Journal of Agricultural Sciences (Belgrade)
Vol. 70, No. 3, 2025
Pages 249-268

https://doi.org/10.2298/JAS2503249A
UDC: 634.22(497)"2007-2024"
Original scientific paper

AMMI, GGE-BIPLOT, AND JOINT REGRESSION TECHNIQUE AS A TOOL IN MEASURING G × E INTERACTION IN 3-WAY CROSS MAIZE (*ZEA MAYS* L.) HYBRIDS

Saidat A. Adeniji, Omolayo J. Ariyo and Gbemisola O. Otusanya[*]

Department of Plant Breeding and Seed Technology,
Federal University of Agriculture, Abeokuta, Ogun State, Nigeria

Abstract: Genotype by environment (GE) interaction has a large impact on selecting adapted and predictable genotypes. Therefore, it is necessary to evaluate maize genotypes across different environments, seasons or locations for a successful selection. Twelve 3-way cross maize hybrids obtained from the International Institute of Tropical Agriculture (IITA) were evaluated on the field of the Federal University of Agriculture, Abeokuta, Nigeria (latitude 7° 15° N and longitude 3° 25° E) across three growing seasons of 2021 and 2022. The experiment was laid out with three replicates. Additive main effect and multiplicative interaction (AMMI), genotype (G) plus GE (GGE) biplot and joint regression techniques were used to identify stable and high-yielding genotypes. The AMMI analysis showed that the total variances in the yield of the three-way maize hybrids accounted for by G, environment (E) and GE interaction were 30.6%, 44.19% and 25.31%, respectively. Based on the AMMI biplot, the genotypes LW1701-10 and OBA SUPER-9, which combined high yield with stability, were the most desirable. The GGE biplot showed that hybrids LW1701-10, OBA SUPER-9 and LW1701-6 were the most stable and desirable genotypes. The joint regression technique showed that the performance of the genotypes could not be revealed in a linear manner as the deviation component variance accounted for 81.05% and identified LW1701-6, LW1701-16, LW1701-12, LW1701-21, LW1701-4 as stable and desirable genotypes. The study revealed that the GGE and AMMI models were more effective than the joint regression technique in examining yield stability of maize hybrids. The study deals with the comparison of AMMI, GGE biplot and joint regression techniques.

Key words: genotype by environment interaction, stable, AMMI, GGE biplot, joint regression technique.

---

[*] Corresponding author: e-mail: igegbemi@gmail.com

Introduction

Maize (*Zea mays* L.), a well-known grain, is important in Nigeria, as it is widely cultivated by a large number of farmers and has high economic value (Adetimirin et al*.,* 2008). However, its productivity remains low across sub-Saharan African countries when compared to the global average production (FAO, 2023). This is due to several abiotic and biotic factors, including low soil fertility, drought and heat stresses, striga infestations, use of low-yielding and un-adapted varieties. High-yielding varieties/hybrids with reliable performance under different environmental conditions are of great importance for sustainable production and productivity. Grain yield is an important agronomic trait that is inherently quantitative and influenced by genes in the crop, the environment and soil management as well as their interactions (Messina et al*.,* 2009).

Multi-environment trials (MET) are conducted worldwide for different crops to identify high-yielding genotypes and the environment(s) that best represent the test environments. In MET, genotypes are tested in different environments, seasons, and years to determine the adaptation of crops. However, the interaction of the genotypes with the environment (GE) makes the selection of the best performing and most reliable genotypes a difficult task. There are numerous stability statistics available to plant breeders which provide different approaches for dealing with GE interactions. These include combined ANOVA, regression analysis and multivariate methods, the additive main effects and multiplicative interaction (AMMI) proposed by Gauch and Zobel (1996) and Gauch (1992), and genotype plus GE interaction (GGE biplot analysis) proposed by Yan et al. (2000).

The AMMI model is one of the most widely used statistical tools in the analysis of different environment trials. It has two uses, namely for understanding complex GE interactions and for accuracy. The model has been used to study grain yields of different crops, select stable genotypes, and investigate GE interactions (Crossa, 1990). The complex relationships among the environments or among genotypes can be adequately represented in a scattered diagram that shows both the genotypes and environments simultaneously. This scattered diagram is called an AMMI biplot (Mohammadi et al., 2007).

The GGE biplot is based on environment-centered data, which removes the main effects of environments (because environments account for a large percentage of variation and are not useful in genotype selection) and integrates the genotypic main effect with the GE interaction effect of a genotype by environment data set (Yan et al., 2000). The GGE biplot is a useful tool for mega-environment analysis (“which-won-where” pattern), whereby specific genotypes can be recommended for specific mega-environments (Yan and Kang, 2003), genotype evaluation (the mean performance and stability), and environmental evaluation (the ability to discriminate among genotypes in the target environments).

Joint regression analysis is an important model for analyzing and interpreting the GEI of two-way classified data and continues to support traditional statistical analysis in genetics and plant breeding in determining the yield stability of different genotypes or agronomic treatments across varying environments (Crossa, 1990). A recent study by Dias et al. (2023) provides a comprehensive overview of joint regression techniques in the context of genotype × environment interaction (GEI) analysis. The authors discuss the application of joint regression models, emphasizing their utility in assessing yield stability and adaptability across diverse environments. This work highlights the continued relevance of joint regression methods in modern crop evaluation and breeding programs. Joint regression analysis combines additive and multiplicative components and thus analyzes both main effects and interaction with main effects, reducing its power for general significance testing (Farshadfar and Stuka, 2006).

Material and Methods

Twelve three-way cross maize hybrids were sourced from the germplasm of the Maize Breeding Unit of the International Institute of Tropical Agriculture (IITA), Ibadan, and were used for this study (Table 1). The experimental sites for the study were the upland and inland valley located at the Teaching and Research Farm of the Federal University of Agriculture, Abeokuta (FUNAAB), Ogun state, Nigeria (Lat 7^{o} 10^{o} N and 7^{o} 58 ^{o}N and Long 3^{o} 20^{o} E and 4^{o} 37^{o} E). The study was conducted in two different cropping seasons, the dry and rainy season of 2021 and 2022. The agro-meteorological data of the FUNAAB experimental sites for the period in which the study was conducted are shown in Table 2.

Table 1. List of genotypes and sources.

Genotypes	Source
LW1701-4	IITA
LW1701-6	IITA
LW1701-7	IITA
LW1701-10	IITA
LW1701-12	IITA
LW1701-16	IITA
LW1701-21	IITA
OBASUPER -7	IITA
OBASUPER-9	IITA
SAMMAZ-23	IITA
SAMMAZ-22	IITA
OSIELE (CHECK)	FUNAAB

Source: IITA: International Institute of Tropical Agriculture, Ibadan.

Table 2. The hydrothermal parameters for 2021 and 2022.

