genotype × environment interaction in yellow melon hybrids in different locations and growing seasons. Bragantia, 84, e20240047. https://doi.org/10.1590/1678-4499.20240047

ABSTRACT: Melon (*Cucumis melo* L.) is cultivated worldwide, with prominence in the Northeast region of Brazil, due to its favorable soil and climate conditions. However, over the years, the genotype × environment (GxE) interaction phenomenon has been occurred, which can complicate the selection process depending on its extent (whether it is a simple or complex interaction). In this context, melon breeding programs aim to identify adaptable and stable genotypes, capable of reaching their maximum potential. Therefore, the objectives of this study were to investigate GxE interactions and identify cultivars with greater adaptability and phenotypic stability using various methods for comparison. Thirteen melon hybrids were assessed in four municipalities in the state of Rio Grande do Norte, across two planting dates, totaling eight distinct environments. The experiments were conducted in randomized complete blocks with three replications. The traits evaluated included the number of fruits per plant and total soluble solids. Several adaptability and stability methods were employed and compared including Wricke, Eberhart and Russell, Lin and Binns, Annicchiarico, GGE Biplot, and Resende (harmonic mean of relative performance of genotypic values). Significant GxE interaction for the number of fruits per plant was found to be simple, whereas for soluble solids, it was crossed. The methods of Linn and Binns, Annicchiarico, and Resende showed strong correlations among them and were all correlated with the trait mean. The HA-08 hybrid emerged as the most promising, exhibiting high number of fruits per plant, high soluble solids content, and exceptional adaptability and stability.

Key words: *Cucumis melo* L., mixed models, cultivars recommendation.

INTRODUCTION

Melon (*Cucumis melo* L.) is globally recognized for its economic significance and it is cultivated in various regions across the world. In Brazil, the states of Rio Grande do Norte and Bahia stand out for their yield and significant contributions to melon cultivation. In 2022, Brazilian melon exports reached the total value of US$ 156.4 million, with major destinations including the Netherlands (80.2 thousand tons), the United Kingdom (60.5 thousand tons), and Spain (55.7 thousand tons) (Kist and Beling 2023).

Melon cultivation occurs practically all year round in the Brazilian semi-arid region, with reduction in area in the rainy season (February to May). In the second semester, when there is practically no rain, the cultivation area is expanded. Farmers take advantage of the European production off-season and produce fruit for export. The Yellow or Valencian melon variety is the most widely produced due to its ease cultivation in comparison to other varieties, as well as its extended post-harvest shelf life, occupying over 60% of the cultivated areas.

In the dry season, cultivation happens in two main periods: the first from June to August and the second from September to December. Although the climatic differences between these seasons are not very pronounced, the presence of genotypes × environments interaction has been observed, leading to concerns and dissatisfaction in the production sector.

The genotype × environment (GxE) interaction phenomenon has been reported on several occasions at Agropolo Mossoró-Assu for various hybrid types (Nunes et al. 2006, Freitas et al. 2007, Nunes et al. 2011b) and families (Silva et al. 2011, Aragão et al. 2015, Guimarães et al. 2016). Therefore, the existence of interactions between genotypes and locations, and genotypes and years, with the prevalence of cross-interaction (complex), underscores the necessity for conducting research aimed at comprehending the extent of both simple and complex variation components and their impact on phenotypic characteristics, as well as their relevance to adaptability and stability.

In the context of melon cultivation, the identification of genotypes displaying high adaptability and stability stands as a crucial approach to mitigate the impact of the GxE interaction, and it forms one of the primary objectives of crop genetic improvement programs. Numerous methods have been proposed to estimate adaptability and stability parameters, encompassing those based on analysis of variance, linear regression, nonlinear regression, and multivariate techniques. More recently, techniques rooted in mixed, Bayesian, and neural network models have been employed in studies of adaptability and phenotypic stability (Silva et al. 2019, Han et al. 2024, Rosa et al. 2024, Shrilatha et al. 2024). These diverse methods differ in their underlying concepts of stability and mathematical properties. When used in conjunction, they assist researchers in the evaluation and selection of genotypes.

Some of the notable methods include Wricke (1965), Eberhart and Russell (1966), Lin and Binns (1988), Annicchiarico (1992), GGE Biplot (Yan and Kang 2003), and Resende's (2007) harmonic mean of relative performance of genotypic values (HMRPGV). Consequently, a range of methods have been utilized to facilitate adaptability and stability estimation (Bornhofen et al. 2017, Rother et al. 2019, Silva et al. 2019, Bishwas et al. 2021, Bai et al. 2023, Li et al. 2023).

With these considerations in mind, the current study aimed to investigate GxE interaction, based on different sowing times during the dry season, determine the magnitude of both simple complex components of this interaction, and identify cultivars that exhibit superior adaptability and phenotypic stability using a variety of methodologies, and compare these different methods.

MATERIAL AND METHODS

Genotypes

A set of simple yellow melon hybrids was assessed, including the following varieties: Goldex, HA-01, HA-02, HA-03, HA-04, HA-05, HA-06, HA-07, HA-08, HA-09, HA-10, HA-11, and HA-12. These hybrids are denoted by the HA code, and they are experimental andromonoic hybrids with white mesocarp, smooth exocarp, and a vibrant yellow color. These hybrids are a product of the genetic improvement program developed at the Universidade Federal Rural do Semiárido, Mossoró, RN, Brazil.

Environments

The evaluation of these hybrids took place in four key municipalities in the Mossoró-Assu Agropolo, spanning two distinct sowing times referred to as E1 and E2, both occurring during the dry season. This arrangement resulted in a total of eight distinct environments. E1 encompassed the months from June to August, while E2 covered the period from September to November (as illustrated in Table 1).

Table 1. Identification, season, city, altitude, soil type, and climatic data for the evaluation environments of melon hybrids at Mossoró-Assu Agricultural Complex, Mossoró, RN, Brazil.

Environments	Season	City	Altitude (m)	Soil	Covariates		
					T_{MAX}	T_{MIN}	RH
Mos-01	E1	Mossoró	18	LVE	30.96	28.82	83.13
Bar-01	E1	Baraúna	94	NEQ	31.71	29.59	71.45
Ass-01	E1	Assu	27	CAH	31.88	29.53	70.98
Apo-01	E1	Apodi	13	CAH	33.11	30.59	64.34
Mos-02	E2	Mossoró	18	LVE	31.60	29.30	66.21
Bar-02	E2	Baraúna	94	NEQ	33.40	30.87	55.71
Ass-02	E2	Assu	27	CAH	29.41	27.24	74.70
Apo-02	E2	Apodi	13	CAH	30.73	28.46	65.50

E1: June-July-August; E2: September-October-November; LVE: Eutrophic Red Latosol; NEQ: Quartzarenic Neosol; CAH: Haplic cambisol; T_{MAX}: maximum temperature (°C); T_{MIN}: minimum temperature (°C), RH: relative humidity (%).

Experimental design

The experiments were conducted using a randomized complete block experimental design, with three replications each. Experimental plots comprised of two 5-m rows, each containing 10 plants, with one plant per drip emitter. To account for the border of the plot, one plant was placed at each line end, resulting in a total of 16 plants available for analysis per replication.

