Adaptability and stability of grain yield and maize tassel traits

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ABSTRACT: Due to the economic importance of maize, it is essential to evaluate the performance of genotypes under environmental variations (years, locations, and seasons). Consequently, researchers have scrutinized genotype-environment (G×E) interactions to ensure reliability in genotype recommendations. Furthermore, when a G×E interaction exists, adaptability and stability analysis can be performed. This analysis enables one to identify genotypes with predictable responses and adaptability to environmental variability. Hence, this study sought to determine if there is a G×E interaction and evaluate the response of 16 maize genotypes across seven environments through adaptability and stability analyses. Seven experiments were conducted with 16 maize genotypes using a randomized complete block design with three replications. Tassel length (TL), tassel branch number (TBN), tassel dry matter (TDM), and grain yield (GY) were evaluated. Individual and joint variance analyses were performed, along with the F-test at a 5% significance level. The complex parts of the interaction between genotypes and pairs of environments were estimated, followed by adaptability and stability analyses using the Eberhart and Russell method. A genotype-environment interaction was found for TL, TBN, TDM, and GY, indicating that genotypes respond differently in various environments. However, considering all four traits, there is no indication of the ideal genotype.
Key words: *Zea mays* L., agronomic traits, plant breeding, biometric models, genotype indication.

Adaptabilidade e estabilidade da produtividade de grãos e de caracteres de pendão de milho

RESUMO: Devido à importância econômica do milho há a necessidade de avaliar o desempenho dos genótipos diante das variações ambientais (anos, locais e épocas), sendo assim, o estudo da interação entre genótipos e ambientes (G×A) têm sido realizado para garantir a segurança nas indicações dos genótipos. Além disso, quando há interação G×A a análise de adaptabilidade e estabilidade pode ser realizada. Essa análise possibilita a identificação de genótipos com resposta previsível e que sejam responsivos a variabilidade ambiental. Assim, os objetivos deste trabalho foram verificar se há interação entre genótipos e ambientes e avaliar a resposta de 16 genótipos de milho em sete ambientes, por meio da análise de adaptabilidade e estabilidade. Foram conduzidos sete experimentos com 16 genótipos de milho, no delineamento experimental blocos completos ao acaso, com três repetições. Foram avaliados o comprimento do pendão (CP), o número de ramificações do pendão (NR), a massa de matéria seca do pendão (MS) e a produtividade de grãos (PROD). Foram realizadas as análises de variância individual e conjunta e o teste F a 5% de significância. As frações da parte complexa da interação entre os genótipos e os pares de ambientes foram estimadas, e, então foram realizadas as análises de adaptabilidade e estabilidade pelo método de Eberhart e Russell. Houve interação genótipos e ambientes para o CP, NR, MS e PROD, o que evidencia que os genótipos respondem de forma diferenciada nos ambientes. Quando considerados os quatro caracteres não há indicação de genótipo ideal.
Palavras-chave: *Zea mays* L., caracteres agronômicos, melhoramento de plantas, modelos biométricos, indicação de genótipos.

INTRODUCTION

Maize (*Zea mays* L.), a member of the Poaceae family, plays a pivotal role in the global agricultural landscape. During the 2022/2023 growing season, Brazil dedicated approximately 22.27 million hectares to maize cultivation, achieving a mean grain yield of 5,922 kg per hectare; this output establishes maize as the country's leading cereal crop (CONAB, 2023). The versatility of maize extends beyond its role as a staple food; it finds widespread applications in industrial and energy sectors, predominantly in animal feed production. Additionally, maize serves as a key ingredient in the manufacturing of essential food products such as cornmeal, flour, hominy, and oils, as well as in more complex formulations such as glucose syrup, maltodextrins, and coloring agents (SOLOGUREN, 2015). Its significance is further underscored by its contribution to bioenergy, particularly in ethanol production.

Given the economic importance of maize, numerous public and private institutions are involved

in the genetic improvement of the crop, developing genotypes with high yield potential coupled with desirable agronomic traits. SOUZA et al. (2015) noted that tassel size is a significant characteristic in maize ideotypes, as larger tassels can adversely affect grain yield and its components. This is due to reduced solar interception in the plant canopy (diminishing photosynthesis) and the role of tassels as a sink for photoassimilates. HALLAUER et al. (2010) argued that the tassel mass is the primary factor responsible for its negative impact since it essentially acts as a drain, directing fewer nutrients to grain production.