2021	JAN	FEB	MAR	APR	MAY	JUN	JUL	AUG	SEPT	OCT	NOV	DEC
Rainfall (cm)	----	4.8	20.02	19.72	8.8	4.94	22.56	13.16	9.35	9.93	10.52	30.85
Max temp°C	34.21	36.21	34.2	33.6	34.02	30.92	30.9	31.02	30.4	32.37	32.85	23
Min temp°C	24.11	25.55	23.3	23.4	24.40	23.12	22.6	22.70	22.55	21.97	22.75	26.93
R.H (%)	62.99	63.05	69.68	80.09	77.36	77.83	74.25	82.76	77.98	78.15	78.18	78.94
Sunshine (hr)	5.15	4.94	5.33	6.3	7.25	4.86	4.6	3.20	6.20	5.69	5.9	4.6
Evaporation (mm)	----	3.5	4.05	3.31	4.7	3.9	3.18	1.90	3.06	3.41	3.43	3.80
2022	JAN	FEB	MAR	APR	MAY	JUN	JUL	AUG	SEPT	OCT	NOV	DEC
Rainfall(cm)	-----	------	11.83	2.3	2.49	15.59	1.95	0.81	11.58	2.79	11.62	
Max temp°C	31.77	33.46	31.23	30.6	30.90	29.36	29.44	26.7	29.7	31.1	32.45	
Min temp°C	22.77	22.2	22.55	22	21.94	21.83	22.33	20.61	21.2	21.4	21.2	
R.H (%)	88.88	75.32	79.25	83.7	80.33	80.74	84.42	83.45	82.7	79.3	77.93	
Sunshine (hr)	4.44	5.19	4.72	3.9	4.92	3.88	4.25	2.76	3.7	4.02	3.92	
Evaporation (mm)	4.36	3.91	3.64	3.4	3.71	3.01	3.16	2.05	2.8	3.3	3.31	

The first and second plantings were carried out during the 2021 rainy season (20th June, 2021 – 30th August, 2021) and the 2022 rainy season (3rd February, 2022 – 26th May, 2022) at upland area, while the third planting was carried out at in-land valley during the 2022 dry season (3rd August, 2022 – 24th November, 2022). Each planting was laid out in a randomized complete block design in three replications. Two seeds of each of the 12 genotypes were sown at the spacing of 75 cm between rows and 50 cm within rows. The blocks were separated by a 1 m wide alley. Weed control was carried out manually if necessary.

Data collection

Data were collected from five (5) plants from the center of each row on the following traits:

i. Days to 50% tasseling: this was determined by counting the number of days from planting to the time when 50% of the plants were tasseling.

ii. Days to 50% silking: this was determined by counting the number of days from planting to the time when 50% of the plants have developed silks.

iii. Plant height (cm): the height of the selected plants was measured from the base to the beginning of tassel branching using a meter rule.

iv. Ear height (cm): this was determined by measuring the height from the base of the plant to the node bearing the upper ear with a meter rule.

v. Field weight (kg): this was measured by weighing the cobs per plot with a weighing scale.

vi. Grain yield per plot (kg): this was done by measuring the total yield per plant at 15% moisture content with a weighing scale.

vii. 1000-seed weight (g): this was determined by counting 1000 seeds and weighing with a weighing scale.

Data analysis

The data collected were subjected to separate and combined analysis of variance (ANOVA) across environments using SAS 9.2 software package to determine the effects of genotype (G), environment (E) and GEI. The means were separated using the least significant difference (LSD) at a 5% probability level.

The yield data were subjected to the additive main effect and multiplicative interaction (AMMI) model according to Gauch and Zobel (1997). The linear model of the technique is:

$$Y_{ger}=\mu + \alpha_g + \beta_e + \sum_n \lambda_n \Upsilon_{gn} \delta_{en} + \rho_{ge} + \epsilon_{ger} \qquad (1)$$

Y_{ge}	is the trait of genotype g in environment e;
μ	is the grand mean;
α_g	is the deviation of the genotype from the grand mean;
β_e	is the environment deviation from the grand mean;
λ_n	is the eigen value of PCA axis n;
$\Upsilon_{gn}\delta_{en}$	are the genotype and environment PCA scores for PCA axis n;
ρ_{ge}	is the residual of the AMMI model.

The AMMI stability value (ASV) was calculated using the formula proposed by Purchase et al. (2000) as follows:

$$\mathrm{ASV}=\sqrt{\left[\frac{IPCA\ 1SS}{IPCA\ 2SS}(\mathrm{IPCA\ 1scores})2\right] + (\mathrm{\ IPCA\ scores})2} \qquad (2)$$

where IPCA 1 SS/IPCA 2 SS is the weight given to the IPCA 1-value.

The IPCA is an indicator of stability to measure the response of both genotypes and environments. The absolute value of the first IPCA score represented the simplest measure of yield and stability.

Genotype plus genotype × environment interaction (GGE) following the procedures of Yan (2001), Yan and Kang (2003), Yan et al. (2007) was used to decompose the GEI into mega-environments and the best-performers according to their visual characteristics. The mean performance and stability of the genotypes were determined, and the discriminatory power and representativeness of the test environments were revealed (Yan, 2001). The GGE biplot was used to identify the ideal genotypes and locations.

The equation of the GGE biplot is as follows (Yan and Kang, 2003):

$$\bar{Y}_{ij} - Y_J = \lambda_1 \Sigma_{I1} \Pi_{ji} + \lambda_2 \Sigma_{I2} \Pi_{j2} + \epsilon_{ij} \quad (3)$$

$\bar{Y}_{ij}$ is the mean yield of genotype I in environment j;
Y_J is the mean yield across all genotypes in environment j;
λ_1 and λ_2 are the singular values for PC1 and PC2, respectively;
Σ_{i1} and Σ_{i2} are the PC1 and PC2 scores for genotype I;
Π_{jI} and Π_{j2} are the PC1 and PC2 scores for environment j;
ϵ_{ij} is the error associated with genotype i in environment j.

Genotype stability index: a stability index recommended by Farshadfar (2008) was calculated for each genotype by adding the overall mean performance and ASV for each trait as follows:

$$GSIi = RASVi + RYi \quad (4)$$

where GSIi = the genotype stability index for the ith genotype across the environment for each trait;

RASVi = the rank of the ith genotype across the environments based on ASV;

RYi = the rank of the ith genotype based on the mean yield across the environment. The genotype with the lowest GSI was considered the best for a particular trait.

Joint regression analysis was carried out according to the procedure of Perkins and Jinks (1968) to identify and select stable genotypes, using a linear regression coefficient (b) and the mean square of deviation (S^2di). The means of the three characters were regressed individually on the means of each environment to determine the response pattern. The GEI was partitioned by the use of variance components to determine the relative magnitude of the variances due to heterogeneity and deviation mean squares according to Breese (1969).