Conduction experimental

A drip irrigation system was employed, with a spacing of 2 m between rows and 0.4 m between individual drippers. The irrigation regimen amounted to an approximate volume of 300 $m^3 \cdot ha^{-1}$.

Soil fertility management was conducted in accordance with soil analysis results obtained from each specific location. The experiment was executed, and the cultural techniques were implemented in alignment with the crop management recommendations outlined for the state (Nunes et al. 2016).

Evaluated characters

The assessment included the determination of two key parameters: the number of fruits per plant, and the total soluble solids content. The number of fruits per plant was calculated by dividing the total number of harvested fruits in the plot by the total number of plants in that plot.

For measuring the soluble solids content, two juice samples were extracted from the fruit mesocarp. This was done using a digital refractometer model (1-877-ATAGO PAL-1), specifically calibrated in °Brix units. Ten fruit per plot sampled by casualization were evaluated. To analysis, the average of the plot was used.

Statistical analyses

Estimation of variance components and prediction of genotypic values

The joint statistical analysis of the genotypes evaluated at seasons and locations, with one observation per plot, followed Eq. 1:

$$y = Xf + Zg + Qp + Ti + Wt + e \quad (1)$$

where: y: vector of observed data; *f*: the vector of fixed effects of the locations-seasons combinations (assumed to be fixed) added to the general mean (μ); g: the vector of genotypic random effects [~NID(0, $\hat{\sigma}^2_g$)]; p: the vector of random effects of the genotypes × season interaction [~NID(0, σ^2_{gs})]; i: the vector of the random effects of the genotypes × locations interaction [~NID(0, 0, σ^2_{gl})]; t: the vector of random effects of the triple interaction genotypes × locations × season [~NID(0, 0, $\hat{\sigma}^2_{gls}$)]; e: the vector of errors or residues assumed to be random [~NID(0, σ^2_e)].

The vector *f* contemplates the effects of replications within seasons, of locations, of seasons and locations × season interaction.

Variance components were estimated using the restricted maximum likelihood (REML) method. The restricted maximum likelihood ratio test was performed to test the significance of the variance components of the model. The function used for this test was Eq. 2:

$$D = 2[\log(L_R 2) - \log(L_R 1)] \tag{2}$$

where: D: the deviance; $\log(L_R 2)$: the logarithm of the likelihood of the model with the tested variance component; $\log(L_R 1)$: the logarithm of the likelihood of the model without the tested variance component.

The analysis was carried out according to model 114 of the SELEGEN-REML/BLUP software (Resende 2016).

Adaptability and stability analysis

Ecovalence (W_i), P_i index, and trust index I_i

Ecovalence was determined using the methodology introduced by Wricke in 1965, relying on the predicted values of the interaction between genotypes and environments. The stability index (P_i) was estimated based on genotypic means using the method proposed by Linn and Binns in 1988. The confidence index (I_i) was calculated following the method outlined by Annicchiarico in 1992. The confidence level used for this calculation was set at 75%, corresponding to α = 0.25.

GGE biplot method

The GGE Biplot analysis was performed using Eq. 3:

$$\hat{g}_i + \widehat{ge}_{ij} = \sum_{k=1}^{p} \lambda_k a_{ik} t_{jk} + \rho_{ij} \tag{3}$$

where: ($\hat{g}_i + \widehat{ge}_{ij}$): the estimate of the genotypic value *i* added with the effect of the interaction of genotype (*i*) environment (*j*) obtained in the REML/BLUP analysis; λ_k: the effect of the singular value (eigenvalue) of the principal component *k*; a_{ik}: the effect of the eigenvector of genotype *i* on the *k*; t_{jk} axis: the effect of the eigenvector of the environment *j* on the *k*; ρ_{ij} axis: the residual effect remaining when all the principal components *p* are not used, that is, p = min(g - 1; *e* - 1).

The genotypes and environment scores were used to obtain a Biplot graph to interpret the structure of the GxE interaction.

Harmonic mean method of relative performance of genotypic values

The HMRPGV was estimated by the REML/BLUP method based on the methodology proposed by Resende (2007).

All adaptability and stability analyses were carried out using the GGEBiplotGUI (Bernal 2016) and Metan (Olivolto and Dal'Col Lúcio 2020) packages of the R software (R Core Team 2023).

Linear regression

The adaptability and stability parameters were estimated using the linear regression model developed by Eberhart and Russell in 1966. The estimates of the parameters of the Eberhart and Russell's model (1966) (β_i and δ_{ij}) were tested using the Student's t-test at a 5% probability level. The grouping of the means of the genotypes was performed using the Scott-Knott's method at a 5% probability level (Scott-Knott 1974).

RESULTS

Main effects and interactions

Significant effects were observed for seasons, locations, and their interaction ($p < 0.01$) for both traits under examination. This highlights variations in growing conditions between the two seasons and among the four locations, as well as the combined impact of these factors (Table 2).

Notably, there was no significant effect observed for the interaction between genotypes and seasons, indicating that the hybrids performed consistently in both evaluation seasons. However, significant effect was observed for the genotypes × seasons × locations interaction ($p < 0.05$) regarding the number of fruits per plant, and for the genotypes × locations interaction ($p < 0.05$) concerning soluble solids (as shown in Table 2). The presence of the genotypes × locations interaction suggests different behavior of genotypes across different locations, emphasizing the need for evaluations in multiple environments, considering different seasons-locations combinations.

To better understand the intensity of these interactions on phenotypic expression, the magnitude of these interactions was estimated. For the number of fruits per plant, the triple interaction had a greater influence, accounting for 20.39% of the phenotypic variance, while for soluble solids the genotypes × locations interaction played a significant role, contributing to 24.67% of the phenotypic variance (Table 2).

Table 2. Estimates of the simple and complex components of the interaction, coefficient of variation, and selective accuracy for the number of fruits per plant and soluble solids in yellow melon hybrids. These hybrids were evaluated in four municipalities (locations) in the Mossoró-Assu Agropolo, during two growing seasons in the dry season sowing, specifically in Mossoró, RN, Brazil, in 2020#.

Effect	Character	
	Number of fruits per plant	Soluble solids (ºBrix)
Random	Estimate (χ^2)	
$\hat{\sigma}^2_g$	0.0252** (33.16)	0.0991*(12.47)
$\hat{\sigma}^2_{gs}$	0.0037^{ns} (4.87)	0.0011^{ns} (0.14)
$\hat{\sigma}^2_{gl}$	0.0003^{ns} (0.39)	0.1960** (24.67)
$\hat{\sigma}^2_{gls}$	0.0155* (20.39)	0.0110ns (1.38)
$\hat{\sigma}^2_e$	0.0447 (58.82)	0.4901 (61.69)
$\hat{\sigma}^2_f$	0.0760**	0.7944**
Fixed	Snedecor's F	
Block/Environment	2.30*	3.87**
Season (S)	51.40**	163.75**
Location (L)	257.74**	123.53**
S × L	16.13**	22.41**
CV (%)	12.73	5.19
SA	0.97	0.72
$\hat{r}_g$	0.78	0.41

$\hat{\sigma}^2_g$: genotypic variance component estimate; $\hat{\sigma}^2_{gs}$: variance component of the genotypes × season interaction estimate; $\hat{\sigma}^2_{gl}$: variance component of the genotypes × locations interaction estimate; $\hat{\sigma}^2_{gls}$: variance component of the genotypes × location × season interaction estimate; $\hat{\sigma}^2_e$: residual variance component; CV (%): coefficient of variation; SA: selective accuracy; $\hat{r}_g$ genotypic correlation between all environments estimate; ns: not significant; *significant at 5% probability; **significant at 1% probability; #values in parentheses refer to the percentage contribution of each variance component to the phenotypic variation.

