

Measures of experimental precision for evaluating melon genotype trials¹

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ABSTRACT - The quality of field trials has traditionally been assessed based on the magnitude of experimental error, commonly measured by the coefficient of variation. However, this classification is often overly broad and fails to account for specific characteristics of the crop or the trait under evaluation, limiting its effectiveness. Consequently, alternative statistics have been proposed to assess experimental precision. We hypothesized that selective accuracy and the F-statistic for genotype, by incorporating genotypic variability, would provide a better assessment of experimental quality than the coefficient of variation. This study aimed to evaluate the suitability of selective accuracy and the F-statistic for genotype as measures of precision in melon experiments. Data on yield and soluble solids content were obtained from 50 trials evaluating melon hybrids conducted in the state of Rio Grande do Norte, Brazil, between 2015 and 2017. The relationships among 10 statistical parameters estimated for each trial were analyzed using correlation and path analysis. Among the 100 trial-trait combinations (50 trials evaluated for two traits), 17 exhibited CV values greater than 20%; however, significant genotype effects were detected in 47% of these trials. Correlation and path analyses showed that selective accuracy and the F-statistic for genotype were associated with both residual variance and genotypic variability. In contrast, the coefficient of variation reflected only residual variation. Therefore, selective accuracy and the F-statistic for genotype were more appropriate indicators of the precision of melon genotype competition trials than the coefficient of variation for both yield and soluble solids content.

Keywords: *Cucumis melo* L. Plant breeding. Experimental quality. Genotype discrimination.

INTRODUCTION

Melon cultivation is of great economic and social importance in the Northeast region of Brazil, particularly in the states of Rio Grande do Norte and Ceará, which are the main national producers and responsible for the majority of the country's melon exports. Due to the economic relevance of this crop, new cultivars are introduced into the national market annually and evaluated in field trials to identify the most promising materials (Araújo Junior *et al.*, 2024a).

As these genotypes are not specifically adapted to the climatic conditions of this region, they may exhibit different responses in yield and fruit quality. Therefore, field experiments are essential for plant breeding programs and cultivar recommendations, requiring high experimental precision and reliable inference regarding genotypic means (Resende; Duarte, 2007).

The quality of trials is commonly evaluated by the magnitude of experimental error, expressed as the coefficient of variation (CV) (Pimentel-Gomes, 2009). Derived from the residual mean square of the analysis of variance and incorporating the mean of the evaluated trait, the CV is widely used as a relative measure of experimental dispersion, with higher values indicating greater experimental heterogeneity (Adedugba *et al.*, 2023).

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Although the classification proposed by Pimentel-Gomes (2009) is widely used as a reference for experimental precision, it is a general approach that does not account for the specific nature of the crop or trait under evaluation. Studies conducted across different species have shown that the magnitudes of coefficients of variation may vary among traits, even within the same species, reflecting differences in genetic architecture and environmental influences (Adedugba *et al.*, 2023; Ramolekwa *et al.*, 2025; Wudu; Mekonnen, 2025; Singh Yadav *et al.*, 2024). Moreover, the CV does not account for the number of replications, a factor that directly affects experimental error reduction and the reliability of inferences, as increasing the number of replications improves the precision of genotype estimation (Araújo Junior *et al.*, 2024a). These aspects demonstrate that interpreting experimental precision solely on the basis of the CV may be limited.

In view of these limitations, alternative statistics have been proposed to evaluate experimental precision. Selective accuracy provides a more direct measure of the precision in predicting genetic or phenotypic values derived from experimental models. This statistic has been applied to several crops, such as soybean, coffee, and common bean, demonstrating its utility for validating estimates across multiple environments (Botelho *et al.*, 2023; Casagrande *et al.*, 2022; Ribeiro; Steckling; Mezzomo, 2018).

In melon trials conducted across multiple environments, experimental precision has been more closely associated with the magnitude of genetic variance and the effectiveness of genotype discrimination than with the residual error expressed by the coefficient of variation (Araújo Junior *et al.*, 2024b). These findings suggest that statistics incorporating genotypic variability may provide a more reliable assessment of experimental precision than the coefficient of variation.