The linear model of Perkins and Jinks (1968) is as follows:

$$Y_{ij} = \mu + d_i + E_j + g_{ij} + e_{ij} \quad (5)$$

Y_{ij} is the yield variable of the ith genotype at the jth environments;
μ is the general mean over all genotypes and environments;
d_i is the additive effects of the ith genotype;
E_j is the effects of the jth environment;
g_{ij} is the GE interaction of the ith genotype with the jth environment;
eij is the error term.

The deviation of bi values from 1.0 was tested using the *t* test for the null hypothesis.

$$\frac{t = (bi-1)}{S.E.}$$

where S.E. = standard error.

If bi is significant, its significant deviation from unity is tested by the following formula:

$$t = \frac{(b-1)}{S.E.}$$

The deviation (S^2di) from zero was tested by dividing the stability values by the pool error M.S.

Results and Discussion

The combined ANOVA of maize genotypes in three environments is presented in Table 3. The result showed that genotype and environments effects were highly significant ($p<0.001$) for all traits evaluated. Similarly, GEI was equally significant for plant height, ear height, 1000-seed weight and grain yield. The maize genotypes evaluated differed significantly in all the characters, suggesting that all twelve genotypes differed from each other. The significant differences observed across the three seasons provided an opportunity to identify reliable genotypes. The environment accounted for more of the total variation than the genotype. This opines with the results of Ojo et al. (2021) and Komolafe et al. (2022).

The result of the AMMI analysis for grain yield of twelve genotypes of 3-way cross maize hybrids is presented in Table 4. Genotype accounted for 30.6% of the total variation, while environments and genotype by environment interaction accounted for 44.19% and 25.13%, respectively. The GEI was divided into the first two IPCA axes and the residual. IPCA 1 and IPCA 2 explained 67.8% and 32.10% of the total GEI variance, respectively. Crossover is present when a genotype performs better in one environment but poor in another, while non-crossover is present when a genotype continues to lead to a change in the IPI values. The AMMI analysis has been used by several authors as a tool to identify the superior and stable genotypes, as well as favorable and high-yielding environments (Tekdal and Kendal, 2018). Based on the results of this study, the AMMI model accounted for a substantial part of the total sum of squares, suggesting that the model was appropriate to explain the GEI. The differences in the amount of rainfall and other climatic conditions in the environments used for the study may have been responsible for the variability in the performance of the genotypes. This is consistent with the report by Komolafe et al. (2022). The significant sum of squares for environment and GEI obtained in the AMMI analysis indicated that the environments used for this study were different from each other, and thus, genotypes responded differently to each environment. The results agree with the findings of Naroui Rad and Bakhshi (2021).

The mean grain yield of 12 genotypes of 3-way cross maize hybrids grown in three environments and their first IPCA scores are presented in Table 5. The results show that the grain yield per plant ranged from 519.94 g/plant to 1011.11 g/plant. SAMMAZ-22, LW1701-10, LW1701-7, OBASUPER-9, LW1701-21 and LW1701-6 performed above average during the 2021 rainy season (E1). In the 2022 dry season (E2), LW1701-10, LW1701-12, LW1701-16, LW1701-6, OBA SUPER-7, and OBA SUPER-9 performed above average. However, in the 2022 rainy season (E3), only 4 genotypes LW1701-10, LW1701-21, LW1701-6, and OBA SUPER-7 performed above average. Environment 3 had the highest mean yield of 881.94 g/plant, while environment 2 had the lowest mean yield of 579.44 g/plant. Osiele Check had the highest IPCA score of 8.11, while Sammaz-22 had the lowest IPCA score of -12.65.

Table 3. Combined analysis of variance for grain-yield and related traits of 12 maize genotypes in three environments.

Source of variation	df	Days to tasseling	Days to silking	Plant height	Ear height	Field weight	1000-seed weight	Grain yield
Environment (E)	2	363.36**	253.48**	115002.96**	17682.06**	2.99**	16893.14**	1047689.58**
Block/E	6	18.19	4.39	1183.45**	217.07*	0.36**	148.28	13736.81
Genotype (G)	11	29.99**	31.42**	1030.21**	290.20**	0.36**	3961.81**	132223.80**
G x E	22	14.41	8.93	1152.45**	539.94**	0.18	1575.15**	54691.60**
Error	66	10.08	7.54	382.52	97.85	0.11	684.16	19248.93

**,* significant at 0.01 and 0.05, respectively.

Table 4. AMMI ANOVA table for grain yield of the twelve genotypes of 3-way cross maize hybrids evaluated across three environments.

Source of variation	Df	SS	MS	% of treatment	% G×E
Total	107	6105906	57065		
Treatment	35	4753056	135802**		
Genotype	11	1454462	132224**	30.6	
Environment	2	2095379	1047690**	44.19	
Block	6	82421	13737		
Interaction	22	1203215	54692**	25.31	
IPCA 1	12	816952	68079**		67.89
IPCA 2	10	386264	38626*		32.10
Residual	0	0	*	*	*
Error	66	1270429	19249		

**, * and IPCA mean significant at 0.01, 0.05 and interaction principal component axes, respectively.

Table 5. Mean and the first IPCA scores of the AMMI analysis of grain yield for the 3-way cross maize hybrids across three environments.

S/N	Environment Genotype	E1	E2	E3	Mean yield	First IPCA
1	Osiele Check	475.00	450.00	633.33	519.94	8.11
2	LW1701-10	1033.33	800.00	1200.00	1011.11	2.37
3	LW1701-12	800.00	583.33	850.00	744.44	2.18
4	LW1701-16	766.67	833.33	866.67	822.22	10.32
5	LW1701-21	900.00	450.00	983.33	777.78	-4.11
6	LW1701-4	866.67	470.00	800.00	712.22	-3.48
7	LW1701-6	966.67	600.00	950.00	838.89	-2.36
8	LW1701-7	1033.33	453.33	766.67	751.11	-9.69
9	OBA-SUPER-7	700.00	583.33	1033.33	772.22	6.55
10	OBA-SUPER-9	1000.00	850.00	833.33	894.44	2.80
11	SAMMAZ-22	1133.33	450.00	850.00	811.11	-12.65
12	SAMMAZ-23	733.33	430.00	816.67	660.00	-0.04
	Mean	867.36	579.44	881.94	776.25	
	First PCA	-17.42	14.48	2.95		

E1= First rainy season of 2021, E2 = Dry season of 2022, E3 = Second rainy season of 2022.