Adaptability and stability

Number of fruits per plant

Regarding ecovalence in the method Wricke (W_i), HA-05 and HA-08 were found to have the lowest contribution to the GxE interaction, while HA-12, HA-02, HA-04, and HA-11 had the highest contributions (as shown in Table 3).

Only three hybrids exhibited regression coefficients (βi) significantly different from 1, with two being specifically adapted to favorable environments (HA-08 and HA-06) and one specifically adapted to unfavorable environments (HA-03). The remaining hybrids demonstrated general or average adaptability. It is worth noticing that the regression bias was non-significant for all hybrids except HA-12 (see Table 3). In terms of this methodology, the ideal genotype is one with a high mean, a regression coefficient of 1, and a regression deviation of 0. In this context, HA-09 performed favorably.

In the Linn and Binns' (1988) method, the 'Goldex' hybrid emerged as the most stable, followed by HA-02, HA-05, HA-09, and HA-11. Conversely, HA-04, HA-043, and HA-01 were characterized by higher instability, as indicated by the Pi values (Table 3). For Annicchiarico's (1992) methodology, the most stable hybrids were HA-09, HA-06, and HA-08. In the context of the HMRPGV methodology, HA-09, HA-06 and HA-08 were identified as the most stable and adapted hybrids, demonstrating the highest number of fruits per plant (Table 3).

Table 3. Adaptability and stability parameters estimates for the number of fruits per plant in yellow melon hybrids, considering the fixed genotypes. Mossoró, RN, Brazil#.

Hybrid	Average	Wricke	Eberhart and Russel			A	B	C
		W_i (%)	β_i	δ_{ij}	R^2 (%)	P_i	I_i (%)	HMRPGV
Goldex	1.45d	4.83	0.82^{ns}	0.01^{ns}	96.55	0.14	86.51	1.43
HA-01	1.50d	4.47	0.98^{ns}	0.07^{ns}	96.76	1.27	98.12	1.48
HA-02	1.61c	13.29	1.04^{ns}	0.01^{ns}	95.05	0.21	96.61	1.61
HA-03	1.41d	7.74	0.75*	0.01^{ns}	89.33	3.67	81.51	1.38
HA-04	1.48d	12.22	0.86^{ns}	0.01^{ns}	91.89	2.49	87.09	1.47
HA-05	1.60c	2.09	0.85^{ns}	0.01^{ns}	90.51	0.21	95.42	1.60
HA-06	1.82a	9.04	1.26*	0.01^{ns}	95.52	0.36	108.97	1.84
HA-07	1.49d	5.11	0.98^{ns}	0.01^{ns}	88.60	0.80	86.85	1.47
HA-08	1.71b	2.51	1.29*	0.01^{ns}	96.15	0.41	100.38	1.72
HA-09	1.91a	4.90	1.10^{ns}	0.05^{ns}	91.16	0.27	116.47	1.96
HA-10	1.66b	7.31	1.11^{ns}	0.01^{ns}	94.19	0.46	99.86	1.67
HA-11	1.55c	10.19	1.00^{ns}	0.01^{ns}	95.71	0.28	92.01	1.54
HA-12	1.59c	16.31	0.98^{ns}	0.70*	70.17	0.89	89.58	1.59

A: Linn and Binns (1988); B: Annicchiarico (1992); C: Resende (2007); HMRPGV: harmonic mean of the relative performance of genotypic values; #means followed by the same letter do not differ from each other using the Scott-Knott's grouping method at a 5% probability level (Scott-Knott 1974); *significant by the Student's t-test at a 5% probability level; ns: not significant by the Student's t-test at a 5% probability level.

Soluble solids

In the context of soluble solids, it was observed that HA-04 and HA-03, with lower ecovalence estimates, had the smallest contribution to the GxE interaction. On the contrary, HA-09 and HA-06 were the most influential contributors to the interaction, making them the most unstable in terms of this trait (as indicated in Table 4).

The hybrids HA-02, HA-011, and HA-09 exhibited regression coefficients (βi) exceeding significantly unity, indicating their specific adaptation to favorable environments. Conversely, HA-07 demonstrated specific adaptability to unfavorable conditions. The remaining hybrids demonstrated general or average adaptability. Significant regression deviations were observed for the hybrids HA-01, HA-05, HA-06, HA-09, and Goldex, showing their pronounced instability (see Table 4). In contrast, the remaining hybrids displayed non-significant regression deviations. The ideal genotype was identified in the standout hybrids HA-08 and HA-03, both showcasing high performance levels that surpassed the minimum commercialization threshold for foreign markets.

Among the hybrids, HA-08 and HA-03 exhibited the lowest Pi index values, showing their superior stability (Table 4). Conversely, HA-09 and HA-05 were the most unstable, as evidenced by their elevated Pi values. According to Annicchiarico's (1992) methodology, the hybrids HA-08 and HA-03 were consistently identified as the most stable. Furthermore, these same hybrids demonstrated remarkable stability and adaptability, while exhibiting the highest soluble solids content when considering the HMRPGV methodology.

Table 4. Adaptability and stability parameters estimates, accounting for the effect of fixed genotypes, for soluble solids in yellow melon hybrids, Mossoró, RN, Brazil#.

Hybrid	Average	Wricke	Eberhart and Russel			A	B	C
		W_i (%)	β_i	δ_{ij}	R^2 (%)	P_i	I_c (%)	HMRPGV
Goldex	13.70b	8.78	0.82^{ns}	0.21*	69.24	0.70	98.24	13.67
HA-01	13.31c	9.69	0.81^{ns}	0.25*	66.58	0.91	95.25	13.33
HA-02	13.36c	9.50	1.55*	0.09^{ns}	97.88	0.99	94.99	13.35
HA-03	14.23a	4.47	0.86^{ns}	0.02^{ns}	83.31	0.15	103.06	14.15
HA-04	13.63b	2.55	0.89^{ns}	0.06^{ns}	90.47	0.59	99.12	13.62
HA-05	13.07c	8.48	0.86^{ns}	0.22*	71.26	1.43	93.70	13.12
HA-06	13.31c	10.23	1.26^{ns}	0.24*	83.16	1.09	94.82	13.31
HA-07	13.92a	8.61	0.66*	0.09^{ns}	67.75	0.30	99.94	13.88
HA-08	14.33a	5.23	0.91^{ns}	0.07^{ns}	81.41	0.05	103.63	14.23
HA-09	13.04c	12.51	1.32*	0.30*	82.58	1.51	92.53	13.08
HA-10	13.27c	5.46	0.80^{ns}	0.04^{ns}	79.49	1.02	95.78	13.31
HA-11	13.48b	7.83	1.35*	0.05^{ns}	91.36	0.80	96.37	13.46
HA-12	13.32c	6.68	0.93^{ns}	0.15^{ns}	78.00	1.00	95.84	13.35

A: Linn and Binns (1988); B: Annicchiarico (1992), C: Resende (2007); HMRPGV: harmonic mean of the relative performance of genotypic values; #means followed by the same letter do not differ from each other using the Scott-Knott's grouping method at a 5% probability level (Scott-Knott 1974); *significant by the Student's t-test at a 5% probability level; ns: not significant by the Student's t-test at a 5% probability level.