Notably, each cultivation context has its own unique characteristics, and the appropriate agricultural practices can vary depending on the region, climate, and soil type. Therefore, it is always recommended that farmers and producers consult experts for specific and up-to-date advice based on the conditions in their growing area. The analysis of variance of a set of genotypes evaluated in a group of environments involving different locations, seasons, and years provides information on the G×E interaction (CRUZ et al., 2012; BORÉM et al., 2021). If the G×E interaction is significant, the researcher needs to know whether the genotypes contribute with the same intensity to the interaction, and this information is not obtained by routine analysis of variance. Therefore, various methods for analyzing adaptability and stability have been developed, complementing the individual and joint analyses of variance. The choice of adaptability and stability analysis method depends mainly on the number of environments available, the required precision, and the desired type of information (CRUZ et al., 2012), as well as simplicity and ease interpretation (BORÉM et al., 2021). Among the methods, those based on linear regression analysis, especially the method proposed by EBERHART & RUSSEL (1966), are commonly used.

Several authors have used the Eberhart and Russel (1966) method for different traits, including grain yield (CHANGIZI et al., 2014; BUSANELLO et al., 2015; PRADO et al., 2016; FARIA et al., 2017; PINTO et al., 2019; BERNINI & GUIMARÃES, 2020; ECKARDT et al., 2022; SHOJAEI et al., 2022), oil content (SANTOS et al., 2018a), and phenological and morphological traits (e.g., male and female flowering and plant and ear height) (BERNINI & GUIMARÃES, 2020; GAMI et al., 2017; PRADO et al., 2016). Nonetheless, no adaptability and stability studies were reported using the EBERHART & RUSSEL (1966) method for tassel traits, which are extremely important when selecting and recommending genotypes. Therefore, this study investigated interactions between genotypes and environments and evaluate the response of 16 maize genotypes in seven environments using adaptability and stability analysis.

MATERIALS AND METHODS

We used data from seven maize (*Zea mays* L.) experiments conducted in the agricultural years 2015/2016 (Environment 1), 2016/2017 (Environment 2), 2017/2018 (Environment 3), 2019/2020 (Environments 4 and 5), and 2020/2021 (Environments 6 and 7) in the experimental area of the Department of Plant Science at the Federal University of Santa Maria (Table 1). The region has a Cfa climate classification (Köppen), which is humid subtropical with hot summers and no defined dry season (ALVARES et al., 2013), and the soil is classified as *Argissolo Vermelho distrófico arênico* (Ultisol) (SANTOS et al., 2018b).

The soil was conventionally prepared in the seven experiments, which included 16 corn genotypes (Table 2). The experimental design was randomized complete blocks with three replications. The plots consisted of two 5 m long rows, spaced 0.80 m apart, with 0.20 m between plants in the row, in the seven experiments. Manual thinning was done to adjust the plant density to five plants per meter of row, totaling 62,500 plants ha^{-1}. General information on base and top dressing fertilization is shown in table 1. These recommendations were based on soil analyses. The other crop treatments followed the guidelines for growing corn, keeping the experiments free of weeds, pests, and diseases (FANCELLI & DOURADO NETO, 2009).

Tassel traits were evaluated using randomly collected tassels from the plot at the end of the reproductive stage. In Environments 1 and 3, 20 tassels were collected per plot, and 11 were collected per plot in the other environments. As per WARTHA et al. (2016), 11 tassels are enough to estimate the mean with 40% precision and a 95% confidence level. After field collection, the tassels were labeled, stored in paper packaging, and taken to a 60ºC oven until constant mass was achieved. The evaluated tassel traits included tassel length (TL, in cm), tassel branch number (TBN), and tassel dry matter (TDM, in g). Grain yield (GY) was assessed for all plants in the plot, in megagrams per hectare (Mg ha^{-1}), at 13% moisture content.

Individual variance analysis was conducted, followed by a joint variance analysis at a 5% significance level, considering the effects of

Table 1 - Sowing date, grain harvest date, weather data, minimum, mean, and maximum temperatures, total rainfall, basal fertilization, commercial formula, top dressing, and plant development stages when the applications were made.

Variable	-----Weather data-----						
	E1	E2	E3	E4	E5	E6	E7
Sowing date	10/21/2015	11/19/2016	10/31/2017	11/25/2019	12/20/2019	10/28/2020	12/01/2020
Grain harvest date	03/30/2016	04/07/2017	03/21/2018	04/13/2020	04/132020	03/24/2021	04/06/2021
Minimum temperature (°C)	14.36	15.92	16.37	12.43	12.43	17.84	17.84
Mean temperature (°C)	22.59	22.92	23.25	23.70	23.84	23.93	23.56
Maximum temperature (°C)	29.45	27.71	29.47	30.78	30.78	36.14	36.14
Total rainfall (mm)	1,101.00	906.20	512.00	452.40	424.00	399.20	417.80
Variable	-----Fertilization (kg ha^{-1})-----						
	E1	E2	E3	E4	E5	E6	E7
Basal fertilization (N-P-K)	750	400	300	300	300	500	500
Commercial formula	05-20-20	05-20-20	05-20-20	05-20-20	05-20-20	05-20-20	05-20-20
N	37.5	20	15	15	15	25	25
P_2O_5	150	80	60	60	60	100	100
K_2O	150	80	60	60	60	100	100
Top dressing (urea)	270	180	250	180	180	180	180
Applied in stages	V4, V8 and V12	V4 and V8	V4 and V8	V4 and V8	V4 and V8	V4 and V8	V4 and V8