In addition, environment 2 had the largest IPCA score of 14.48, while E1 had the lowest IPCA score of -17.42. Thus, when a genotype and an environment have the same sign on their respective first IPCA axes, their interaction is positive, if different, their interaction is negative. The AMMI stability values revealed variations in grain ranking yield among the twelve genotypes. G12 (Sammaz-23) and G3 (LW1701-12) were considered stable according to ASV, but unstable according to GSI. This agrees with the report by Komolafe et al. (2022), who found some genotypes stable according to ASV but slightly unstable according to GSI. The AMMI biplot enables the simultaneous selection for yield and stability of genotype performance. This selection is always based on genotype yield responses to the environments, adaptability of the genotypes to the environments and the minimum deviation from zero score on IPCA 1 (Ariyo and Ayo-Vaughan, 2000).

The polygon view of the GGE biplot of twelve genotypes of maize grown in three environments is presented in Figure 1. The PC1 explained 55.5% of the total variation, whereas PC2 explained 30% of the variation in grain yield. The two principal axes accounted for 85.5% of the total variation in grain yield across three environments. The polygon view grouped the three environments into two mega-environments, with environment 1 in one mega-environment and environments 2 and 3 in the second mega-environment. The genotypes at the vertex of each sector denote the highest yielding genotype in the environments that fall within that sector. The vertex genotypes are G2 (LW1701-10) for mega-environment 1 and G11 (SAMMAZ-22) for mega-environment 2. G2 (LW1701-10) was the best in environment 3 and G11 (SAMMAZ-22) was the best in environment 1. The genotypes that fell out of the mega-environments are low-yielding and therefore not desirable in any of the environments and probably the poorest in some or all environments (Yan, 2001). The GGE biplot ranks the genotypes according to the average yield and stability. G2 (LW1701-10), G10 (Oba Super-9), and G7 (lw1701-6) combined high yield with stability, indicating that these genotypes possess the ability to maintain constant performance in terms of yield over a range of environmental conditions. This is in agreement with Kusmiyati and Setiawan (2022), who defined yield stability as the ability of a genotype to avoid significant yield fluctuation over a range of environmental conditions.

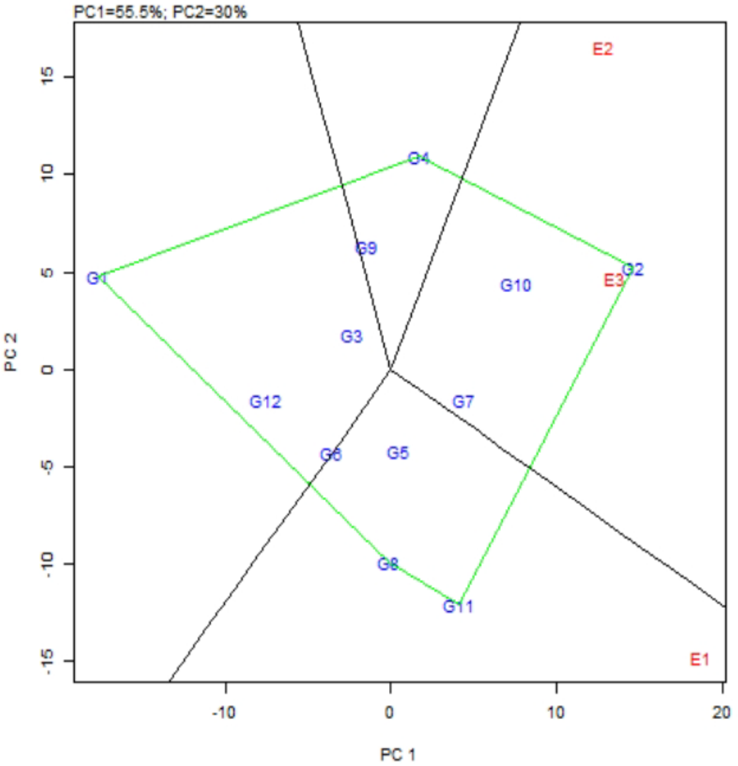

Figure 1. Polygon view of GGE biplot for grain yield data of twelve 3-way cross maize hybrid genotypes evaluated across 3 environments between 2021 and 2022. E1=Rainy; June 2021 – Aug 2021, E2=Dry; Feb 2022 – May 2022, E3=Rainy; Aug 2022 – Nov 2022. G1=Osiele Check, G2=LW1701-10, G3=LW1701-12, G4=LW1701-16, G5=LW1701-21, G6=LW1701-4, G7=LW1701-6, G8=LW1701-7, G9=OBA SUPER-7, G10=OBA SUPER-9, G11=SAMMAZ-22, G12=SAMMAZ-23.

Though G11 (Sammaz-22) and G4 (LW 17101-16) were high-yielding, they were not stable and therefore unpredictable. G12 (Sammaz-22) and G3 (LW 1701-12) were stable but low-yielding genotypes, making them undesirable for selection. G1 (Osiele Check), G8 (LW 1701-7) and G9 (Oba- Super 7) were low-yielding and unstable, making them the most undesirable. Yan and Kang (2003) defined an ideal genotype on the basis of mean performance and stability. Kaya et al. (2006) have also reported that a genotype is only stable when it translates to high yields. This ideal genotype rarely occurs in nature, thus the genotype closest to the small circle is called ideal. Based on this information, G2 (LW 1701-10) was classified as the ideal genotype in terms of grain yield, as it combines yield and stability. This is in contrast to Jalata (2011), who have argued that there is no ideal genotype.

The discriminatory and representative view of the environments and ranking of the test environment relative to an ideal environment is presented in Figure 2. An environment is called discriminative when it is able to identify the best genotypes, while representativeness refers to the ability of a test location to represent the test environments (Kassaye et al., 2024). The length of the environment vectors (which approximates the standard deviation within each environment) from the biplot origin and the angle formed with the abscissa of the AEC reveal the discriminatory ability and representativeness of the test environment, respectively. A test environment that has the longest vector is more discriminatory when compared with other test environments. Hence, environment 1 was the most discriminatory environment. A test environment is more representative when it has the smallest deviation angle with the AEC abscissa compared with the other test locations. Thus, environment 3 was identified as the most representative. An ideal environment is the most discriminatory of genotypes and yet representative for the other test environments. Hence, the dark circle in the ring of circles determines the ideal environment and the environment closest to the best environment. This biplot shows that E3 comes closest to the ideal environment. The GGE biplot evaluates the test locations through their discriminatory power and representativeness. The environment with the highest discriminatory power is the environment that provides the best information on the genotype differences among the tested genotypes, while the ability to represent the average environment confers representativeness (Kassaye et al., 2024). Kassaye et al. (2024) defined an ideal test environment as a virtual environment that has the longest vector of all the test environments (most discriminating) and located on the AEC abscissa (most representative). In terms of grain yield, the 2021 rainy season was the least representative and most discriminatory among the environments. This is true as the means of genotypes in the 2021 rainy season were not significantly different from each other.