GGE Biplot

In terms of the number of fruits per plant, the first and second principal components captured 68.85 and 17.17% of the GxE sum of squares, respectively, resulting in an accumulated variation of 79.59%. When considering soluble solids, the first two principal components explained 47.97 and 21.11% of the variation attributable to the sum of squares of GxE.

When considering the polygon by the number of fruits per plant, this was composed of six vertices, effectively segmenting the graph into six distinct sections. The environments were categorized into two mega-environments: the first comprised only the AP-01 environment, while the second encompassed the remaining environments (Fig. 1a). The apex of the first mega-environment was defined by the hybrid HA-11, whereas the hybrid HA-08 occupied the apex of the second mega-environment. The genotypes located at each vertex represented those with the highest number of fruits per plant in most of the environments in their respective mega-environment. Notably, no mega-environment fell in sectors in which the genotypes HA-02, HA-03, and HA-06 were the vertex genotypes, suggesting that these particular genotypes exhibited lower yield in the evaluation environment.

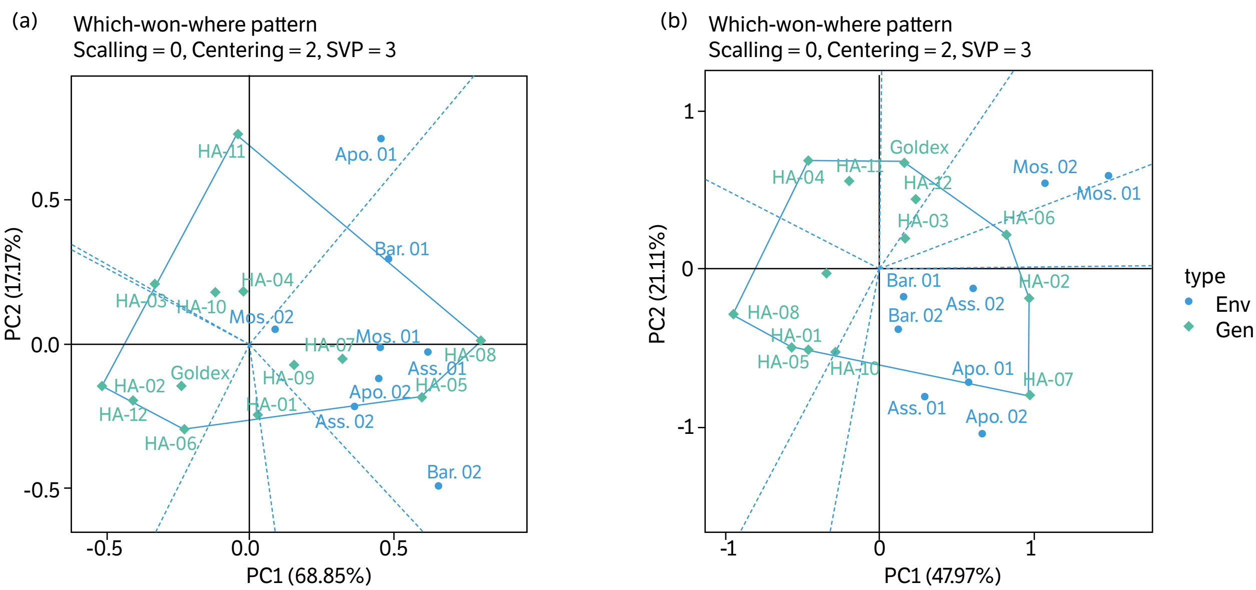
In the context of soluble solids, the polygon encompassed seven vertices, each representing a genotype (HA-04, Goldex, HA-06, HA-02, HA-07, HA-05, and HA-08), effectively dividing the graph into seven distinct sections. Environments, on the other hand, were grouped into just two sections, while the genotypes were distributed into four separate sectors. The genotype at the apex of each sector exhibited the highest average for the specific trait in the environments comprising that sector (Fig. 1b).

We identified two prominent mega-environments. The first mega-environment encompassed the following environments: AS-01, AS-02, BA-01, BA-02, AP-01, and AP-02, with the vertex genotype HA-07. This genotype demonstrated superior performance in most of these environments. In contrast, the second mega-environment featured only the MO-01 and MO-02 environments, with its apex genotype being HA-06. Notably, the remaining hybrids, except for HA-02, were not associated with either of the two mega-environments.

Regarding the study environments and the results of the mega-environment formation in the GGE Biplot analysis, it is essential to initially contextualize the melon-producing region in Rio Grande do Norte state. The municipalities of Mossoró and Baraúna account for over 90% of the production and export of melons in the state. These municipalities are very close to each other, about 37 km apart. However, due to water scarcity in these municipalities in recent years, farmers have been seeking new alternatives, with two of them being the municipalities of Apodi and Assu. Apodi is located 79 km from Mossoró and 91 km from Baraúna. The municipality of Assu is 70 km from Mossoró and over 110 km from Baraúna and Apodi. All four municipalities are situated in the Mesorregion of Western Potiguar, with Mossoró and Baraúna in the Mossoró Microrregion, Apodi in the Apodi Microrregion, and Assu in the Açu Valley Microrregion.

The climatic characteristics are similar in terms of temperature and relative humidity during the trial period (June to November), as shown in Table 1. Additionally, sunlight and rainfall are comparable between the locations and favorable for melon cultivation. However, the municipality of Baraúna has a higher altitude compared to the other ones. The GGE Biplot analysis reflected the similarities among the municipalities, as one of the two mega-environments formed for the number of fruits per plant included all environments except Apo-01. In contrast, for soluble solids, the first mega-environment included all municipalities except Mos-01 and Mos-02, which were part of the second mega-environment.

The formation of mega-environments in the GGE Biplot analysis for the two studied traits, with one mega-environment consisting of practically all environments in both cases, reflects, at least in part, the minor contribution of interactions between genotypes × seasons, genotypes × locations, as well as the three-way interaction genotypes × seasons × locations on phenotypic expression, especially for the number of fruits per plant (Table 2). However, more detailed analyses with factor regression analysis would be necessary to quantify the effect of environmental covariates on the genotypes and, consequently, the effect on the genotype × environment interaction. In a previous study, Nunes et al. (2011a) concluded that average, maximum, and minimum temperatures have the greatest influence on the genotype × environment interaction in melons for yield.



Env: environments; Gen: genotypes.

Figure 1. GGE Biplot Which-Won-Where graph for (a) the number of fruits per plant and (b) soluble solids evaluated in yellow melon hybrids.

In the context of the GGE Biplot method, the visualization of the mean and stability of genotypes is achieved by drawing an average environment coordinate (AEC) on the biplot. First, an average environment, represented by a small circle, is defined by the mean scores of PC1 and PC2 for all environments. The line that passes through the origin of the biplot and the AEC can be referred to as the mean. The ordinate AEC distinguishes hybrids with performance below and above the general average. Consequently, hybrids with a higher number of fruits per plant than the general average included HA-08, HA-05, HA-07, HA-09, and HA-01 (Fig. 2a). For soluble solids, the hybrids with the highest averages were HA-07, HA-02, HA-06, HA-12, and HA-03 (Fig. 2b).