All seven experiments employed basic fertilization on the day of sowing.
N: nitrogen; P: phosphorus; K: potassium.
Plant development stages: V4 (four expanded leaves), V8 (eight expanded leaves), and V12 (twelve expanded leaves).
The weather data was obtained from the Automatic Weather Station in Santa Maria/RS and provided by the National Institute of Meteorology (INMET).

genotypes as fixed and environments as random. To determine the homogeneity of the residual variances, the ratio between the largest and smallest residual mean square (RMS) of the environments (>RMS/<RMS) was calculated. When this value was less than seven, joint variance analysis was carried out to assess the significance of genotype (G), environment (E), and G×E interaction effects. Estimates of the mean, coefficient of variation (CV), F-value calculated for genotype (Fc), and selective accuracy (SA) were recorded for each of the four traits. The fractions of the complex part of the interaction between genotypes and pairs of environments were estimated. Subsequently, for traits showing significant G×E interaction, adaptability, and stability analyses were performed using the EBERHART & RUSSELL (1966) method. Statistical analyses were conducted using the Office Excel® and Genes software (CRUZ, 2016).

RESULTS AND DISCUSSION

Significant genotype effects (P ≤ 0.05) were observed for TL, TBN, TDM, and GY in the individual variance analyses across the seven environments (Table 3). The highest to lowest mean square residual ratio of the environments (>RMS/<RMS) was less than seven, indicating homogeneity of residual variances and enabling a joint analysis of the data for the four traits. The joint variance analysis showed significant effects for genotype, environment, and G×E interaction for all four traits (Table 4). Similar results for G×E interactions were observed by CHANGIZI et al. (2014), BUSANELLO et al. (2015), PRADO et al. (2016), GAMI et al. (2017), FARIA et al. (2017), SANTOS et al. (2018a), PINTO et al. (2019), BERNINI & GUIMARÃES (2020), Eckardt et al. (2022), and SHOJAEI et al. (2022) in maize traits, demonstrating the necessity of evaluating genotypes over multiple years, seasons, or cultivation locations.

In the individual variance analyses, the CV (%) ranged from 1.90% for TL (Environment 4) to 16.03% for GY in Environment 6 (Table 3). In the joint variance analysis, the CV ranged from 3.32% for TL to 12.46% for GY (Table 4). According to PIMENTEL-GOMES (2009), the CV is classified as low under 10%, medium between 10 and 20%, high between 20 and 30%, and very high over 30%.

Table 2 - Technology, company, type, cycle, use, grain, color, and investment of the 16 maize genotypes.

Genotype	Version	Technology[1]	Company	Type[2]	Cycle[3]	Use[4]	Grain	Color[5]	Investment[6]
20A55	PW	PowerCore	Morgan Sementes	TCH	E	G/S	Semi-hard	LO	Medium
30F53	YH	Optimum Intrasect	Pioneer	SCH	E	G/S	Semi-dented	O	High
AG8780	PRO 3	VT PRO 3	Sementes Agroceres	SCH	E	G	Semi-dented	LO	High
AG9025	PRO 3	VT PRO 3	Sementes Agroceres	SCH	SE	G	Semi-dented	LO	High
AM9724	-	Conventional	Melhoramento Agropastoril	SCH	SE	G	Dented	Y/LO	High
AS1666	PRO 3	VT PRO 3	Agroeste	SCH	SE	G	Semi-dented	Y/LO	High
AS1677	PRO 3	VT PRO 3	Agroeste	SCH	SE	G	Semi-dented	LO	High
BM3066	PRO2	VT PRO 2	Biomatrix	SCH	E	G/S	Semi-dented	O	High
DKB230	PRO 3	VT PRO 3	Dekalb	SCH	SE	G	Semi-dented	Y	High
DKB290	PRO 3	VT PRO 3	Dekalb	SCH	E	G	Semi-dented	LO	High
MS2010	-	Conventional	Melhoramento Agropastoril	SCH	E	G	Semi-dented	Y/LO	High
MS2013	-	Conventional	Melhoramento Agropastoril	SCH	E	G	Semi-hard	LO	High
MS3022	-	Conventional	Melhoramento Agropastoril	TCH	E	G	Hard	O	Medium
P1630	H	Herculex I	Pioneer	SCH	SE	G	Semi-dented	LO	High
P2530	-	Conventional	Pioneer	SCH	SE	G	Semi-hard	O	High
StatusVIP	VIP	Agrisure Viptera	Syngenta Seeds	SCH	E	G	Hard	LO	High