However, despite their increasing use in plant breeding, comparative evaluations of experimental precision statistics for assessing the quality of melon trials remain limited in the literature. Therefore, this study

aimed to evaluate the suitability of selective accuracy and the F-statistic for genotype as measures of experimental precision in melon genotype trials.

MATERIAL AND METHODS

This study utilized data from 50 experiments evaluating 48 melon hybrids of the Honey Dew, Yellow, Piel de Sapo, Cantaloupe, and Galia types, assessing the traits yield and soluble solids content, totaling 100 trial–trait combinations. The trials were conducted between 2015 and 2017 for all melon types with three years of experiments, except for the Yellow type, for which trials were carried out in two growing seasons in 2017. The number of hybrids, locations, evaluation years, and experiments for each melon type are presented in Table 1. All trials were conducted in municipalities within the Mossoró-Assú Agro-Cluster in the state of Rio Grande do Norte, Brazil.

The experiments followed a randomized complete block design with three replications. Each plot comprised two 5-m-long rows, spaced at 2.0×0.5 m, totaling 20 plants per plot. Border plants at the ends of each row were considered buffer plants and were not evaluated. Crop management followed standard cultural practices recommended for melon cultivation in the state of Rio Grande do Norte, Brazil (Cavalcante Neto *et al.*, 2025; Nunes *et al.*, 2016).

The traits evaluated in this study were commercial yield and soluble solids content, which growers consider the primary commercial characteristics of this crop. Yield was determined by weighing all marketable fruits harvested from the plot for each melon type. Soluble solids content was measured by extracting a sample corresponding to approximately two-thirds of the pulp thickness at the equatorial region of the fruit, toward the seed cavity. The sample was manually pressed until a portion of juice was deposited onto a digital refractometer (Digital Refractometer Palette 100), which was used to determine the soluble solids content. Eight fruits per plot were sampled for the measurement of soluble solids.

Table 1 - Number of genotypes, locations, years, and trials for each type of melon studied

Melon type	Number of genotypes	Number of locations	Number of years	Number of trials
Honey Dew	10	4	3	12
Yellow	13	4	2	8
Piel del sapo	8	3	3	9
Cantaloupe	8	3	3	9
Galia	9	4	3	12
Total	48	-	-	50

For each experiment, analysis of variance (ANOVA) was performed at a nominal significance level of $\alpha = 0.05$, using the following statistical model: $y = Xr + Zg + e$, where y is the data vector; r is the vector of replication effects (assumed fixed) added to the overall mean; g is the vector of genotypic effects (assumed random); and e is the vector of random errors or residuals. The capital letters represent incidence matrices (Resende, 2007).

From the ANOVA results, estimates of the block mean square (BMS), genotype mean square (GMS), error mean square (EMS), and the F-test value for genotype (Eq. 1) were obtained. In addition, the overall experiment mean (m), the range of the means ($R = \text{maximum mean} - \text{minimum mean}$), and the coefficient of variation (Eq. 2) were calculated:

$$F_G = \frac{GMS}{EMS} \quad (1)$$

$$CV = 100 \frac{\sqrt{EMS}}{m} \quad (2)$$

Selective accuracy (SA) was estimated using Eq. (3). Broad-sense maximum heritability (h^2) was estimated using Eq. (4), where J is the number of replications. The genotypic determination coefficient (R^2), which represents the reliability of predicting the true value of the selected genotypes based on J measurements, was calculated using Eq. (5) (Cruz; Regazzi; Carneiro, 2012).

$$SA = \sqrt{1 - \frac{1}{F_G}} \quad (3)$$

$$h^2 = \frac{(GMS - EMS)}{(GMS - EMS) + EMS} \quad (4)$$

$$R^2 = \frac{Jr}{1 + r(J-1)} \quad (5)$$

The honestly significant difference (HSD) between cultivars, determined using Tukey's test at the 5% significance level and expressed as a percentage of the mean, was obtained using Eq. (6), where Δ is the estimate of the overall mean of the trial and Δ represents the minimum significant difference between cultivars determined using Tukey's test at the 5% significance level, obtained using Eq. (7), in which q is the critical value for use in Tukey's test; n is the number of cultivars, and df_e is the number of degrees of freedom for the error.