On the other hand, the ordinate of the AEC is the line that passes through the origin of the biplot and is perpendicular to the abscissa of the AEC. Therefore, if the AEC abscissa represents the genotype, the AEC ordinate quantifies the stability of the genotype (Yan et al. 2007). Thus, a greater projection on the AEC ordinate, regardless of the direction, indicates greater instability. Therefore, in terms of the number of fruits per plant, hybrids HA-09, HA-07, and HA-08 were the most stable (Fig. 2a). In contrast, hybrids HA-11 and HA-06, with longer vectors farthest from the AEC abscise line, were the most unstable. As for soluble solids, hybrids HA-07, HA-03 and HA-09 demonstrated the most stability, while hybrids HA-08, Goldex, HA-01, HA-10, and HA-05 exhibited the highest degree of instability (Fig. 2b).

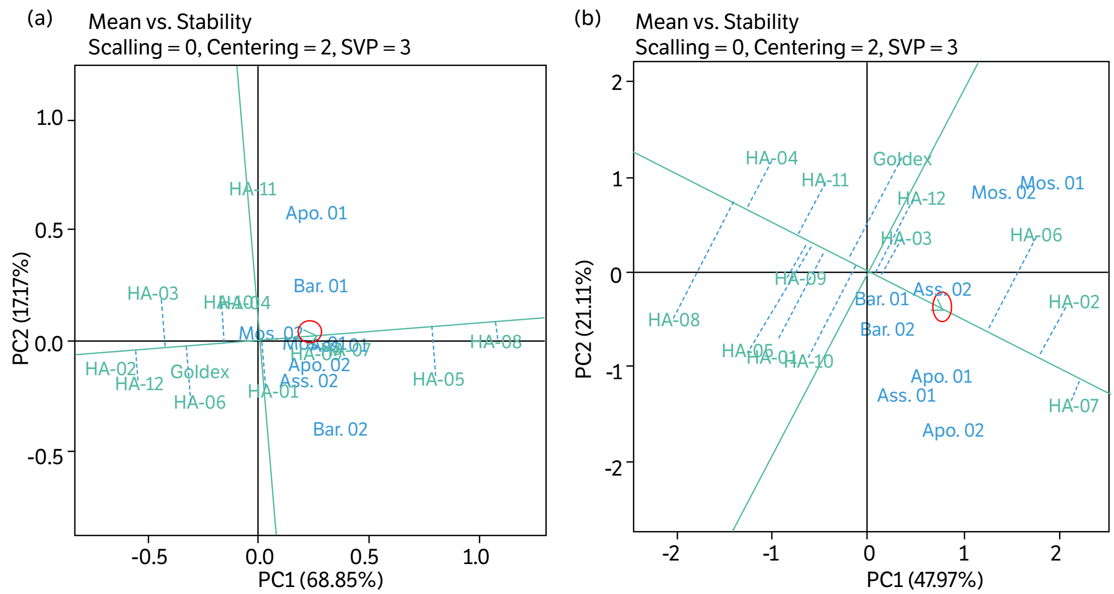
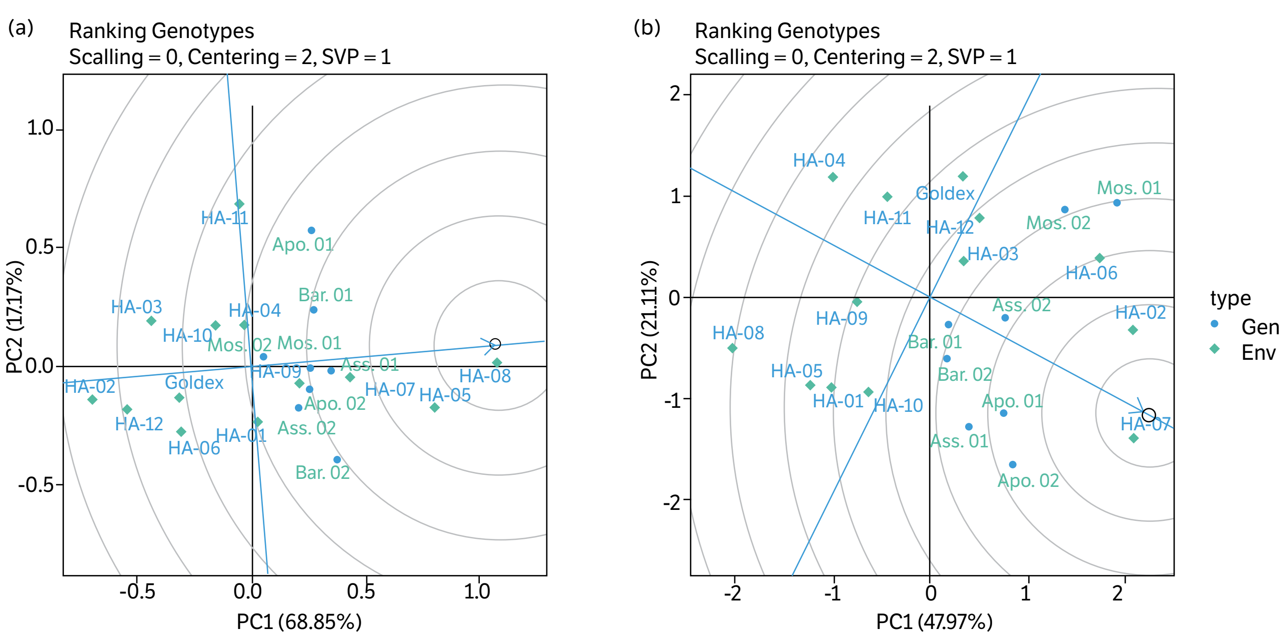


Figure 2. GGE Biplot graph showing mean and instability for (a) the number of fruits per plant and (b) soluble solids in evaluated yellow melon hybrids.

In the context of the number of fruits per plant, the hybrids positioned near the first concentric circle, namely HA-08, HA-05, and HA-07, were in proximity to the ideal genotype, thus establishing them as desirable genotypes (Fig. 3A). For soluble solids, hybrids HA-07, HA-02, and HA-06, situated close to the first concentric circles, held promise (Fig. 3B).



Env: environments; Gen: genotypes.

Figure 3. GGE Biplot graph showing mean and instability for (a) the number of fruits per plant and (b) soluble solids in evaluated yellow melon hybrids.

Regarding result consistency, it was observed that the Linn and Binns' (1988) method exhibited a negative correlation with both the character average and the methods proposed by Annicchiarico (1992), Eberhart and Russell (1966), and Resende (2007) for number of fruits per plant (Figs. 4 and 5).