[1] The genetic composition of maize plants is modified and may confer inherent resistance or tolerance in the development of maize hybrids, that is, development of materials with specific characteristics, such as: resistance to attack of pest insects andtolerance to different herbicides. [2] SCH: single-cross hybrid; TCH: triple-cross hybrid. [3] E: early; SE: super-early. [4] G: grain; S: silage. [5] LO: light orange; O: orange; Y: yellow. [6] Financial investment applied in technology and management. Information provided by the Fundação Estadual de Pesquisa Agropecuária (FEPAGRO).

Based on this classification, the CV varied from low to medium, conferring reliability to the dataset.

Experimental precision, determined by SA, was very high (SA ≥ 0.90) for all traits in the seven environments, except for GY. For this trait, precision was high ($0.70 \leq SA < 0.90$) in Environments 1, 4, and 5 and very high in the others, as classified by RESENDE & DUARTE (2007) (Table 3). When analyzing the seven experiments jointly, all traits exhibited very high experimental precision (SA ≥ 0.90) (Table 4). Given this extensive dataset (four traits evaluated in 16 genotypes across seven environments), the high experimental precision, and the existing variability among genotypes, one can infer that the database is suitable for adaptability and stability studies. Furthermore, CARGNELUTTI FILHO & GUADAGNIN (2018) reported that seven experiments are enough to analyze the adaptability and stability of maize genotypes using the Eberhart and Russell method.

For TL and GY, most of the pairs of environments had a complex interaction (Table 5), meaning there was inconsistency in the superiority of the genotypes with the environmental variation, which makes it difficult to indicate genotypes (CRUZ & CASTOLDI, 1991), given there is no way of making a single recommendation for all locations without considerable damage to TL and GY, hindering the selection of superior genotypes. For TBN and TDM, all pairs of environments had a simple interaction, as the responses of the different genotypes are similar in relation to the characteristics evaluated in the different environments.

For TL, we found that most genotypes (56.25%) had a mean below the overall mean, which is desirable since a smaller tassel length is preferred. In the adaptability and stability parameter analysis for TL, 62.50% of the genotypes had regression coefficients not statistically different from one ($\beta 1i = 1$), indicating broad adaptability to environments (i.e., they respond satisfactorily to environmental improvements) (Table 6). The genotypes AM9724, P1630, and P2530 showed specific adaptability to favorable environments ($\beta 1i > 1$), responding positively to environmental improvements. Genotypes BM3066, DKB230, and MS2013 had $\beta 1i$ statistically less than one ($\beta 1i < 1$), demonstrating adaptability to unfavorable environments. Regarding stability, only the genotype BM3066 exhibited a regression deviation of zero ($S^2d = 0$), indicating high stability and a highly predictable response. The other genotypes had significant regression deviations ($S^2d \neq 0$), showing low stability and, thus, unpredictable responses in different environments.

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Table 3 - Individual analysis of variance with degree of freedom and the mean square for the sources of variation block, genotype and error, F-test value for genotype, mean, coefficient of variation, and selective accuracy for four traits in 16 maize genotypes in seven environments.