$$HSD = 100 \frac{\Delta}{\bar{m}} \quad (6)$$

$$\Delta = q_{\alpha(n; df_e)} \left(\frac{EMS}{J} \right)^{0.5} \quad (7)$$

Regarding the statistics GMS, EMS, m , R , h^2 , R^2 , CV, HSD, F-statistic, and SA, obtained from trials for each melon type, the minimum, average, and maximum values were calculated, along with the dispersion measure (standard deviation). The Kolmogorov–Smirnov normality test was performed. Subsequently, the Pearson linear correlation coefficient was calculated between the statistics, and its significance was assessed using Student's t -test at

the 5% significance level. Additionally, multicollinearity diagnostics and path analysis (Cruz; Regazzi; Carneiro, 2012) of the dependent variables, which were candidates for precision measures (CV, HSD, F-statistic, and SA), in relation to the independent variables (GMS, EMS, m), were performed using the Programa GENES (Cruz, 2001).

RESULTS AND DISCUSSION

There was a significant genotype effect in 33 trials for yield (66%) and in 36 trials for soluble solids (72%), indicating genetic variability among melon hybrids for these traits. In the remaining trial–trait combinations, no significant genotype effect was observed. From the perspective of cultivar discrimination based on quality control criteria, only trials in which no cultivar effect was detected could be discarded. However, this result should be interpreted with caution, as the absence of a genotypic effect may reflect either a true lack of genetic variability or excessive experimental error (Cargnelutti Filho; Storck, 2007).

The CV ranged from 3.81% to 46.61% for yield and from 1.22% to 17.50% for soluble solids (Table 2). The CV values for soluble solids were lower than those observed for yield. In general, yield-related traits tend to exhibit wider ranges of CV values (Adedugba *et al.*, 2023). Tukey's HSD among genotypes, expressed as a percentage of the mean, ranged from 11.06% to 136.44% for yield and from 3.54% to 50.42% for soluble solids at the 5% significance level (Table 2).

According to the classification proposed by Pimentel-Gomes (2009), CV values ranged from low to very high for yield and from low to medium for soluble solids. Trials with high CV values, typically associated with lower experimental precision, could in principle be discarded. However, among the 100 situations analyzed (50 for yield and 50 for soluble solids), 17 presented CV values higher than 20%, and in 9 of these no significant genotypic effect was detected. Therefore, in 47% of the situations with $CV > 20\%$, which might initially be considered for exclusion, significant genotype effects were observed, and the results should not be disregarded.

The detection of significant genotypic effects does not necessarily indicate that an experiment is precise, as this test only reveals differences between two or more genotypes. Therefore, it is important to classify trials using additional experimental precision statistics (Benin *et al.*, 2013; Cargnelutti Filho *et al.*, 2012).

There was variation among the statistics EMS, GMS, m , R (range), h^2 , R^2 , CV, HSD, the F-statistic (FG), and selective accuracy (SA) obtained for each of the 50 trials for yield ($25.56\% \leq CV \leq 237.10\%$) and soluble solids ($19.46\% \leq CV \leq 197.31\%$). This broadens the

scope of the inferences by including extreme scenarios. Among these statistics, only GMS, EMS, FG, and SA for yield, and R^2 , FG, and SA for soluble solids, did not conform to the normal distribution according to the Kolmogorov–Smirnov test, presenting p -values ≤ 0.05 . However, the large number of trials (50), combined with the variability among the statistics, supports the adequacy of the dataset for the proposed analyses.

There was a positive linear correlation ($p \leq 0.05$) between CV and HSD ($r = 1.00$) for both yield and soluble solids (Table 3), indicating that the simultaneous use of these statistics to classify experimental precision provides redundant information. This occurs because both statistics are directly derived from the experimental error mean square of the analysis of variance. This phenomenon has also been reported when assessing experimental precision in grain yield trials in maize (Cargnelutti Filho; Storck, 2007)

and cowpea (Teodoro *et al.*, 2016). A strong positive linear association was also observed between h^2 and R^2 and the statistics FG and SA for both yield and soluble solids, indicating similarity among these statistics. Therefore, it is unnecessary to adopt all of them to assess experimental precision. Instead, FG and SA may be preferred due to their ease of calculation. For example, the F-statistic for treatment effects in the analysis of variance can serve as a reference for evaluating the quality of cultivar competition trials, as this statistic is independent of the cultivated species and the trait under evaluation (Resende; Duarte, 2007).