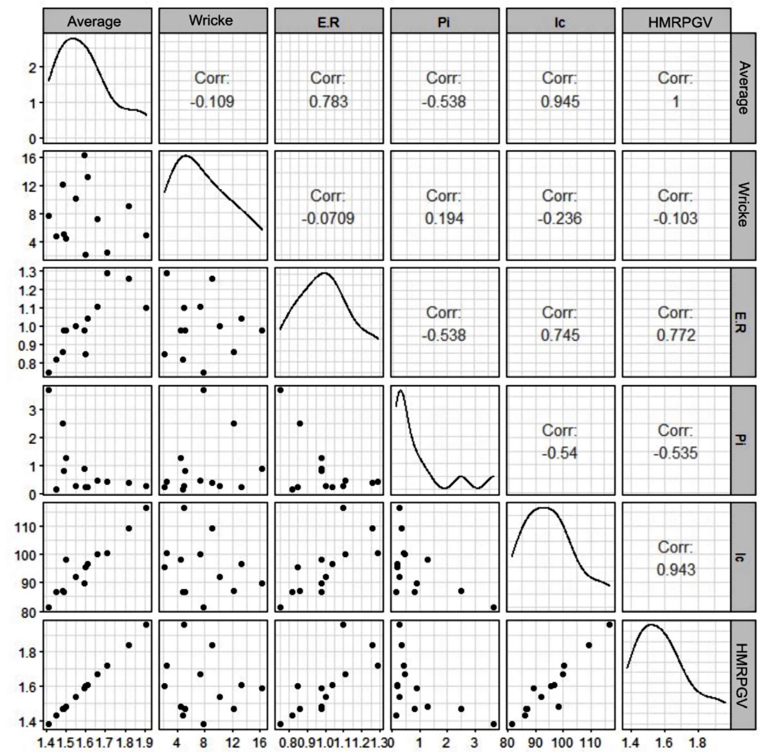


Figure 4. Correlations between adaptability and stability parameters estimated by six methods, average, Wricke, Eberhart (E.R) and Russel, Linn and Binns (Pi), Annicchiarico (Ic), and Resende (harmonic mean of the relative performance of genetic values), for the number of fruits per plant evaluated in yellow melon hybrids.

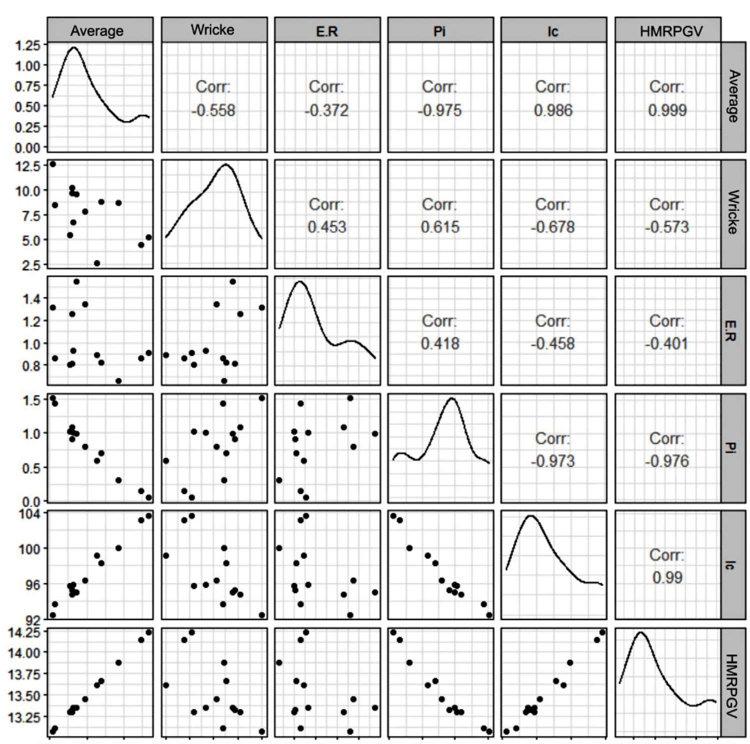


Figure 5. Correlations between adaptability and stability parameters estimated by six methods, average, Wricke, Eberhart (E.R) and Russel, Linn and Binns (Pi), Annicchiarico (Ic), and Resende (harmonic mean of the relative performance of genetic values), for soluble solids evaluated in yellow melon hybrids.

DISCUSSION

The identification of melon cultivars with high adaptability and stability stands as a paramount practice crucial for achieving success in the final stages of crop genetic improvement programs. It represents a fundamental and indispensable aspect, considering that phenotypic instability poses challenges for breeding programs. This difficulty underscores the complexity of selecting stable genotypes across diverse environments. In our study, we observed that employing various methods for estimating adaptability and stability facilitated the identification of genotypes demonstrating stability and adaptability. These findings hold valuable implications, recommending these stable genotypes for cultivation in this region.

Experimental accuracy

In the evaluation of cultivars, the initial concern revolves around the quality of the trials. This holds relevance in current genetic improvement programs for melon trees, in which the discernible differences between hybrids have diminished owing to enhanced selection processes and the increased relatedness of evaluated genotypes.

Therefore, selective accuracy is an essential parameter. This parameter gauges the correlation between the true genotypic value of the genetic treatment and the value estimated or predicted based on experimental information (Resende and Duarte 2007). According to the classification provided (Resende and Duarte 2007), the precision for the number of fruits per plant and soluble solids is very high (≥ 0.90) and high (≥ 0.70), respectively (Table 2).

GxE interaction

The presence of GxE interaction has been consistently observed in melon studies at Agropolo Mossoró-Assu, particularly concerning yield and soluble solids (Silva et al. 2011, Nunes et al. 2011b, Aragão et al. 2015, Guimarães et al. 2016). Variances in results across studies primarily stem from variations in the genotypic groups and environmental conditions considered. Then, differences are observed in the cultivation regions (Table 1).

The GxE interaction can be classified as simple and complex. The simple interaction is due to differences in the magnitude of genotypic effects in different environments, without altering the genotypic classifications. On the other hand, the complex or crossover interaction is due to the absence of genotypic correlation across environments. In the present study, based on the magnitudes of the genotypic correlation coefficients estimated across all environments (Table 2), it was found that the simple interaction predominated for the number of fruits per plant, while the complex or crossover interaction predominated for the soluble solids content.

Literature reports consistently indicate that the GxE interaction in melon is primarily driven by the complex component for soluble solids and yield (Nunes et al. 2006, Nunes et al. 2011b, Aragão et al. 2015, Guimarães et al. 2016). However, some studies have reported a more substantial impact of the simple component on soluble solids (Silva et al. 2011).

The quantification of the types of interaction is important because it informs the breeder about the degree of difficulty at the time of selecting or recommending cultivars. When the simple component predominates, the task of breeder is facilitated, as the genotypic classification does not change. Conversely, when the complex component is more expressive, the decision becomes more difficult, since in this case there are genotypes that are well adapted to specific environments (Nunes et al. 2011a, 2011b).

It is emphasized that the GxE interaction can be exploited by breeders through the selection of specific genotypes for a particular environment or region. In this case, the interaction is capitalized, increasing the phenotypic value of the trait (Nunes et al. 2002). However, executing such a strategy in the Mossoró-Assu Agricultural Hub to melon crop remains challenging. Despite the change in classification due to environmental variation, mainly driven by the complex component, it does not preclude the selection of stable materials with broad adaptation (Vencovsky and Barriga 1992).

In genetic improvement programs, the interaction between genotypes and environments is a pivotal consideration that should never be overlooked, as it significantly influences the process of selecting or recommending cultivars (Nunes et al.