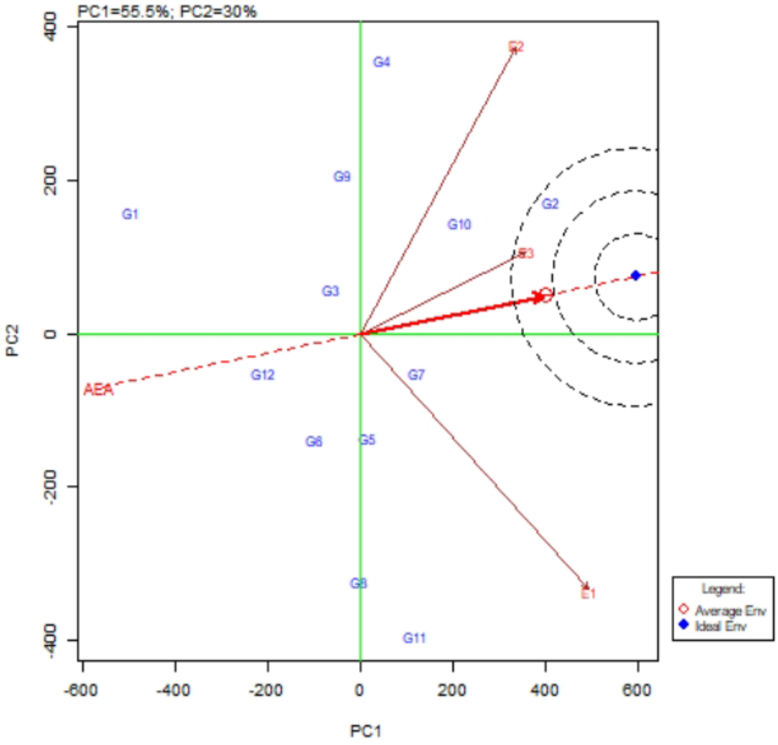

Figure 2. The biplot showing discrimination and representativeness based on genotype by environment grain yield data of twelve genotypes of 3-way cross maize hybrids evaluated across 3 environments between 2021 and 2022.
E1=Rainy; June 2021 – Aug 2021, E2=Dry; Feb 2022 – May 2022, E3=Rainy; Aug 2022 – Nov 2022, G1=Osiele check, G2=LW1701-10, G3=LW1701-12, G4=LW1701-16, G5=LW1701-21, G6=LW1701-4, G7=LW1701-6, G8=LW1701-7, G9=OBA SUPER-7, G10=OBA SUPER-9, G11=SAMMAZ-22, G12=SAMMAZ-23.

According to Yan and Tinker (2006), such an environment gives little or no encouragement to good genotypes with the potential to upgrade poor genotypes. The rainy season (2022), which had the smallest angle with the AEC abscissa, is the most representative environment and is ideal for selecting superior genotypes. This is true as the test location is the closest to the ideal environment. The most representative environment can therefore be used to select sample environments with wide adaptation, lowering the cost of multi-environment trials while the non-representative environments are useful for selecting specifically adapted genotypes.

The performance of twelve maize genotypes based on the mean grain yield/plant and stability across the three environments is presented in Figure 3. The single-arrowed line, called the Average Environment Coordinate (AEC) abscissa, indicates the direction of increasing mean genotype performance across test environments. The double-arrowed line, orthogonal to the AEC abscissa and passing through the origin, is the AEC ordinate**.** This axis divides the genotypes into two groups: those on the right performed above the overall mean**,** while those on the left yielded below the average**.** G2 (LW1701-10) was the best performer across the three environments based on yield. The projections on the ordinate are measures of the stability of the genotypes. The shorter the vector, irrespective of the direction, the more stable is the associated genotype. A short vector denotes high stability (Yan and Kang, 2003). LW1701-10 (G2) was identified as the most stable, followed by LW1701-6 (G7), OBA-SUPER-9 (G10), while Osiele-Check (G1), LW1701-7(G8), SAMMAZ-22(G11), LW1701-16(G4), OBA-SUPER-7 (G9), LW1701-21(G5) had long vectors and were unstable. An ideal genotype is the genotype that combines high yield and stability. It is represented by the small circle with the arrow pointing to it. LW1701-10 (G2) was identified as the most desirable genotype near the ideal genotype.

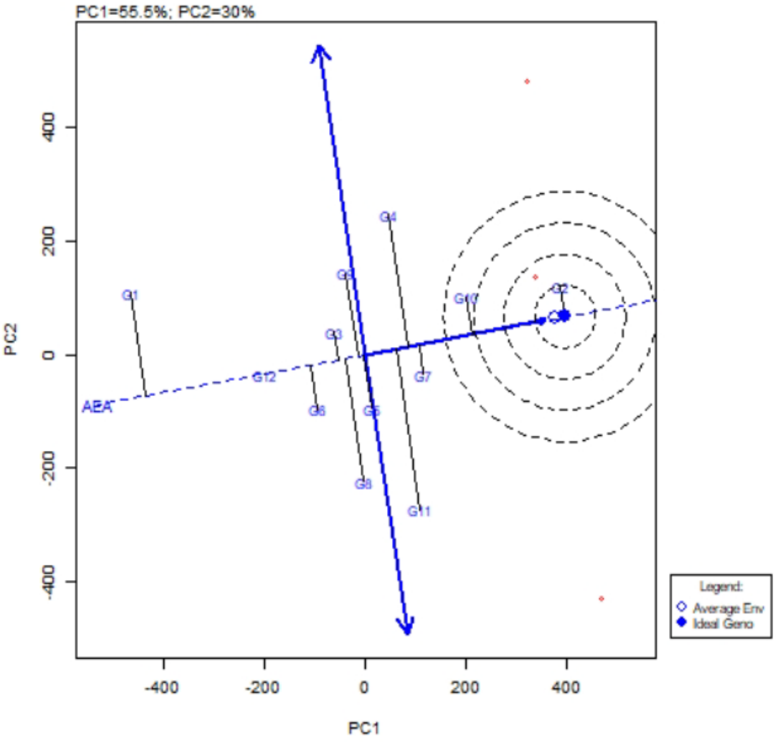

Figure 3. The GGE biplot showing the performance of the 3-way cross maize hybrid genotypes for both grain yield and stability evaluated across 3 environments between 2021 and 2022.

E1=Rainy; June 2021 – Aug 2021, E2=Dry; Feb 2022 – May 2022, E3=Rainy; Aug 2022 – Nov 2022, G1=Osiele check, G2=LW1701-10, G3=LW1701-12, G4=LW1701-16, G5=LW1701-21, G6=LW1701-4, G7=LW1701-6, G8=LW1701-7, G9=OBA SUPER-7, G10=OBA SUPER-9, G11=SAMMAZ-22, G12=SAMMAZ-23.