SV	DF	---Mean square for tassel length (TL, in cm)---						
		E1	E2	E3	E4	E5	E6	E7
Block	2	3.575	2.306	5.896	2.130	21.996	2.151	14.640
Genotype	15	17.688*	24.636*	30.209*	35.434*	18.668*	15.909*	18.945*
Error	30	1.559	2.251	2.755	0.833	2.843	1.310	4.431
Mean		46.910	47.500	43.890	47.970	46.000	44.260	41.760
CV(%)		2.66	3.16	3.78	1.90	3.67	2.59	5.04
Fc		11.344	10.945	10.964	42.544	6.567	12.145	4.275
SA[1]		0.955	0.953	0.953	0.988	0.921	0.958	0.875
Precision		VH	VH	VH	VH	VH	VH	VH
EI		1.441	2.027	-1.580	2.503	0.529	-1.212	-3.708
SV	DF	---Mean square for tassel branch number (TBN)---						
		E1	E2	E3	E4	E5	E6	E7
Block	2	8.610	4.518	0.185	13.942	0.110	0.147	0.200
Genotype	15	96.074*	60.719*	60.031*	58.523*	54.246*	72.899*	55.650*
Error	30	2.601	2.143	0.950	1.084	0.916	1.016	0.711
Mean		13.920	12.330	11.150	14.940	13.920	13.430	15.090
CV(%)		11.58	11.87	8.74	6.97	6.88	7.51	5.59
Fc		36.934	28.338	63.164	54.010	59.249	71.769	78.226
SA[1]		0.986	0.982	0.992	0.991	0.992	0.993	0.994
Precision		VH	VH	VH	VH	VH	VH	VH
EI		0.384	-1.207	-2.390	1.396	0.377	-0.112	1.553
SV	DF	---Mean square for tassel dry matter (TDM, in g)---						
		E1	E2	E3	E4	E5	E6	E7
Block	2	0.145	0.015	0.180	0.052	0.180	0.112	0.170
Genotype	15	2.877*	1.363*	1.999*	4.848*	1.768*	2.365*	2.958*
Error	30	0.086	0.024	0.082	0.061	0.083	0.069	0.108
Mean		3.080	2.330	2.570	4.200	3.650	2.920	3.350
CV(%)		9.51	6.67	11.14	5.87	7.90	9.02	9.79
Fc		33.608	56.235	24.408	79.951	21.339	34.178	27.488
SA[1]		0.985	0.991	0.979	0.994	0.976	0.985	0.982
Precision		VH	VH	VH	VH	VH	VH	VH
EI		-0.079	-0.823	-0.587	1.041	0.490	-0.239	0.197
SV	DF	---Mean square for grain yield (GY, in Mg ha^{-1})---						
		E1	E2	E3	E4	E5	E6	E7
Block	2	2.208	1.266	2.950	1.535	2.774	3.998	0.422
Genotype	15	5.478*	8.507*	4.239*	1.836*	0.825*	7.294*	24.518*
Error	30	1.864	0.894	0.746	0.639	0.291	0.562	0.684
Mean		9.890	9.140	8.110	8.120	5.100	4.680	5.570
CV(%)		13.81	10.35	10.65	9.84	10.58	16.03	14.84
Fc		2.939	9.511	5.679	2.874	2.832	12.984	35.854
SA[1]		0.812	0.946	0.908	0.807	0.804	0.961	0.986
Precision		H	VH	VH	H	H	VH	VH
EI		2.659	1.910	0.883	0.892	-2.131	-2.555	-1.657

*Significant effect by the F test at 5% significance. DF: degree of freedom. SV: source of variation.[1]Class limits for selective accuracy (SA), established by RESENDE & DUARTE (2007): VH: very high (SA ≥ 0.90), H: high (0.70 ≤ SA < 0.90), and M: moderate (0.50 ≤ SA < 0.70). Environmental index (EI): when EI values are positive, environments are classified as favorable; when EI values are negative, environments are classified as unfavorable.

Table 4 - Summary of the joint analysis of variance with the number of degrees of freedom and the mean square for the sources of variation (block/environment, genotype, environment, genotype × environment, and residual mean square), mean, coefficient of variation, the ratio between the highest and lowest residual mean square between environments (>RMS/<RMS), F value calculated for genotype and selective accuracy in maize.

Source of variation	DF	Mean square			
		TL	TBN	TDM	GY
Block/environment	14	7.528	3.959	0.122	2.165
Genotype	15	87.720*	434.309*	16.019*	26.612*
Environment	6	243.583*	94.631*	19.579*	208.850*
Genotype × environment	90	12.295*	3.972*	0.360*	4.347*
Residual	210	2.283	1.346	0.073	0.812
Mean		45.470	13.540	3.155	7.230
CV(%)		3.32	8.57	8.57	12.46
>RMS/<RMS		5.321	3.656	4.441	6.402
Fc		7.135	109.346	44.523	6.122
SA[1]		0.927	0.995	0.989	0.915
Precision		VH	VH	VH	VH

Traits: Tassel length (TL, in cm), tassel branch number (TBN), tassel dry matter (TDM, in g) and grain yield (GY, in Mg ha^{-1}). *Significant effect by the F test at 5% significance. >RMS/<RMS when the value is less than seven; in experiments with the same number of repetitions, we proceeded with the joint analysis of variance.[1]Class limits for selective accuracy (SA), as established by RESENDE & DUARTE (2007): VH: very high (SA ≥ 0.90), H: high (0.70 ≤ SA < 0.90), and M: moderate (0.50 ≤ SA < 0.70).

For TL, an ideal genotype is one with a lower mean, as breeding programs aim to develop maize plants with shorter tassels and fewer branches while maintaining sufficient pollen production for fertilization (FISCHER & EDMEADES, 2010). According to SOUZA et al. (2015), a smaller tassel allows more sunlight to penetrate the plant canopy, thereby increasing the photosynthetic capacity of modern maize hybrids. Additionally, the same authors stated that a smaller tassel has higher reproductive efficiency, as the plant's energy will be directed toward grain production rather than the growth of vegetative structures (e.g., the tassel). Therefore, genotypes with lower means, broad adaptability, and high stability for TL should be considered ideal. Thus, none of the studied genotypes were deemed ideal.