Due to the high correlation between the variables GMS and range (R), both for yield ($r = 0.70$) and soluble solids ($r = 0.91$), the variable R was excluded from the path analysis. The exclusion of one or more highly correlated independent variables is recommended,

Table 2 - Mean, minimum and maximum, standard deviation, coefficient of variation (CV), and p -value of the Kolmogorov–Smirnov normality test for yield and soluble solids data from 50 melon trials

Statistic ⁽¹⁾	Mean	Minimum	Maximum	Standard deviation	CV	p -value
Yield (t ha ⁻¹)						
GMS	161.1935	11.02750	478.7885	130.1017	80.71	0.0270
EMS	45.1028	0.95040	309.5361	61.4152	136.17	0.0016
m	30.8423	19.84467	55.1670	7.8843	25.56	0.4014
R	0.6806	0.21365	1.2179	0.2946	43.28	0.4548
h^2	0.4955	0.00220	0.9861	0.3075	62.05	0.8126
R^2	0.6578	0.00656	0.9953	0.3074	46.73	0.1001
CV	17.8071	3.80930	46.6132	9.2738	52.08	0.8340
HSD	51.8620	11.0625	136.4446	27.0328	52.12	0.7653
F_G	16.0106	1.00661	213.9782	37.9612	237.10	0.0000
SA	0.7675	0.08102	0.9977	0.2648	34.50	0.0181
Soluble solids (°Brix)						
GMS	4.39887	0.471500	21.4969	4.38281	99.63	0.0569
EMS	0.65722	0.012700	2.1163	0.48836	74.31	0.7547
M	10.54249	6.540700	14.5828	2.05117	19.46	0.4298
R	0.33664	0.082822	1.3114	0.21387	63.53	0.4687
h^2	0.53433	0.003049	0.9884	0.31914	59.73	0.2885
R^2	0.68764	0.009092	0.9961	0.30486	44.33	0.0286
CV	7.23701	1.218066	17.5025	3.67489	50.78	0.6391
HSD	21.0535	3.5374	50.4243	10.5814	50.26	0.7591
F_G	25.51304	1.009175	255.9155	50.33908	197.31	0.0000
SA	0.78740	0.095351	0.9980	0.26271	33.36	0.0039

Note: GMS = genotype mean square; EMS = error mean square; m = overall trial mean; R = mean range; h^2 = broad-sense heritability; R^2 = genotypic coefficient of determination; HSD = honestly significant difference among genotypes using Tukey's test at 5%, expressed as a percentage of the mean; F_G = F-statistic for genotype; SA = selective accuracy

as increasing multicollinearity reduces the ability to estimate individual variable effects (Souza, 2013). The multicollinearity diagnosis performed using the Pearson linear correlation matrix (Table 3) among the statistics GMS, EMS, and m resulted in condition numbers of 7.43 for yield and 2.28 for soluble solids, indicating weak collinearity ($CN < 100$) and therefore allowing a reliable path analysis (Cruz; Regazzi; Carneiro, 2012).

The main statistics were grouped into two sets using path analysis, presenting similar results within each group and distinct results between them (Tables 4 and 5).

The CV and HSD formed the first group, whereas FG and SA formed the second. The strong positive linear association between CV and HSD ($r = 1.00$) for both yield and soluble solids, together with the positive associations between FG and SA for yield ($r = 0.32$) and soluble solids ($r = 0.37$), and the weak and/or negative associations between statistics belonging to different groups, confirmed two distinct clusters. These results

are consistent with those reported by Cargnelutti Filho and Storck (2007), Cargnelutti Filho *et al.* (2012), and Teodoro *et al.* (2016), who concluded that FG and SA were more appropriate than CV and HSD for evaluating experimental precision in trials with maize, irrigated rice, and cowpea genotypes, respectively.

