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RESEARCH PAPER

Analysis of genotype environment interaction and yield stability of elite maize hybrids using integrated parametric and non-parametric biometric approaches

Aditya Pratap Singh • Dinesha M. Chiplonker • Vijay Bhan Singh • Saurabh Rathi

Abstract: Maize (*Zea mays* L.), ubiquitously known as the "Queen of Cereals" due to its exceptional genetic yield potential, stands as a pillar of global food security and the industrial bio-economy. However, achieving consistent genetic gain is inherently challenged by the Genotype Environment (G×E) interaction, which complicates the selection of broadly adapted and stable hybrids for cultivation across diverse agro-climatic zones. Stability and adaptability of thirteen elite maize hybrids were evaluated across six distinct environments which are representative of major *Kharif* maize growing regions. The combined ANOVA revealed highly significant effects ($P < 0.001$) for genotype (G) and environment (E), whereas the genotype × environment (G×E) interaction was comparatively small and statistically non-significant ($P = 0.36$), although multivariate analyses were subsequently used to explore genotype response patterns across environments. Environment Aurangabad (AUR) recorded the highest mean yield (11.66 t/ha), while VRN recorded the lowest (5.42 t/ha), indicating strong environmental influence. The first two AMMI interaction principal component axes (IPCA1 and IPCA2) together explained 79.2% of the G×E interaction sum of squares. GGE biplot analysis suggested the presence of distinct environmental sectors, indicating differential genotype adaptation across the test locations. Crucially, the multi-trait stability index (MTSI) identified VMAH 236 as the most desirable hybrid, combining high mean grain yield with broad stability, positioning it as a promising candidate for advanced multi-location evaluation and possible commercial release. GAJA 031 and VMAH 322 emerged as the subsequent stability leaders. These findings provide an empirical basis for stratified maize breeding and targeted hybrid deployment in the face of climatic variability.

Keywords: Maize • Mega-environment • Multi trait stability index • Stability • Yield

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Introduction

Maize (*Zea mays* L.) is globally significant, serving as a vital source of human food, livestock feed, and industrial raw material. Its global production consistently ranks highest among cereals, reflecting its paramount role in agricultural economies worldwide (Shrestha *et al.*, 2024; Sleper and Pohler, 2024). The relentless pursuit of higher and more consistent yields is fundamental to maize breeding programs, driven by escalating population growth and the pervasive threats of climate change (Ma *et al.*, 2024). Breeding efforts, while successful in increasing the genetic yield potential, face an inherent, complex challenge: the Genotype Environment (G×E) interaction (Van Eeuwijk *et al.,* 2024). This interaction refers to the differential ranking or magnitude of genotypic performance across varying environmental conditions, making the selection of superior, widely-adapted genotypes a probabilistic and intricate process (Eeuwijk *et al.,* 2023; Kambiranda *et al.,* 2024).

Therefore, a successful breeding strategy must move beyond simply selecting the highest mean yielding genotype and instead focus on hybrids that exhibit yield stability,

defined as consistent performance across a range of environments, or specific adaptability to defined mega-environments (Tadesse *et al.*, 2023; Olivoto *et al.*, 2023).

Historically, stability analysis relied on univariate parametric methods like the Eberhart and Russell (1966) model, which defines stability based on the regression coefficient and the deviation from regression. A genotype with a regression coefficient (bi≈1) and non-significant deviation from regression ($S^2di\approx0$) is considered broadly adapted (Eberhart and Russell, 1966; Balakrishnan *et al.*, 2024). However, these methods only partially explain the G×E component, allowing for simultaneous visualization of genotypic mean performance, stability, and the delineation of mega-environments (Yan and Kang, 2020; Yan *et al.*, 2023). More recently, sophisticated metrics have emerged to address the limitations of single-parameter stability indices (Olivoto and Nardino, 2020). The WAASB index, derived from AMMI analysis, provides a highly accurate measure of stability by incorporating all significant IPCA scores (Olivoto *et al.*, 2023; Oladosu *et al.*, 2021). Critically, a key challenge remains: integrating the various stability and performance traits into a single, comprehensive selection index (Yan and Kang, 2020). To overcome this, the multi-trait stability index (MTSI) offers a powerful solution by combining selection pressure across multiple traits and stability indices, facilitating the identification of hybrids that simultaneously maximize yield, minimize environmental responsiveness, and maintain high performance across key secondary traits (Olivoto *et al.*, 2023; Abhinandan *et al.*, 2024).