Using the procedures described by Perkins and Jinks (1968), analysis of variance for performance stability revealed that genotype, environment and GEI were significant for grain yield (Table 6). The significant remainder mean square also indicated that a significant portion of the variation was non-linear due to the genotype × environment interaction. However, the variance component was used to examine the relative contribution of heterogeneity and deviation from regression to GEI. It was found that the larger proportion of GEI was accounted for by the deviation component (81.05%) and the heterogeneity between regressions accounted for 8.53%.

Table 6. Mean squares from the stability analyses of variance of 3-way cross hybrid maize (Perkins and Jinks, 1968).

Source	DF	Grain yield	Component of GEI variance
Genotype	11	44074.59*	
Environment (joint regression)	2	349231.83**	
Genotype × environment	22	18230.31**	
Heterogeneity between regression	11	19015.75	8.53
Remainder	12	15991.14**	81.05
Pooled error	72	6416.31	

The average grain yields per plant and the regression coefficient of each genotype are presented in Table 7. Since the regression coefficients measure the responses of the genotypes to an increment in an improving environment, G11 (SAMMAZ-22), G5 (LW1701-21) and G8 (LW1701-7) showed above average responses with regression coefficients greater than 1.00 and were considered good yielders in above average environments. G2 (LW1701-10) and G9 (OBA – SUPER-7) with regression coefficients averaging 1.09 and 1.00 were also consistent in all environments. Other genotypes such as G1 (OSIELE CHECK), G3 (LW1701-12), G4 (LW1701-16), and G10 (OBA-SUPER-9) had regression coefficients smaller than 1 and only performed well in below-average environments. Six genotypes were found stable among the twelve genotypes: LW 1701-12(G3), LW 1701-16(G4), LW 1701-21(G5), LW1701-4 (G6), LW1701-6 (G7) and SAMMAZ-23 (G12). LW 1701-16(G4), LW1701-6 (G7) and LW1701-21(G5) were high-yielding and stable. The non-significant heterogeneity between the regressions in this study indicated that the response of the genotypes was not different and therefore the relative performance of maize grain yields cannot be accurately predicted. Genotypes are regarded as being stable based on t of their stability deviation being zero. The following genotypes LW 1701-12(G3), LW 1701-16(G4), LW 1701-21(G5), LW1701-4 (G4), LW1701-6 (G7) and SAMMAZ-23 (G12) were regarded as stable across the test location. LW1701-16 (G4), LW1701-6 (G7) and LW1701-21(G5) combined both high yield and stability, while SAMMAZ-23 had a low yield and was stable. Differences in environments are an important factor and largely determine the usefulness of b_i values (Pfahler and Linskens, 1979). The significance and non-significance of pooled deviation and heterogeneity between regressions in the joint regression indicated the presence of a GE interaction and that the response of genotypes to the maize grain yield was non-linear.

Table 7. Mean yield for genotypes, regression coefficient and stability value of each maize hybrid.

S/N	Genotypes	Mean grain yield/plant (g)	Regression coefficients b_i	Stability
1	OSIELE CHECK	519.4	0.37 ± 0.45	5294.96**
2	LW1701-10	1011.11	1.09± 0.44	4967.40**
3	LW1701-12	744.44	0.82 ± 0.11	-5693.29
4	LW1701-16	822.22	-0.04 ± 0.30	-1342.96
5	LW1701-21	777.78	1.67 ± 0.17$^+$	-4676.53
6	LW1701-4	712.22	1.22 ± 0.25	-2842.68
7	LW1701-6	838.89	1.21 ± 0.10$^+$	-5826.68
8	LW1701-7	751.11	1.48 ± 0.85	35188.75**
9	OBA-SUPER-7	772.22	1.00 ± 0.94	44477.40**
10	OBA-SUPER-9	894.44	0.20 ± 0.50	8001.06**
11	SAMMAZ-22	811.11	1.80 ± 0.91	41573.22**
12	SAMMAZ-23	660.00	1.18 ± 0.19	-4222.68
	Average	776.25	1.00	

$^+$Regression coefficients (b_i), significantly greater than 1.0, the other genotypes have regression coefficients not significantly different from 1.0 or less than 1.0. **Stability, significantly greater than 0.

Further partitioning of the GE interaction into components according to Breese (1969) revealed that the deviation from linearity was larger than the heterogeneity between regressions. The present study on maize clearly demonstrates that it is not reasonable to simply assume that GEI may always be explained by a linear function of the environment. The result of this study is in agreement with the findings of Perkins and Jinks (1968), where the remainder M.S. is significant against the error M.S. This result also aligns with recent findings that report highly significant deviation components for yield-related traits, highlighting the presence of substantial genotype × environment interactions. Such findings underscore the need to assess genotypic stability and adaptability in crop breeding programs (Adu et al., 2019; Ajala et al., 2021). This result is in contrast to the findings of Perkins and Jinks (1968), who showed that there was a significant linear regression which accounted for the entire GEI. This result is also in contrast to the results of Anil et al. (2013) and Khathod et al. (2006), who observed a significant linear and nonlinear response of genotype to environment. In contrast, Breese (1969) found a linear response to yield in the five grass populations studied.

The relative effectiveness of joint regression, AMMI and the GGE biplot in discriminating desirable genotypes is presented in Table 8. AMMI identified four genotypes as desirable, while GGE biplot and joint regression identified three (3) and five (5) genotypes, respectively, as the desirable genotypes. These three techniques identified LW1710-6 as the desirable genotype. AMMI and GGE biplot also agreed on LW1701-10, LW1701-6 and OBA SUPER-9 as high-yielding and stable and therefore the most desirable. In the order of the superiority, the GGE biplot was found to be the most sensitive, while the AMMI was superior to the joint regression. This result is in agreement with the findings of Yan et al. (2007), who observed the superiority of the GGE biplot over the AMMI analysis.

Table 8. Relative effectiveness of AMMI, GGE biplot, and joint regression in discriminating desirable maize genotypes in terms of grain yield.

S/N	AMMI	GGE BIPLOT	Joint regression
1	LW1701-10	LW1701-10	LW1701-6
2	LW1701-21	LW1701-6	LW1701-16
3	OBA SUPER-9	OBA SUPER-9	LW1701-12
4	LW1701-6		LW1701-21
5			LW1701-4

The GGE biplot was found to be more informative in the “which-won-where’’ view, mega-environment evaluation and identification of ideal genotypes and environment than the AMMI model. Yan et al. (2010) suggested that the GGE biplot analysis should be supported by conventional statistical analysis. This is because the GGE biplot use is only justified when either G or G × E in the data is statistically significant and an analysis of variance should be conducted to see if it is worthwhile to perform a GGE biplot analysis. The AMMI analysis combines the analysis of variance and principal component analysis (PCA) into a unified approach (Gauch and Zobel, 1988). Using this tool, larger sum of squares was recorded for the interaction components when compared to the joint regression analysis. A similar result was found by Ariyo and Ayo-Vaughan (2000). This study suggests that the AMMI model has been found superior to regression techniques by being more effective in explaining the GEI. Zobel et al. (1988) reported that AMMI analysis significantly improved the probability of successful selection.