Across the 50 trials, significant correlations were observed between GMS and CV ($r = 0.48$) and between GMS and HSD ($r = 0.49$). However, the direct effects of GMS on CV (-0.1457) and HSD (-0.1380) were negative, in contrast to the positive r values, indicating the absence of a cause-and-effect relationship. These results suggest that, for melon yield, there is no association between genetic variability (GMS) and either CV or HSD. This indicates that the classification of experimental precision based on these statistics is independent of genetic variability. Similar findings have been reported for irrigated rice (Cargnelutti Filho *et al.*, 2012) and cowpea (Teodoro *et al.*, 2016).

Table 3 - Pearson correlation coefficients among the statistics from 50 melon trials regarding yield and soluble solids content

Statistic ¹	EMS	m	R	h ²	R ²	CV	HSD	F _G	SA
Yield (t ha ⁻¹)									
GMS	0.70*	0.49*	0.70*	0.19 ^{ns}	0.26 ^{ns}	0.48*	0.49*	0.07 ^{ns}	0.30*
EMS		0.56*	0.18 ^{ns}	-0.43*	-0.33 ^{ns}	0.84*	0.85*	-0.25 ^{ns}	-0.22 ^{ns}
M			-0.11 ^{ns}	-0.17 ^{ns}	-0.05 ^{ns}	0.22 ^{ns}	0.22 ^{ns}	-0.23 ^{ns}	0.04 ^{ns}
R				0.61*	0.59*	0.13 ^{ns}	0.13 ^{ns}	0.40*	0.59*
h ²					0.95*	-0.63*	-0.63*	0.53*	0.88*
R ²						-0.53*	-0.52*	0.39*	0.98*
CV							1.00*	-0.44*	-0.42*
HSD								-0.44*	-0.41*
F _G									0.32*
Soluble solids (°Brix)									
GMS	0.13 ^{ns}	-0.37*	0.91*	0.60*	0.55*	0.13 ^{ns}	0.12 ^{ns}	0.49*	0.49*
EMS		-0.02 ^{ns}	0.04 ^{ns}	-0.42*	-0.26 ^{ns}	0.92*	0.92*	-0.51*	-0.18 ^{ns}
m			-0.62*	-0.47*	-0.43*	-0.28*	-0.27 ^{ns}	-0.39*	-0.39*
R				0.65*	0.61*	0.15 ^{ns}	0.15 ^{ns}	0.59*	0.56*
h ²					0.95*	-0.37*	-0.37*	0.62*	0.87*
R ²						-0.21 ^{ns}	-0.21 ^{ns}	0.46*	0.98*
CV							1.00*	-0.50*	-0.13 ^{ns}
HSD								-0.50*	-0.14 ^{ns}
F _G									0.37*

Note: GMS = genotype mean square; EMS = error mean square; m: overall trial mean; R = mean range; h² = broad-sense heritability; R² = genotypic coefficient of determination; CV = coefficient of variation; HSD = honestly significant difference among genotypes using Tukey's test at 5%, expressed as a percentage of the mean; F_G = F-statistic for genotype; SA = selective accuracy. ^{ns} = Not significant; * = Significant at the 5% significance level according to the t-test with 48 degrees of freedom

Table 4 - Estimates of Pearson correlation coefficients and respective estimates of direct and indirect effects of the statistics genotype mean square (GMS), error mean square (EMS), and overall trial mean (M) on the statistics coefficient of variation (CV), honestly significant difference (HSD) using Tukey's test at the 5% significance level expressed as a percentage of the mean, F-statistic for genotype (FG), and selective accuracy (SA) for yield data from 50 melon trials