The present study was undertaken to comprehensively analyze G×E interaction and yield stability in a set of elite maize hybrids using an integrated framework of parametric and non-parametric biometric approaches, with the goal of generating actionable recommendations for hybrid deployment across diverse Indian agro-ecologies.

Materials and methods

Experimental sites and environmental characterization

The multi-environment trial (MET) comprised six testing environments across central and eastern India, representing diverse agro-climatic zones with significant variation in soil characteristics and rainfall patterns (Vannozzi *et al.*, 2023).

1. *Aurangabad (AUR), Maharashtra:* Characterized by Vertisols (Black Cotton Soil), this site typically experiences moderate to high rainfall but can face intermittent dry spells. The soil's high clay content influences water holding capacity, often leading to high yield potential under adequate moisture (Rai *et al.*, 2023).
2. *Raipur (RPR), Chhattisgarh:* Located in the Chhattisgarh Plains, this region has Alfisols/ Inceptisols. It is generally high-yielding with moderate heritability, benefiting from consistent *Kharif* rainfall, positioning it as a highly favorable environment for maize production.
3. *Dhamnod (DMD), Madhya Pradesh:* Situated in the Malwa Plateau, the soil is primarily Black Cotton Soil. This environment is generally favorable and high-yielding, similar to AUR, but often shows higher vulnerability to minor moisture stress, resulting in high environmental variance (Shrestha *et al.*, 2024).
4. *Jagdalpur (JDP), Chhattisgarh:* Located in the Bastar Plateau, this environment is characterized by acidic, nutrient-poor Oxisols/Ultisols and heavy, high-intensity rainfall. This often presents constraints related to soil fertility and waterlogging stress, making it a marginal environment.
5. *Chittorgarh (CHI), Rajasthan:* Representing the semi-arid western region, this location is characterized by light-textured Aridisols/Entisols and a higher risk of terminal drought and heat stress, leading to low mean yields and high variability.
6. *Varanasi (VRN), Uttar Pradesh:* Located in the Upper Gangetic Plains, this environment often exhibits highly unpredictable conditions, including periods of waterlogging and mid-season drought.

Experimental design and agronomic management

The thirteen maize hybrids (including checks) were evaluated in a randomized complete block design (RCBD) with two replications at each of the six environments (Table 1). The sowing was done at the onset of monsoon and sowing at all the locations were completed within June, 2025. The total number of experimental plots was 26 at each location. Each plot consisted of four rows of 5.0 meters length, with an inter-row spacing of 75 cm and an inter-plant spacing of 25 cm (Setiyono *et al.*, 2022). Standard agronomic practices were uniformly

Table 1. List of hybrids tested for stability and other statistical parameters

Hybrid	Remarks
VMAH 291	Pre-commercial / Trial stage
VMAH 303	Pre-commercial / Trial stage
VMAH 313	Pre-commercial / Trial stage
VMAH 394	Pre-commercial / Trial stage
VMAH 158	Pre-commercial / Trial stage
VMAH 236	Pre-commercial / Trial stage
VMAH 248	Pre-commercial / Trial stage
VMAH 249	Pre-commercial / Trial stage
VMAH 322	Pre-commercial / Trial stage
VMAH 083	Pre-commercial / Trial stage
VMAH 256	Non-commercial internal check
VMAH 002	Pre-commercial / Trial stage
GAJA 031	Commercial Check (year of commercialization- 2025)

applied across all locations (Rai *et al.*, 2023). This included a balanced dose of Nitrogen (N), Phosphorus (P), and Potassium (K) fertilizer, typically in the ratio of kg/ha, applied in split doses as per local recommendations (Balakrishnan *et al.*, 2024). Irrigation was provided only as supplemental to the natural rainfall, following local best practices for *kharif* maize cultivation.

Data recording

The primary trait recorded was grain yield, recorded from the central harvest area of each plot, adjusted to a standard moisture content of 15% (Tadesse *et al.*, 2023) and converted to tonnes/ha (designated as GYDTH). Additionally, plant height (average total height of 10 plants), ear height (average ear height from ground of 10 plants), final plant population (at harvest), number of ears harvested per plot and shelling percentage were recorded.

Statistical analysis

All statistical analyses were conducted using the R statistical computing environment (version 4.3.2) and the metan package (version 1.22.0) (Olivoto and Nardino, 2020).