Conclusion

The study revealed significant differences among the twelve maize genotypes, indicating the potential for selecting high-yielding and stable genotypes. The AMMI analysis identified LW1701-10 as the most stable genotype with high yields, while LW1701-16, OBA-SUPER-9, LW1701-6, and SAMMAZ-22 also showed high yield performance but were unstable. A specific genotype adaptation was observed: OBA-SUPER-9 was best suited for the 2022 rainy season, Osiele-1 for the 2022 dry season, and SAMMAZ-22 for the 2021 rainy season. GGE biplot analysis further confirmed LW1701-10 as the highest yielding and most stable genotype, particularly well suited to the 2022 rainy season. Among the testing environments, the 2021 rainy season was identified as the most discriminating, while the 2022 rainy season was the most representative.

References

Adetimirin, V., Vroh-Bi, I., The, C., Menkir, A., Mitchell, S., & Kresovich, S. (2008). Diversity Analysis of Elite Maize Inbred Lines Adapted to West and Central Africa Using SSR Markers. *Maydica, 53*, 143-149.

Adu, G.B., Badru-Apraku, B.A., Akinwale, R., Rowland, O., & Oyekunle, M. (2019). Stability and adaptability of extra-early maturing quality protein maize hybrids under multiple environments in West Africa. *Field Crops Research*, *239,* 107942. https://doi.org/10.1016/j.fcr.2019.107942

Ajala, A. R., Aremu, C.O, Makinde, S.C., & Olakojo, S.A (2021). Stability analysis of okra *(Abelmoschus esculentus L)* genotypes for pod yield and related traits under diverse environments. *Journal of Plant Breeding and Crop Science*, *13* (1), 1-10. https://doi.org/10.5897/JPBCS2020.0924

Anil, C.D., Rahimul, A.M., & Abdul, Khaleque, M. (2013). Joint Regression Analysis of Some Quantitative Characters of F_1 Sugarcane Genotypes. *International Journal of Plant Breeding, 7* (2), 141-144.

Ariyo, O.J., & Ayo-Vaughan M.A. (2000). Analysis of Genotype Environment Interaction of Okra (*Abelmoschus esculentus* L. Moech). *Journal of Genetics and Breeding*, *54*, 35-40.

Breese, E. L. (1969). The measurement and significance of genotype environmental interactions in grasses. *Heredity,* 24, 181-200.

Crossa, J. (1990). Statistical Analyses of Multi-Location Trials. *Advances in Agronomy, 44*, 55-85.

Dias, C., Santos, C., & Mexia, J.T. (2023). Genotype × Environment Interaction: A Comparison between Joint Regression Analysis and the Additive Main and Multiplicative Interaction Model. *WSEAS Transactions on Environment and Development*, *19*, 1476-1485.

FAO (Food and Agriculture Organization of the United Nations) (2023). FAOSTAT Statistical Database; FAO: Rome, Italy.

Farshadfar, E. (2008). Incorporation of AMMI stability value and grain yield in a single non-parametric index (GSI) in bread wheat. *Pakistan Journal of Biological Science, 11*, 1791-1796.

Farshadfar, E. & Sutka, J. (2006). Biplot analysis of genotype-environment interaction in durum wheat using the AMMI model. *Acta Agronomy Hungary, 54*, 459-467.

Gauch, H.G. (1992). *Statistical Analysis of Regional Yield Trials: AMMI Analysis of Factorial Designs*. Elsevier, Amsterdam.

Gauch, H.G., & Zobel. R.W. (1988). Predictive and post-dictive success of statistical analyses of yield trials. *Theoretical and Applied Genetics*, *76*, 1-10.

Gauch, H.G., & Zobel, R.W. (1996). AMMI analyses of yield trials. In: M.S. Kang & H.G. Gauch (Eds.) *Genotype by environment interaction*, (pp. 85-122). CRC, Boca Raton, Florida, USA.

Gauch, H.G., & Zobel, R.W. (1997). Identifying mega-environments and targeting genotypes. *Crop Science, 37*, 311-326.

Jalata, Z. (2011). GGE-biplot Analysis of Multi-Environment Yield Trials of Barley Genotypes in Southeastern Ethiopia Highlands. *International Journal of Plant Breeding and Genetics, 5* (1) 59-75.

Kassaye, B., Asfaw, A., Tadesse, M., & Daba, C. (2024). Genotype-by-environment interaction and yield stability analysis of faba bean (Vicia faba L.) genotypes using GGE biplot and AMMI model. *BMC Plant Biology, 24* (1), 197. https://doi.org/10.1186/s12870-024-05829-4

Kaya, Y., Akcura, M., & Taner, S. (2006). GGE-biplot analysis of multi- environment yield trials in bread wheat. *Turkish Journal of Agriculture and Forestry, 30*, 325-337.

Khathod, R.P., Garkar, R.M., & Pawar, S.M. (2006). Genotype x environment interaction and stability analysis in sugar cane. *Indian sugar, 56* (7), 17-22.

Komolafe, R.J., Ariyo, O.J., & Alake, C.O. (2022). Yield performance and stability analysis of okra (*Abelmoschus esculentus*) accessions using AMMI and GGE biplots. *Journal of Agricultural Sciences (Belgrade), 67* (4), 335-354.

Kusmiyati, N., & Setiawan, B. (2022). Genotype × Environment interaction and yield stability analysis in maize hybrids using AMMI and GGE biplot models. *Agronomy*, *12* (3), 741. https://doi.org/10.3390/agronomy12030741

Messina, C.D., Hammer, G.L., Dong, Z., Podlich, D., & Cooper, M. (2009). Modelling crop improvement in a G*E*M framework via gene- trait – phenotype relationships. In: Sadras V, & Caldeini D, (Eds.), *Crop Physiology: Interfacing with genetic improvement and agronomy.* (pp. 235-265). The Netherlands: Elsevier.

Mohammadi, R., Armion, M., Shabani, A., & Daryaei, A. (2007). Identification of stability and adaptability in advanced durum genotypes using AMMI analysis. *Asian Journal of Plant Science*, *6*, 1261-1268.

Naroui, Rad, M.R., & Bakhshi, B. (2021). GGE biplot tool to identify melon fruit weight stability under different drought conditions.). *International Journal of Vegetable Science, 27*, 220-230.

Ojo, A.A, Ariyo, O.J., Ayo-Vaughan M.A., & Otusanya G.O. (2021). Effect of planting time on yield and related –traits of 24 three –way cross maize (*Zea mays* L.) Hybrids. *Vegetos, 35*, 642-648.

Perkins, J.M., & Jinks, J.L. (1968). Environmental and Genotype-Environmental Components of Variability, III: Multiple Lines and Crosses. *Heredity, 23*, 339-356.