2002, Guimarães et al. 2016). Consequently, when a significant (GxE) interaction is identified, efforts are made to mitigate its impact on the phenotypic expression. One approach involves identifying hybrids that exhibit both favorable yield and fruit characteristics while demonstrating greater stability.

In adaptability and stability studies, researchers employ uni- or multivariate methods, and the choice often depends on existing models and parameter estimation processes. The recommendation is to use a variety of methods to characterize a genotype's profile in terms of adaptability and stability. This approach allows for the complementary information provided by each method to enhance the overall understanding of a genotype's performance.

Adaptability and stability

Based on the results, the most employed procedures are those utilizing linear regression, with the Eberhart and Russel's method (1966) standing out as the predominant choice. According to this method, the ideal genotype should possess a high trait average, regression coefficient equals to 1, and regression deviation equals to 0, thereby characterizing type II stability, also known as agronomic stability (Becker and León 1988, Yan and Kang 2003). It is noteworthy that, in the context of melon cultivation, genotypes with regression coefficients significantly greater than 1, indicating responsiveness to improved environmental conditions, are particularly desirable due to the advanced technology utilized in the production sector. Therefore, the hybrids HA-08 and HA-06 for the number of fruits per plant, as well as HA-02, HA-09, and HA-11 for soluble solids, deserve special attention considering the specific requirements of melon cultivation.

However, it is crucial to highlight the significant differences among the hybrids in terms of Wricke's (1965) stability criterion, with HA-05 and HA-08 exhibiting the highest stability for the number of fruits per plant, and HA-04 and HA-03 demonstrating superior stability for soluble solids. It is important to note that this type of stability, while characterized by lower variability, is not always desired, as it is generally associated with lower average trait values (Ramalho et al. 2012). This observation is consistent with the findings of the present study (Figs. 4 and 5).

In the Linn and Binns' (1988) method, the Pi parameter indicates a measure of genotype stability, with the genotype possessing the lowest Pi value considered the most stable. Annicchiarico's (1992) method estimates the confidence coefficient (Ic), while Resende's (2007) method calculates the HMRPGV. In both Annicchiarico's (1992) and Resende's (2007) methods, higher estimates of their respective parameters indicate greater adaptability and/or phenotypic stability. Notably, Pi is negatively correlated with Ic and HMRPGV, and the latter two are closely related. These parameters are linked to the mean, suggesting that selecting genotypes using any of these methods will also influence the mean trait values.

All evaluated hybrids exhibit high averages for the two traits under consideration. This outcome was anticipated, given that these genotypes originated from lines selected under the specific cultivation conditions of this study. While this high average complicates the recommendation of specific cultivars, a common challenge in this stage of genetic improvement programs for numerous crops, the HA-08 hybrid emerges as the most promising. It embodies the most desirable characteristics, contributes minimally to GxE interaction, and maintains a high average for both traits. Consequently, it stands out as the most promising candidate for recommendation as a cultivar.

Among the models studied, simultaneous selection for yield, stability, and adaptability can be performed using the method of HMRPGV. This method is highly correlated to the methodologies by Lin and Binns (1988) and Annicchiarico (1992), in addition to presenting other advantages such as considering genotypic effects as random, thereby providing genotypic stability and adaptability, and allowing for handling unbalanced data, heterogeneity of variances, correlated errors within locations, and can be applied to any number of environments. Furthermore, it provides genetic values already adjusted (penalized) for instability in the same unit or scale as the evaluated trait, which can be directly interpreted as genetic values.

Hence, comprehending the impact of GxE interaction concerning yield and soluble solids, the primary attributes of the melon tree, is imperative for steering forthcoming crop improvement strategies during the final phases of breeding programs. Our findings strongly indicate that employing diverse methods to estimate adaptability and stability provides a reliable means of selecting genotypes capable of responding optimally to environmental variations. This approach is pivotal for advancing and refining crop improvement efforts.

CONCLUSION

The GxE interaction for number of fruits per plant and soluble solids is simple and crossed, respectively.

The HA-08 hybrid is the most promising, with a high number of fruits per plant, high soluble solids content, high adaptability, and stability.

Simultaneous selection for yield, stability, and adaptability can be performed using the HMRPGV method.

CONFLICT OF INTEREST

Nothing to declare.

AUTHORS' CONTRIBUTION

Conceptualization: Cavalcante Neto, J. G. and Nunes, G. H. S.; **Methodology:** Cavalcante Neto, J. G., Silva, E. M. and Nunes, G. H. S.; **Data curation:** Cavalcante Neto, J. G.; **Formal Analysis:** Silva, E. M. and Nunes, G. H. S.; **Supervision:** Nunes, G. H. S.; **Project administration:** Nunes, G. H. S.; **Visualization:** Cavalcante Neto, J. G. and Silva, E. M.; **Original – draft writing:** Cavalcante Neto, J. G., Nunes, E. W. L. P., Silva, E. M., Martins, A. F., Diógenes, L. J. P., Melo, S. B. and Costa Filho, J. H.; **Writing – review and editing:** Nunes, E. W. L. P., Silva, E. M., Martins, A. F., Diógenes, L. J. P., Melo, S. B. and Costa Filho, J. H.; **Final approval:** Silva, E. M.

DATA AVAILABILITY STATEMENT

The datasets generated analyzed during the current study are available from the corresponding author on reasonable request.

FUNDING

Conselho Nacional de Desenvolvimento Científico e Tecnológico ROR
Grant No.: 313410/2021-6

ACKNOWLEDGMENTS

To the Conselho Nacional de Desenvolvimento Científico e Tecnológico for providing the research productivity scholarship for the last author.

REFERENCES

Annicchiarico, P. (1992). Cultivar adaptation and recommendation from alfalfa trials in Northern Italy. Journal of Genetics and Breeding, 46, 269-278.

Aragão, F. A. S., Nunes, G. H. S. and Queiroz, M. A. (2015). Genotype x environment interaction of melon families based on fruit quality traits. Crop Breeding Applied Biotechnology, 15, 79-86. https://doi.org/10.1590/1984-70332015v15n2a15

Bai, L., Huang X., Li, Z., Li S., Lv C. and Zhang K. (2023). Stability and adaptability of wheat cultivars with low cadmium accumulation based on farmland trials. European Journal of Agronomy, 144, 126764. https://doi.org/10.1016/j.eja.2023.126764

Becker, H. C. and Léon, J. (1988). Stability analysis in plant breeding. Plant Breeding, 101, 1-23. https://doi.org/10.1111/j.1439-0523.1988.tb00261.x

Bernal, E. F. (2016). GGEBiplotGUI: Interactive GGE Biplots in R.

Bishwas, K. C., Poudel, R. M. and Regmi, D. (2021). AMMI and GGE biplot analysis of yield of different elite wheat line under terminal heat stress and irrigated environments. Heliyon, 7, e07206. https://doi.org/10.1016/j.heliyon.2021.e07206

Bornhofen, E., Benin, G., Stock, L., Woyann, L. G., Duarte, T., Stoco, M. G. and Marchioro, S. V. (2017). Statistical methods to study adaptability and stability of wheat genotypes. Bragantia, 76, 1-10. https://doi.org/10.1590/1678-4499.557

Eberhart, S. A. and Russel, W. A. (1966). Stability parameters for comparing varieties. Crop Science, 6, 36-40. https://doi.org/10.2135/cropsci1966.0011183X000600010011x

Freitas, J. G., Crisóstomo, J. R., Silva, F. P., Pitombeira, J. B. and Távora, F. J. A. F. (2007). Interação entre genótipo e ambiente em híbridos de melão-amarelo no Nordeste do Brasil. Ciência Agronômica, 38, 176-181.