Combined analysis of variance (ANOVA)

Environment was treated as a fixed effect, whereas genotype, replication within environment, and genotype × environment interaction were modeled according to the analytical framework implemented in the metan package. The heritability for yield was estimated for each environment and across environments.

AMMI and GGE biplot analysis

The AMMI model was used to partition the G×E variance. The GGE biplot analysis was employed using the singular value decomposition (SVD) of the centered and standardized data matrix containing only the G and G×E components (Yan, 2021). The biplot functions were used to visualize the which-won-where pattern to identify mega-environments; assess the discriminating ability and representativeness of the test environments and to evaluate the mean performance & stability of the hybrids graphically.

Stability and Multi-trait stability index (MTSI)

Eberhart and Russell Regression (Eberhart and Russell, 1966) and weighted average of absolute scores (WAASB) were computed. (Eeuwijk *et al.*, 2023; Olivoto *et al.*, 2023). The multi-trait stability index (MTSI) was computed to simultaneously select hybrids based on both high mean yield and high stability (low WAASB). This index uses factor analysis and a selection differential approach to rank genotypes across multiple desirable traits (Olivoto and Nardino, 2020). Genotypes with lower MTSI scores are closer to the ideal stability-performance combination (Abhinandan *et al.*, 2024). For this study, the target traits included grain yield (GYDTH), plant height, ear height, final plant population, number of ears harvested, shelling percentage, and WAASB, with the desired ideotype defined as high grain yield, improved agronomic performance, and high stability.

Table 2. Descriptive statistics across environments. RPR- Raipur, CHI- Chittorgarh, DMD- Dhamnod, JDP- Jagdalpur, VRN- Varanasi, AUR- Aurangabad

Environment (Location)	Mean yield of genotypes	CV	h^2
Raipur (RPR)	10.50	7.46	0.60
Chittorgarh (CHI)	6.40	17.32	0.36
Dhamnod (DMD)	10.74	11.83	0.03
Jagdalpur (JDP)	9.32	16.19	0.19
Varanasi (VRN)	5.42	34.34	0.18
Aurangabad (AUR)	11.66	10.84	0.59

Table 3. Individual ANOVA for GYDTH

Source	df	Sum square	Mean square	F value	Pr(>F)	Proportion of variance explained	Cumulative proportion of variance explained
ENV	5	833.86	166.77	6.94	0.0177	–	–
REP(ENV)	6	144.21	24.03	13.75	<0.0001	–	–
GEN	12	57.10	4.76	2.72	0.0043	–	–
GEN × ENV	60	113.88	1.90	1.09	0.3670	–	–
IPCA1	16	50.19	3.14	1.79	0.0494	44.1	44.1
IPCA2	14	39.98	2.86	1.63	0.0916	35.1	79.2
IPCA3	12	15.06	1.26	0.72	0.7270	13.2	92.4
IPCA4	10	6.13	0.61	0.35	0.9630	5.4	97.8
IPCA5	8	2.52	0.32	0.18	0.9930	2.2	100.0
Residuals	72	125.87	1.75	–	–	–	–
Total	215	1388.80	6.46	–	–		

Table 4. Pooled ANOVA for GYDTH

Source	df	Sum square	Mean square	F value	Pr(>F)
ENV	5	833.85	166.7	6.9388	0.01765
REP(ENV)	6	144.2	24.0	13.7480	0.00000
GEN	12	57.1	2.50	2.5071	0.009693
GEN:ENV	60	113.8	1.08	1.0857	0.367203
Residuals	54	947.7	8.34	8.3403	
CV(%)	14.67		10.56		
MSR+/MSR-	6.14				
Overall mean	9.01				

Results

Analysis of variance (ANOVA) and environmental effects

The combined ANOVA results revealed that environment and genotype effects were significant, whereas the genotype × environment interaction was not statistically significant (P = 0.367), although AMMI and GGE analyses were performed to explore patterns of genotype response (Table 3 & 4). The magnitude of the Environmental SS was overwhelmingly the largest, accounting for approximately 60.0% of the total SS, which shows the profound influence of diverse environmental conditions on maize grain yield (Tadesse *et al.*, 2023). Although the G×E interaction was not statistically significant, decomposition of the interaction matrix through AMMI and GGE analyses facilitated visualization of genotype responses across environments (Van Eeuwijk *et al.*, 2024).