Purchase, J.L., Hatting, H., & Vandeventer, C.S. (2000). Genotype × environment interaction of winter wheat (Triticum aestivum L.) in South Africa: Stability analysis of yield performance. *South African Journal of Plant and Soil*, *17*, 101-107.

Pfahler, P.L., & Linskens, H.F. (1979). Yield stability and population diversity in oats (*Avena sp.*). *Theoretical and Applied Genetics*, *54*, 1-5.

Tekdal, S., & Kendal, E. (2018). AMMI model to assess durum wheat genotypes in multi-environment trials. *Journal of Agricutural Science and Technology, 20*, 153-166.

Yan, W., Hunt, L.A., Sheng, Q., & Szlavnics, Z. (2000). Cultivar evaluation and mega-environment investigation based on the GGE biplot. *Crop Science, 40*, 597-605.

Yan, W. (2001). GGE biplot a windows application for graphical analysis of multi-environment trial data and other types of two-way data. *Agronomy Journal*, *93*, 1111-1118.

Yan, W., Kang, M.S., Ma, B., Woods, S., & Cornelius, P.L. (2007). GGE Biplot vs AMMI Analysis of Genotype by Environment Data, *Crop Science, 47*, 643-655.

Yan, W., & Kang, M.S. (2003). GGE biplot analysis: a graphical tool for breeders, In M. S. Kang (Ed.), *Geneticists and Agronomist,* (pp. 63-88). CRC Press, Boca Raton, FL, USA.

Yan, W., & Tinker, N.A. (2006). Biplot analysis of multi-environment trial data: Principles and applications. *Canadian Journal of Plant Science, 86*, 623-645.

Yan, W., Glover, K.D., & Kang, M.S. (2010). Letter to Editor. *Crop Science, 50*, 1121–1123.

Zobel, R.W., Wright, M.J., & Gauch, Jr, H.G. (1988). Statistical analysis of a yield trial. *Agronomy Journal*, *80* (3), 388-393.

Received: August 3, 2023
Accepted: June 8, 2025

Appendix 1: Means of seven traits for 12 three-way cross maize hybrids across three environments.

Genotype	DYTS (days)	DYSK (days)	PLHT (cm)	EHT (cm)	FDWT (g)	1000-SW (g)	GYLD (g/plant)
OSIELE-1	63.67	65.78	182.43	97.72	0.59	248.27	519.44
LW1701-10	58.11	60.67	169.81	90.14	1.18	316.87	1011.11
LW1701-12	57.11	59.89	189.19	91.68	1.16	315.75	744.4
LW1701-16	59.22	61.56	183.08	87.61	1.03	301.12	822.22
LW1701-21	57.44	60.33	187.31	94.35	1.22	304.84	777.78
LW1701-4	59.00	62.44	187.63	96.13	1.14	292.78	712.22
LW1701-6	59.22	61.67	190.30	94.14	1.19	284.52	838.89
LW1701-7	57.67	62.00	185.16	93.43	1.03	283.83	751.11
OBA SUPER-7	58.72	58.94	192.02	84.29	0.68	303.59	772.22
OBA SUPER-9	56.67	58.56	195.36	97.47	1.11	277.93	894.44
SAMMAZ-22	60.00	61.33	162.80	84.10	0.97	326.48	811.11
SAMMAZ-23	59.17	61.44	165.42	80.56	1.06	301.75	660.00
LSD	2.58	2.58	18.41	9.31	0.31	24.62	74.98

DYST=Days to 50% tasselling, DYSK=Days to 50% silking, PLHT=Plant height. HT=Ear height, FDWT=Field weight, 1000-SWT=1000-seed weight. GYLD=Grain yield/plant.

ADITIVNI GLAVNI EFEKTI I VIŠESTRUKA INTERAKCIJA, GLAVNI EFEKAT GENOTIPA I INTERAKCIJE GENOTIP × SREDINA, ZDRUŽENA REGRESIJA U KVANTIFIKACIJI INTERAKCIJE GENOTIP × SREDINA TROLINIJSKIH HIBRIDA KUKURUZA

Saidat A. Adeniji, Omolayo J. Ariyo i Gbemisola O. Otusanya[*]

Department of Plant Breeding and Seed Technology,
Federal University of Agriculture, Abeokuta, Ogun State, Nigeria

Rezime

Interakcija genotipa i spoljašnje sredine (engl. *genotype by environment – GE*) ima veliki uticaj pri odabiru adaptiranih i superiornih genotipova. Zbog toga je neophodno ocenjivati genotipove kukuruza u različitim okruženjima, sezonama ili lokacijama radi uspešnog odabira. Dvanaest trolinijskih hibrida kukuruza dobijenih iz Međunarodnog instituta za tropsku poljoprivredu (engl. *International Institute of Tropical Agriculture – IITA*) ocenjivano je na oglednom polju Saveznog univerziteta za poljoprivredu u Abeokuti, Nigerija (7°15′ severne geografske širine i 3°25′ istočne geografske dužine) tokom tri vegetacione sezone 2021. i 2022. godine. Ogled je postavljen u tri ponavljanja. Za identifikaciju stabilnih i visokoprinosnih genotipova korišćeni su aditivni glavni efekti i višestruka interakcija (engl. *additive main effect and multiplicative interaction – AMMI*), glavni efekat genotipa i interakcije genotip × spoljašnja sredina (engl. *genotype and genotype environment interaction*), združena regresija. Analiza AMMI je pokazala da je ukupna varijansa u prinosu trolinijskih hibrida kukuruza bila raspodeljena na genotip, sredinu i interakciju genotip × sredina sa udelima od 30,6%, 44,19% odnosno 25,31%. Na osnovu AMMI analize, genotipovi LW1701-10 i OBA SUPER-9, koji su kombinovali visok prinos sa stabilnošću, bili su najpoželjniji. GGE biplot analiza je pokazala da su hibridi LW1701-10, OBA SUPER-9 i LW1701-6 najstabilniji i najpoželjniji genotipovi. Združena regresija je pokazala da se učinak genotipova ne može prikazati na linearan način, jer je varijansa komponente odstupanja iznosila 81,05% i identifikovala je LW1701-6, LW1701-16, LW1701-12, LW1701-21, i LW1701-4 kao stabilne i poželjne. Studija je pokazala da su modeli GGE i AMMI bili efikasniji od združene regresije u ispitivanju stabilnosti prinosa hibrida kukuruza. Studija se bavi poređenjem modela AMMI, GGE i združene regresije.

Ključne reči: interakcija genotip × sredina, stabilnost, AMMI, GGE biplot analiza, združena regresija.

Primljeno: 3. avgusta 2023.
Odobreno: 8. juna 2025.

---

[*] Autor za kontakt: e-mail: igegbemi@gmail.com