For TBN, genotypes 30F53, AG9025, AS1666, AS1677, DKB230, P1630, and P2530 exhibited means lower than the general mean. Furthermore, 81.25% of the genotypes had regression coefficients equal to one (β1i = 1), thus showing broad adaptability (Table 6). Specific adaptability to favorable environments (β1i > 1) was observed in BM3066 (1.693) and P2530 (1.843). The genotype AG8780 had a β1i of 0.616, less than one (β1i < 1), indicating adaptability to unfavorable environments.

As for stability for TBN, the genotypes 30F53, AG9025, AM9724, AS1666, AS1677, DBK230, and MS2013 showed zero regression deviations (S²d = 0), indicating high predictability. The other genotypes had significant regression deviations (S²d ≠ 0), showing unpredictable responses in different environments (Table 6).

Moreover, TBN is evaluated similarly to TL, meaning a lower mean is desirable. Larger tassels (higher number of branches) impede the passage of solar radiation to the plant canopy and act as a sink for photoassimilates, which could otherwise be allocated for grain production (EDWARDS, 2011). In terms of simultaneous analysis of mean, adaptability, and stability parameters (β1i and S²d) for TBN, genotypes 30F53, AG9025, AS1666, AS1677, and DKB230 demonstrated broad adaptability, high stability, and lower means, ideas being considered (Table 6).

For TDM, lower means are also preferred. This was observed in genotypes 30F53, AG8780, AG9025, AS1666, AS1677, DKB230, P1630, and P2530. Regarding adaptability parameters for TDM, 25.00% of the genotypes (30F53, AG9025, AS1666, and P2530) had regression coefficients equal to one (β1i = 1), indicating broad adaptability (Table 6). Genotypes 20A55, MS2013, and MS3022 had

Table 5 - Pairs of environments, the correlation between environments, and percentage of the complex part resulting from the decomposition of the interaction between genotypes and pairs of environments as per the method of CRUZ & CASTOLDI (1991) in 16 maize genotypes in seven environments.

-----Tassel length (cm)-----			-----Tassel branch number-----		
Pair	Correlation	Complex part	Pairs	Correlation	Complex part
1 × 2	0.74	48.19s	1 × 2	0.97	8.47s
1 × 3	0.55	62.36	1 × 3	0.98	4.97s
1 × 4	0.62	53.47	1 × 4	0.94	15.84s
1 × 5	0.47	72.78	1 × 5	0.94	13.99s
1 × 6	0.49	70.91	1 × 6	0.96	17.28s
1 × 7	0.53	68.68	1 × 7	0.96	10.15s
2 × 3	0.80	43.10s	2 × 3	0.97	18.02s
2 × 4	0.73	49.46s	2 × 4	0.95	22.57s
2 × 5	0.57	64.30	2 × 5	0.92	27.29s
2 × 6	0.45	71.26	2 × 6	0.94	23.71s
2 × 7	0.38	77.80	2 × 7	0.94	23.50s
3 × 4	0.60	62.68	3 × 4	0.94	24.42s
3 × 5	0.27	82.35	3 × 5	0.92	28.31s
3 × 6	0.26	80.18	3 × 6	0.93	24.63s
3 × 7	0.45	70.94	3 × 7	0.94	23.63s
4 × 5	0.58	57.83	4 × 5	0.93	25.27s
4 × 6	0.64	48.78s	4 × 6	0.95	19.83s
4 × 7	0.13	88.28	4 × 7	0.95	22.42s
5 × 6	0.37	79.20	5 × 6	0.96	16.47s
5 × 7	-0.19	109.23	5 × 7	0.97	16.63s
6 × 7	0.29	83.60	6 × 7	0.97	14.39s
-----Tassel dry matter (g)-----			-----Grain yield (Mg ha^{-1})-----		
Pair	Correlation	Complex part	Pairs	Correlation	Complex part
1 × 2	0.88	21.34s	1 × 2	0.70	50.70
1 × 3	0.95	15.99s	1 × 3	0.39	76.96
1 × 4	0.93	18.63s	1 × 4	0.21	74.34
1 × 5	0.86	30.24s	1 × 5	0.54	32.88s
1 × 6	0.93	24.40s	1 × 6	0.31	81.64
1 × 7	0.95	22.76s	1 × 7	0.62	35.08s
2 × 3	0.92	23.75s	2 × 3	0.70	45.15s
2 × 4	0.88	12.45s	2 × 4	0.45	47.21s
2 × 5	0.77	46.42s	2 × 5	0.48	29.54s
2 × 6	0.90	22.00s	2 × 6	0.58	64.27
2 × 7	0.87	22.99s	2 × 7	0.71	35.95s
3 × 4	0.91	13.89s	3 × 4	0.44	64.34
3 × 5	0.83	40.47s	3 × 5	0.19	62.78
3 × 6	0.89	31.67s	3 × 6	0.47	68.21
3 × 7	0.90	26.78s	3 × 7	0.60	30.95s
4 × 5	0.91	12.39s	4 × 5	0.50	60.87
4 × 6	0.94	11.45s	4 × 6	0.37	56.96
4 × 7	0.90	23.93s	4 × 7	0.30	35.28s
5 × 6	0.89	30.64s	5 × 6	0.10	54.67
5 × 7	0.87	28.61s	5 × 7	0.33	21.99s
6 × 7	0.91	28.46s	6 × 7	0.82	20.31s