The mean grain yield varied markedly across the six environments. Aurangabad (AUR) recorded the highest mean yield (11.66 t/ha), followed closely by Dhamnod (DMD) at 10.74 t/ha, indicating these locations served as the most favorable, high-input potential environments (Setiyono *et al.*, 2022). Conversely, Varanasi (VRN) recorded the lowest mean yield (5.42 t/ha) and the highest coefficient of variation (CV), confirming its role as the most stressful and low-yielding environment, likely due to a combination of water stress and high temperature. Heritability estimates varied substantially among environments, ranging from a critically low 0.03 in DMD to moderate 0.60 in RPR and 0.59 in AUR (Table 2). The low heritability in DMD, despite high mean yield, suggests that observed phenotypic differences were largely environmental, while the higher values in RPR and AUR indicated a greater potential for selection and genetic advancement within these environments (Ma *et al.*, 2024).

AMMI and GGE biplot

The AMMI analysis indicated that the first two interaction principal component axes (IPCA1 and IPCA2) together explained 79.2% of the genotype × environment interaction variation, with IPCA1 accounting for 44.1% and IPCA2 for 35.1%, providing an adequate summary of the interaction pattern for graphical interpretation (Figure 1). This high percentage suggests that the multiplicative effects were largely accounted for by the first two axes, providing a robust fit for the AMMI model and allowing

for effective visualization and interpretation using biplots (Gauch *et al.*, 2024).

The GGE Biplot analysis, which focused on the variance, corroborated the AMMI findings. The polygon (which-won-where) view suggested the existence of distinct environmental sectors, indicating differential genotype adaptation across the evaluated environments (Yan and Kang, 2020).

1. *Mega-environment 1 (High potential/broadly favorable):* Comprising AUR, RPR, and DMD. This group represents the higher-yielding, less stressful environments where genetic potential is more fully expressed.
2. *Mega-environment 2 (Low-moderate potential/ Moderate Stress):* Represented by JDP and CHI. These sites exhibit moderate yield reductions, likely due to soil acidity/waterlogging (JDP) and heat/moisture stress (CHI).
3. *Mega-environment 3 (High stress/low potential):* Singularly represented by VRN. This environment had the lowest mean yield and served as the highest stress environment, confirming its unique environmental challenges (Rai *et al.*, 2023).

Hybrid, VMAH 256 was positioned at the vertex of the polygon encompassing Mega-Environment 1, indicating its specific adaptation and high performance under the most favorable conditions (AUR and RPR). Hybrid GAJA 031 was associated with the polygon vertex corresponding to the Mega-Environment 2 group, suggesting its superior performance under moderate-stress conditions (Oladosu *et al.*, 2021). Hybrid VMAH 322 exhibited relatively small interaction effects together with above-average grain yield, indicating broad adaptation across the test environments (Yan *et al.,* 2023).

Parametric and non-parametric stability indices

The Eberhart and Russell regression analysis provided insight into the responsiveness and predictability of the hybrids. The environment mean index clearly separated the environments, with AUR and DMD having the highest positive indices, confirming their superior potential (Table 5). The hybrid, VMAH 256 exhibited a regression coefficient significantly greater than unity, suggesting that it was highly responsive hybrid ideally suited for high-input, non-stress environments where it can maximize yield (Shrestha *et al.*, 2024). Its deviation from regression was high (S^2_{di}= 0.33), indicating significant instability.

The hybrids, VMAH 322 and VMAH 303 showed regression coefficients approximating unity and low, with non-significant deviations from regression. This combination signifies highly predictable performance and broad adaptation across the tested environments (Eberhart and Russell, 1966).

Whereas, hybrid VMAH 158 had a very low coefficient (b_i= 0.68), indicating unresponsiveness to environmental improvement, making it a reliable performer in low-input or marginal areas (Balakrishnan *et al.*, 2024).