Guimarães, I. P., Dovale, J. C., Antônio, R. P., Aragão, F. A. S. and Nunnes, G. H. S. (2016). Interference of genotype-by-environment interaction in the selection of inbred lines of yellow melon in an agricultural center in Mossoró-Assu, Brazil. Acta Scientiarum Agronomy, 38, 51-59. https://doi.org/10.4025/actasciagron.v38i1.26045

Han, Y., Wang, K., Zhang, Q., Yang, F., Pan, S., Liu, Z. and Zhang, Q. (2024). Developing a comprehensive evaluation model of variety adaptability based on machine learning method. Field Crops Research, 301, 109203. https://doi.org/10.1016/j.fcr.2023.109203

Kist, B. B. and Beling, R. R (2023). Anuário brasileiro de Horti&Fruti. Santa Cruz do Sul: Gazeta Santa Cruz.

Li, Z. and Wu, W. (2023). Genotype recommendations for high performance and stability based on multiple traits selection across a multi-environment in rapeseed. European Journal of Agronomy, 145, 126787. https://doi.org/10.1016/j.eja.2023.126787

Lin, C. S. and Binns, M. R. (1988). A superiority measure of cultivar performance for cultivar x location data. Canadian Journal of Plant Science, 68, 193-198. https://doi.org/10.4141/cjps88-018

Nunes, G. H. S., Andrade Neto, R. C., Costa Filho, J. H. and Melo, S. B. (2011a) Influência de variáveis ambientais sobre a interação genótipos x ambientes em meloeiro. Revista Brasileira de Fruticultura, 33, 1194-1199. https://doi.org/10.1590/S0100-29452011000400018

Nunes, G. H. S., Madeiros, A. E. S., Granjeiro, L. C., Santos, G. M. and Sales Júnior, R. (2006). Estabilidade fenotípica de híbridos de melão amarelo avaliados no Pólo Agroindustrial Mossoró-Assu. Pesquisa Agropecuária Brasileira, 41, 57-67. https://doi.org/10.1590/S0100-204X2006000900004

Nunes, G. H. S., Resende, G. D. S. P., Ramalho, M. A. P. and Santos, J. B. (2002). Implicações da interação genótipo x ambientes na seleção de clones de eucalipto. Cerne, 8, 49-58.

Nunes, G. H. S., Santos Júnior, H., Granjeiro, L. C., Bezerra Neto, F., Dias, C. T. S. and Dantas, M. S. M. (2011b). Phenotypic stability of hybrids of Gália melon. Anais da Academia Brasileira de Ciências, 83, 1421-1433. https://doi.org/10.1590/S0001-37652011005000034

Nunes, G. H. S., Aragão, F. A. S., Nunes, E. W. L. P., Costa, J. M. and Ricarte, A. O. (2016). Melhoramento de Melão. In C. Nick and A. Borém (Eds.). Melhoramento de hortaliças (1, p. 331-363).

Olivolto, T. and Dal'Col Lúcio, A. (2020). Metan: An R package for multi-environment trial analysis. Methods in Ecology and Evolution, 11, 783-789. https://doi.org/10.1111/2041-210X.13384

Ramalho, M. A. P., Abreu, A. F. B., Santos, J. B. and Nunes, J. A. R. (2012). Aplicações da genética quantitativa no melhoramento de plantas autógamas. Lavras: UFLA.

R Core Team (2023). R: A language and environment for statistical computing. Vienna: R Foundation for Statistical Computing.

Resende, M. D. V. (2007). Matemática e estatística na análise de experimentos e no melhoramento genético. Colombo: Embrapa Florestas.

Resende, M. D. V. (2016). Software Selegen-REML/BLUP: a useful tool for plant breeding. Crop Breeding and Applied Biotechnology, 16, 330-339. http://dx.doi.org/10.1590/1984-70332016v16n4a49

Resende, M. D. V. and Duarte, J. B. (2007). Precisão e controle de qualidade em experimentos de avaliação de cultivares. Pesquisa Agropecuária Tropical, 37, 182-194. https://doi.org/10.1590/1984-70332016v16n4a49

Rosa, G. B., Follmann, D. N., Pereira, A. C., Bolzan, F. T., Marchioro, V. S. and Maldaner, I. C. (2024). Adaptability and stability of maize hybrids using the Eberhart and Russell and AMMI models in subtropical environments. Ciência e Agrotecnologia, 48, 1-10. https://doi.org/10.1590/1413-7054202448008824

Rother, V., Verdi, C. A., Thurow, L. B., Carvalho, I. R., Oliveira, V. F., Maia, L. C., Venske, E., Pegoraro, C. and Oliveira, A. C. (2019). Uni- and multivariate methods applied to the study of the adaptability and stability of white oat. Pesquisa Agropecuária Brasileira, 54, 1-10. https://doi.org/10.1590/S1678-3921.pab2019.v54.00656

Shrilatha, K. A., Parmar, V. K., Patel, R. K., Patel, A. I., Srivastava, A., Bhanderi, D. R., Patel, S. Y. and Parekh, V. (2024). Stability Analysis of Yield and Its Components in Snap Melon (Cucumis melo var momordica). International Journal of Environment and Climate Change, 14, 200-207. https://doi.org/10.9734/ijecc/2024/v14i84342

Silva, E. M., Nunes, E. W. P., Costa, J. M., Ricarte, A. O., Nunes, G. H. S. and Aragão, F. A. S. (2019). Genotype x environment interaction, adaptability and stability of 'Piel de Sapo' melon hybrids through mixed models. Crop Breeding and Applied Biotechnology, 19, 402-411. https://doi.org/10.1590/1984-70332019v19n4a57

Scott, A. and Knott, M. (1974). Cluster-analysis method for grouping means in analysis of variance. Biometrics, 30, 507-512.

Silva, J. M., Nunes, G. H. S., Costa, G. G., Aragão, F. A. S. and Maia, L. K. R. (2011). Implicações da interação genótipos x ambientes sobre ganhos com a seleção em meloeiro. Ciência Rural, 41, 51-56. https://doi.org/10.1590/S0103-84782011000100009

Vencovsky, R. and Barriga, P. (1992). Genética biométrica no fitomelhoramento. Ribeirão Preto: Sociedade Brasileira de Genética.

Wricke, G. (1965). Zur Berechning der okovalenz bei sommerweizen und hafer. Zeitschrift fur Pflanzenzuchtung, 52, 127-138.

Yan, W. and Kang, A. M. S. (2003). GGE Biplot Analysis: A graphical tool for breeders, geneticists, and agronomists. Boca Raton: CRC Press.

Yan, W., Kang, M. S., Ma, B., Woods, S. and Cornélio, P. L. (2007). GGE biplot vs. AMMI analysis of genotype-by-environment data. Crop Science, 47, 643-655.