s: identifies the pairs of environments whose interaction with the genotypes is predominantly simple.

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Table 6 - Estimates of stability and adaptability parameters for 16 maize genotypes for tassel length, tassel branch number, tassel matter, and grain yield obtained using the EBERHART & RUSSELL (1966) method in seven environments.

Genotypes	---Tassel length (cm)---				---Tassel branch number---			
	Mean	$\beta^1i^{(1)}$	$S^2d^{(2)}$	R^2 (%)	Mean	$\beta^1i^{(1)}$	$S^2d^{(2)}$	R^2 (%)
20A55	48.200	0.874ns	1.923*	63.404	15.505	0.934ns	1.688*	49.143
30F53	45.386	1.255ns	3.186*	70.858	7.461	0.862ns	-0.144ns	85.230
AG8780	48.069	0.964ns	1.510*	71.357	15.154	0.616*	0.656*	44.870
AG9025	45.428	0.986ns	1.884*	69.109	10.449	1.058ns	0.215ns	79.978
AM9724	44.227	1.393*	1.090*	86.453	14.516	1.104ns	0.422ns	76.783
AS1666	43.934	1.211ns	2.977*	70.491	8.806	0.631ns	-0.302ns	86.555
AS1677	43.331	0.832ns	2.434*	56.893	9.835	1.053ns	-0.186ns	90.906
BM3066	42.951	0.115*	0.206ns	7.678	21.010	1.693*	1.082*	81.585
DKB230	42.348	0.607*	4.108*	31.509	11.792	0.995ns	-0.260ns	92.552
DKB290	46.534	0.808ns	3.830*	46.434	14.868	0.772ns	1.146*	46.962
MS2010	48.328	0.815ns	2.241*	57.420	16.508	0.866ns	0.846*	57.812
MS2013	45.925	0.645*	1.707*	50.686	16.977	1.090ns	0.336ns	78.183
MS3022	43.973	1.065ns	1.558*	74.869	16.010	0.924ns	0.615*	65.527
P1630	48.598	2.207*	8.082*	77.029	8.179	0.829ns	0.636*	59.986
P2530	46.178	1.516*	3.979*	74.709	7.681	1.843*	3.761*	65.624
StatusVIP	44.116	0.707ns	1.044*	62.754	21.891	0.729ns	2.119*	32.849
Genotypes	---Tassel dry matter (g)---				---Grain yield (Mg ha^{-1})---			
	Mean	$\beta^1i^{(1)}$	$S^2d^{(2)}$	R^2 (%)	Mean	$\beta^1i^{(1)}$	$S^2d^{(2)}$	R^2 (%)
20A55	4.498	1.247*	0.185*	78.445	7.868	0.702*	0.481*	77.382
30F53	2.551	0.855ns	0.006ns	92.230	6.884	1.466*	0.906*	90.505
AG8780	3.132	0.677*	0.043*	76.905	7.773	1.322*	0.192ns	95.172
AG9025	2.793	0.937ns	0.039*	87.208	6.243	1.133ns	0.964*	84.447
AM9724	3.397	1.298*	0.009ns	96.068	7.385	1.179ns	0.558*	89.754
AS1666	2.452	0.904ns	0.092*	77.496	6.305	0.909ns	0.083ns	92.430
AS1677	2.144	0.726*	0.040*	79.918	6.843	1.006ns	0.453*	87.966
BM3066	4.287	1.398*	0.041*	93.621	9.175	0.788*	3.151*	48.682
DKB230	1.825	0.666*	0.004ns	88.596	6.561	0.837ns	0.455*	83.452
DKB290	3.395	0.600*	0.076*	63.695	7.771	1.139ns	0.386*	91.163
MS2010	3.435	1.361*	0.074*	90.220	8.370	1.190ns	2.168*	75.187
MS2013	4.192	1.393*	0.049*	92.856	8.881	0.545*	1.989*	40.716
MS3022	4.114	1.583*	0.162*	86.795	7.163	0.806ns	0.057ns	91.202
P1630	2.060	0.653*	0.074*	67.899	5.607	0.992ns	2.303*	66.610
P2530	2.335	0.913ns	0.020ns	90.277	5.067	1.005ns	2.118*	68.824
StatusVIP	3.873	0.792*	0.079*	74.878	7.792	0.982ns	1.115*	78.412

β^1i: Regression coefficient as adaptability parameter.