Table 5. Regression based (Eberhart and Russel model) stability parameters

GEN	b_0	b_1	t(b_1=1)	$p_{val\ t}$	s^2di	F(s^2di=0)	$p_{val\ f}$	RMSE	R^2
VMAH 291	8.82	1.14	0.82	0.41	0.33	1.38	0.25	0.90	0.90
VMAH 303	8.94	1.00	-0.02	0.98	0.91	2.04	0.10	1.09	0.82
VMAH 313	9.04	1.05	0.32	0.75	-0.44	0.50	0.74	0.54	0.95
VMAH 394	8.63	0.97	-0.18	0.86	-0.65	0.26	0.90	0.39	0.97
VMAH 158	8.90	0.68	-1.96	0.05	-0.26	0.70	0.60	0.64	0.86
VMAH 236	9.06	0.90	-0.62	0.54	-0.75	0.14	0.97	0.29	0.98
VMAH 248	8.93	1.13	0.77	0.45	0.47	1.54	0.20	0.95	0.88
VMAH 249	8.29	0.99	-0.08	0.94	0.24	1.28	0.29	0.86	0.88
VMAH 322	10.21	1.02	0.11	0.91	1.04	2.19	0.08	1.13	0.81
VMAH 083	8.63	1.03	0.18	0.86	-0.30	0.66	0.62	0.62	0.94
VMAH 256	10.13	1.41	2.47	0.02	0.33	1.38	0.25	0.90	0.93
VMAH 002	8.05	0.91	-0.53	0.60	-0.68	0.22	0.93	0.36	0.97
GAJA 031	9.52	0.79	-1.28	0.20	-0.36	0.59	0.67	0.59	0.91

AMMI analysis

Analysis of the AMMI1 biplot (Figure 1), where genotype mean grain yield was plotted against IPCA1 scores accounting for 44.1% of the interaction variation, identified AUR as the highest-yielding environment and VRN as the lowest-yielding environment. Genotype VMAH 256 achieved the highest mean yield overall but showed significant vertical distance from the horizontal origin line, reflecting high responsiveness to favorable environments like AUR, DMD, and RPR. Genotype VMAH 313 demonstrated maximum stability with near-average yield.

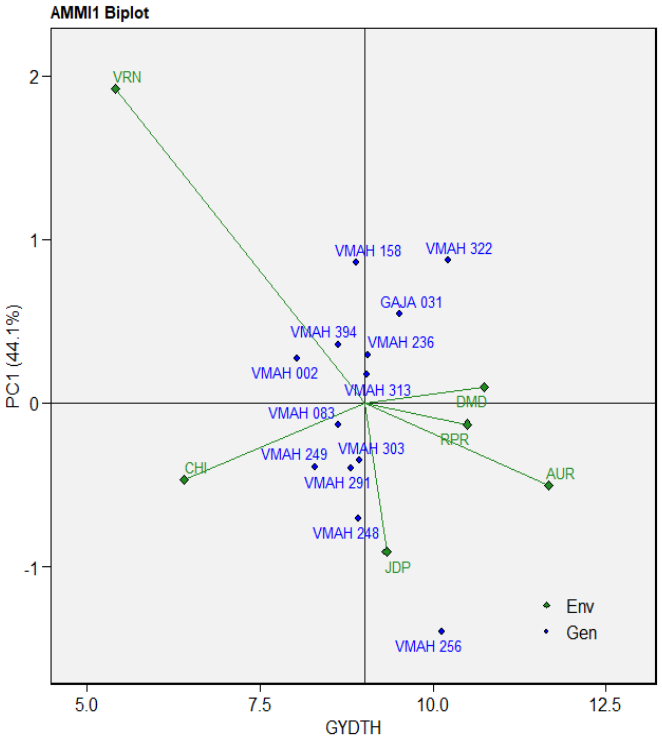


Figure 1. AMMI1 biplot showing genotype mean grain yield (GYDTH) versus IPCA1 scores

The AMMI2 biplot displays IPCA1 (44.1%) against IPCA2 (35.1%), jointly explaining 79.2% of the genotype × environment interaction variation (Figure 2). Strong specific positive interactions were observed between environment VRN and genotypes VMAH 322 and VMAH 158. Additionally, environments AUR and CHI showed specific adaptation with genotype VMAH 303. Genotypes VMAH 236 and VMAH 313 sit closest to the biplot origin, confirming minimal interaction and high overall stability.