Variable	Effect	Dependent variable			
		CV	HSD	FG	SA
GMS	Direct effect	-0.1457	-0.1380	0.5198	0.8683
	Indirect effect via EMS	0.7942	0.8011	-0.3492	-0.6241
	Indirect effect via m	-0.1686	-0.1731	-0.1006	0.0558
	Pearson correlation (r)	0.48*	0.49*	0.07 ^{ns}	0.30*
EMS	Direct effect	1.1346	1.1444	-0.4989	-0.8916
	Indirect effect via GMS	-0.1020	-0.0966	0.3639	0.6078
	Indirect effect via m	-0.1926	-0.1978	-0.1150	0.0637
	Pearson correlation (r)	0.84*	0.85*	-0.25 ^{ns}	-0.22 ^{ns}
m	Direct effect	-0.3440	-0.3533	-0.2053	0.1138
	Indirect effect via GMS	-0.0714	-0.0676	0.2547	0.4255
	Indirect effect via EMS	0.6354	0.6409	-0.2794	-0.4992
	Pearson correlation (r)	0.22 ^{ns}	0.22 ^{ns}	-0.23 ^{ns}	0.04 ^{ns}
Coefficient of determination		0.8075	0.8274	0.2083	0.4612
Residual effect		0.4388	0.4154	0.8898	0.7340

Note: ^{ns} = Not significant; * = Significant at the 5% level using the *t*-test, with 48 degrees of freedom

Table 5 - Estimates of Pearson correlation coefficients and respective estimates of direct and indirect effects of the statistics genotype mean square (GMS), error mean square (EMS), and overall trial mean (m) on the statistics coefficient of variation (CV), honestly significant difference (HSD) using Tukey's test at the 5% significance level expressed as a percentage of the mean, F-statistic for genotype (FG), and selective accuracy (SA) for soluble solids data from 50 melon trials

Variable	Effect	Dependent variable			
		CV	HSD	FG	SA
GMS	Direct effect	-0.1011	-0.1086	0.4825	0.4348
	Indirect effect via EMS	0.1205	0.1207	-0.0750	-0.0314
	Indirect effect via m	0.1106	0.1079	0.0825	0.0866
	Pearson correlation (r)	0.13 ^{ns}	0.12 ^{ns}	0.49*	0.49*
EMS	Direct effect	0.9272	0.9283	-0.5772	-0.2412
	Indirect effect via GMS	-0.0131	-0.0141	0.0627	0.0565
	Indirect effect via m	0.0060	0.0058	0.0045	0.0047
	Pearson correlation (r)	0.92*	0.92*	-0.51*	-0.18 ^{ns}
m	Direct effect	-0.2989	-0.2916	-0.2230	-0.2339
	Indirect effect via GMS	0.0374	0.0402	-0.1785	-0.1609
	Indirect effect via EMS	-0.0185	-0.0186	0.0115	0.0048
	Pearson correlation (r)	-0.28*	-0.27 ^{ns}	-0.39*	-0.39*
Coefficient of determination		0.9235	0.9197	0.6178	0.3477
Residual effect		0.2765	0.2833	0.6182	0.8076

Note: ^{ns} = Not significant; * = Significant at the 5% level using the *t*-test, with 48 degrees of freedom

A positive linear association was observed between EMS and the statistics CV ($r = 0.84$) and HSD ($r = 0.85$), with high direct effects of EMS in the same direction as the correlation coefficients, both on CV (1.1346) and HSD (1.1444), indicating that these statistics are associated with the residual variance. No linear association was observed between the mean and the statistics CV ($r = 0.22$) and HSD ($r = 0.22$), and the direct effects of the mean on CV (-0.3440) and HSD (-0.3533) had opposite signs compared to r , indicating the absence of a causal relationship. These findings suggest that more precise experiments (lower CV and HSD values) are associated with lower residual variances and are independent of the mean yield and the genetic variability of the evaluated melon genotypes.

Even though they are independent of the mean for yield, which is an important characteristic of experimental precision statistics, the CV and HSD statistics do not account for genetic variability. Consequently, evaluating the quality of cultivar competition trials based solely on these statistics may be inadequate. It may lead to misleading interpretations of experimental quality, particularly in trials with greater environmental heterogeneity. In this context, selective accuracy has been indicated as a more appropriate statistic for assessing the discriminatory capacity of treatments (Santos *et al.*, 2017).