[1]$H0=\beta^1i=1$, *significant at 5% probability by t-test; ns: not significant.

S^2d: Regression deviation as a stability parameter.

[2]$H0=S^2d=0$, *significant at 5% probability by the F test; ns: not significant.

R^2: Coefficient of determination as a measure of stability.

coefficients greater than one ($\beta 1i > 1$), showing adaptability to favorable environments. Genotypes AG8780, AS1677, DKB230, DKB290, P1630, and StatusVIP had $\beta 1i$ less than one ($\beta 1i < 1$), indicating specific adaptability to unfavorable environments.

For the stability of TDM, the genotypes 30F53, AM9724, DKB230, and P2530 obtained zero regression deviations ($S^2d = 0$), indicating high stability. Significant regression deviations ($S^2d \neq 0$) were noted for the other genotypes, thus showing unpredictable responses or low stability in these environments. Considering the coefficient of determination (R^2) as an auxiliary measure of stability, genotype AG9025 also stood out, presenting a mean lower (2.793) than the overall mean (3.155) and an R^2 above 85% (Table 5). The TDM is interpreted in the same way as the TL and TBN (i.e., a lower mean is desired). By simultaneously evaluating the mean and parameters of adaptability ($\beta 1i$) and stability (S^2d), the genotypes 30F53 and P2530 were found to have lower means, broad adaptability, and high stability. Hence, they were considered ideal genotypes for TDM (Table 6).

Higher means for GY were observed in 20A55, AG8780, AM9724, BM3066, DKB290, MS2010, MS2013, and StatusVIP. Regarding genotype adaptability, 68.75% exhibited broad adaptability ($\beta 1i = 1$). Genotypes 30F53 and AG8780 had regression coefficients greater than one ($\beta 1i > 1$), indicating adaptability to favorable environments and high productive capacity responsive to environmental improvements. Genotypes 20A55, BM3066, and MS2013, with $\beta 1i$ less than one, demonstrated specific adaptability to unfavorable environments, meaning high productive capacity but no responsiveness to environmental improvement (Table 6).

For the stability parameter S^2d, AG8780, AS1666, and MS3022 showed zero regression deviations ($S^2d = 0$), indicating high stability and predictability. Other genotypes had significant regression deviations ($S^2d \neq 0$), thus considered unpredictable in these environments. However, genotypes AM9724 and DKB290, with higher means than the general mean and R^2 over 85%, also demonstrated good stability (Table 6). Additionally, 81.25% of genotypes had significant regression deviations, indicating unpredictable responses. This may be related to the high number of single hybrids in this study, as HALLAUER et al. (2010) noted that single hybrids have a genetic constitution of low stability due to being derived from the crossing of two contrasting lines.

In the simultaneous analysis of adaptability and stability parameters ($\beta 1i$ and S^2d) and the mean for GY, a minority of genotypes (AM9724, AS1666, DKB290, and MS3022) demonstrated broad adaptability and high predictability. Nevertheless, genotypes AS1666 and MS3022 had grain yield means below the general mean. Therefore, AM9724 and DKB290 were considered ideal, exhibiting higher means, broad adaptability, and high stability. When considering all four traits (TL, TBN, TDM, and GY), there is no clear indication of an ideal genotype, as none simultaneously meet the appropriate parameters. Similar to this study, when investigating adaptability and stability in maize using the Eberhart and Russell method, other researchers were also unable to identify an ideal genotype for the traits studied (PRADO et al., 2016; GAMI et al., 2017; FARIA et al., 2017; SHOJAEI et al., 2022).

It is important to emphasize that the search for a shorter shoot must be balanced with agricultural practices, suitable varieties, and the growing environment, as shoot tassel length is just one of the many variables influencing maize grain yield. Proper management, including the correct use of fertilizers, irrigation, pest and disease control, and planting density, among other factors, is key to optimizing the crop's grain yield.

CONCLUSION

There is an interaction between genotypes and environments regarding the following traits: tassel length, tassel branch number, tassel dry matter, and grain yield in maize; in other words, genotypes respond differently to different environments. When the four traits are considered, tassel length, tassel branch number, tassel dry matter, and grain yield, there is no indication of an ideal genotype, as they do not exhibit the desired parameters simultaneously.

DECLARATION OF CONFLICT OF INTEREST

We have no conflicts of interest to declare.

AUTHORS' CONTRIBUTIONS

All the authors critically reviewed the manuscript and approved the final version.

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