The GGE biplot for discriminativeness versus representativeness (PC1, 38.7%; PC2, 29.21%) identifies

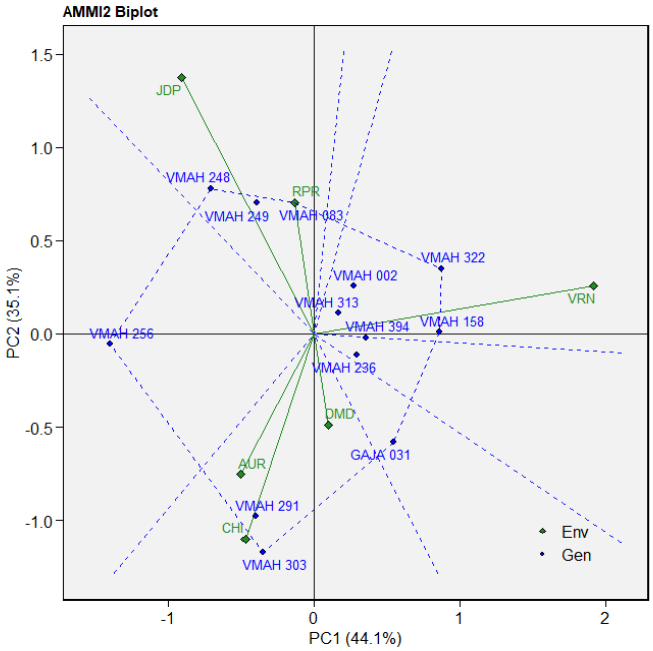


Figure 2. AMMI2 biplot showing IPCA1 versus IPCA2 scores for genotypes and environments

AUR as the most ideal test environment, featuring a long vector (high discriminating ability) and a very small angle with the average environment axis (AEA), indicating high representativeness of the target mega-environment. DMD also serves as a strong, representative test site. Conversely, VRN and JDP possess large angles from the AEA, rendering them unrepresentative of the overall trial conditions, though VRN's long vector makes it useful for culling unstable genotypes (Figure 3 and 4).

The mean vs. stability plot positions genotypes along the AEA (representing mean yield, PC1) and the axis perpendicular to it (representing stability, PC2). Genotype VMAH 313 was positioned close to the average environment axis (AEA), indicating relatively high stability with near-average grain yield. While genotypes VMAH 322, GAJA 031, and VMAH 256 project further along the positive PC1 axis indicating higher mean yields, VMAH 256 exhibits significant deviation from the AEA (high PC2), highlighting genotype-specific vulnerabilities and instability. Genotype VMAH 158 falls into a low-mean, unstable zone (Figure 5).

Environment ranking identifies AUR and DMD as the top-ranked environments, plotting closest to the ideal environment point represented by the concentric circles on the AEA. This confirms their status as the most effective locations for evaluating and selecting superior genotypes. JDP and VRN rank the lowest due to extreme

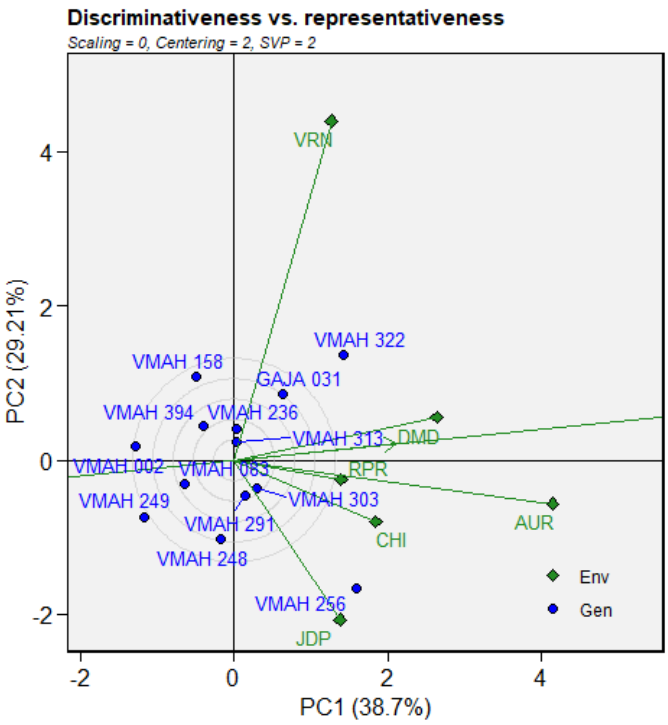


Figure 3. Discriminativeness vs. Representativeness (GGE Biplot)