Regarding the statistics FG and SA, no significant association was observed between GMS and FG ($r = 0.07$). However, the direct effect of GMS on FG (0.5198) was high and had the same sign as r , indicating a cause-and-effect relationship. For SA, a positive correlation ($r = 0.30$) and a high direct effect of GMS (0.8683) were observed. Although the correlation coefficients between EMS and FG (-0.25) and between EMS and SA (-0.22) were low, the direct effects on FG (-0.4989) and SA (-0.8916) were higher and had the same sign as r , indicating a true negative linear association. As for the mean, no correlation was found with FG ($r = -0.23$) or SA ($r = 0.04$), and the direct effects were negligible (Table 4).

Based on these results, more precise trials for melon yield (higher FG and SA values) are associated with greater genetic variances and lower residual variances and are independent of the mean. These characteristics confirm the adequacy of these statistics as measures of experimental precision for trials with melon genotypes.

For soluble solids, no linear association was observed between GMS and the statistics CV ($r = 0.13$) and HSD ($r = 0.12$), and the direct effects of GMS on CV (-0.1011) and HSD (-0.1086) had opposite signs to r , indicating the absence of a cause-and-effect relationship. However, a positive linear association was

observed between EMS and the statistics CV ($r = 0.92$) and HSD ($r = 0.92$), with high direct effects of EMS on CV (0.9272) and HSD (0.9283), both with the same sign as r . Regarding the mean, a negative linear correlation was observed with CV ($r = -0.28$), with a greater direct effect and the same sign as r (-0.2989) on CV. Although no significant association was observed between the mean and HSD ($r = -0.27$), the direct effect of the mean on HSD (-0.2916) was greater and shared the same sign as r , indicating a true negative linear association between them (Table 5).

These results indicate that more precise experiments (lower CV and HSD values) for soluble solids in melon are associated with lower residual variances and higher means and are independent of genetic variability. This finding shows that, for soluble solids in melon—as observed for yield—using only CV and HSD as statistics to assess experimental quality may be an inadequate strategy because a precision statistic should also reflect genetic variability. This limitation of the CV was also reported by Valle *et al.* (2024), who emphasized that statistics incorporating genetic variance, such as selective accuracy, are more appropriate for inferring the discriminatory capacity of trials.

A positive linear association was observed between GMS and the F-statistic ($r = 0.49$) and SA ($r = 0.49$), with direct effects on the F-statistic (0.4825) and SA (0.4248) showing the same sign and similar magnitudes to r . A negative linear association was observed between EMS and the F-statistic ($r = -0.51$), with a stronger direct effect (-0.5772) and the same sign as r . Although the linear correlation between EMS and SA was low ($r = -0.18$), the direct effect of EMS on SA was greater (-0.2412) and had the same sign as r , indicating a true negative linear association. Unlike what was observed for yield, for soluble solids there was a negative linear correlation between the mean and the statistics F-statistic and SA ($r = -0.39$ for both), with a greater direct effect of the mean and the same sign as r on the F-statistic (-0.2230) and SA (-0.2339).

Therefore, more precise experiments (higher F-statistic and SA values) are associated with greater genetic variability, lower residual variance, and lower means. Although these statistics for soluble solids are not independent of the mean, they proved more suitable for evaluating trial quality because they account for genetic variability, which was not observed for CV and HSD. Thus, the statistics CV and HSD, traditionally used to assess the quality of cultivar competition trials, can be replaced by the F-statistic and SA, which have been identified in several studies as more appropriate for this purpose (Cargnelutti Filho *et al.*, 2012; Santos *et al.*, 2017; Resende; Duarte, 2007; Ribeiro; Steckling; Mezzomo, 2018).

CONCLUSIONS

1. The assessment of the quality of melon cultivar competition trials based solely on the coefficient of variation and the least significant difference was inadequate, as these statistics do not account for the level of genotypic variation expressed in the trait;
2. In contrast, the use of the F-statistic for the genotype effect and the selective accuracy statistic proved more appropriate for evaluating experimental precision in trials with melon genotypes, both for fruit yield and soluble solids content, as they incorporate genotypic variability. Therefore, these two statistics are recommended as more reliable indicators for assessing the quality of melon cultivar trials.

DATA AVAILABILITY STATEMENT

The research data is available only upon request to the corresponding author.

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