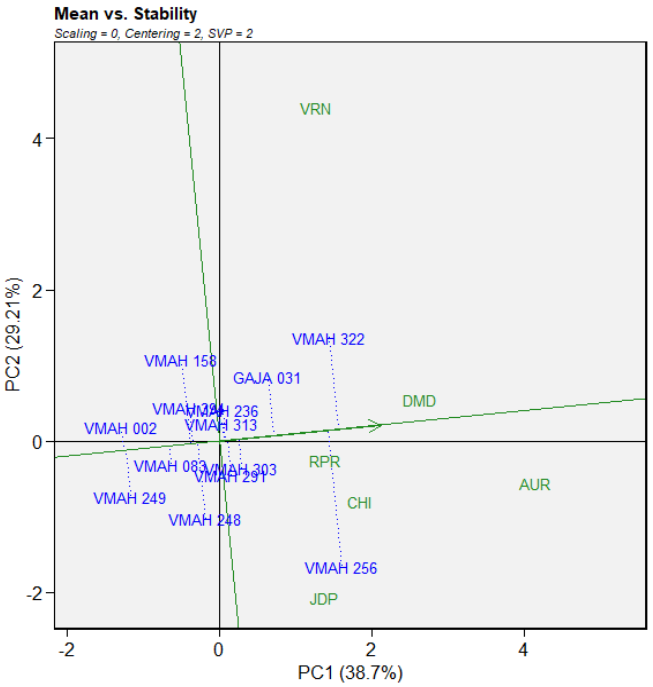


Figure 5. Mean performance versus stability view of the GGE biplot based on the average environment coordination (AEC)

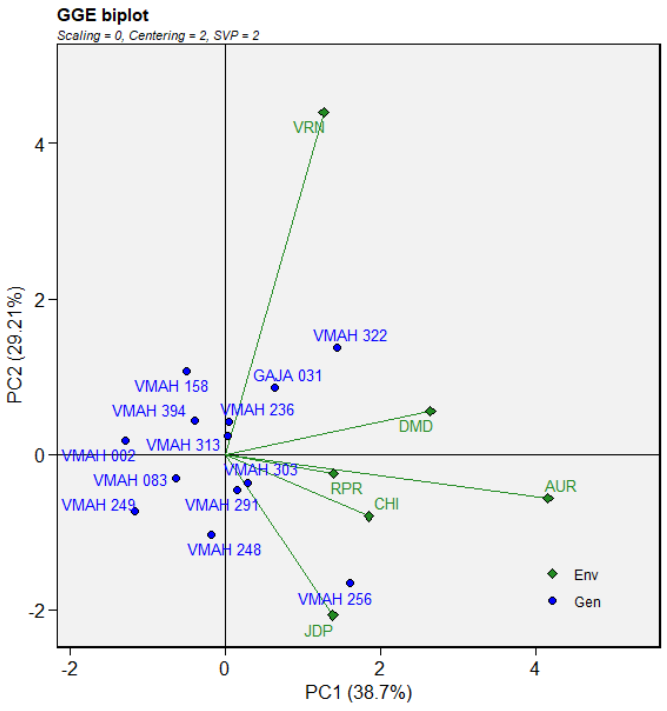


Figure 4. GGE biplot showing the average environment coordination (AEC) view

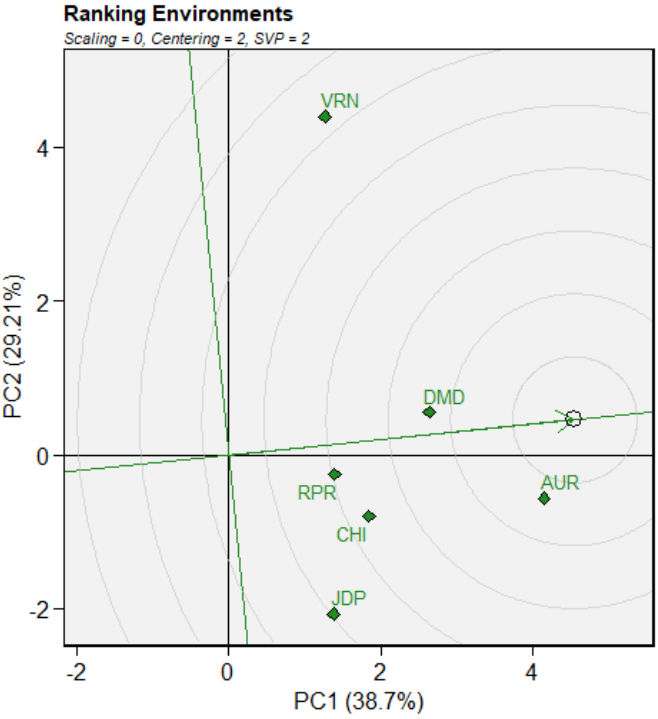


Figure 6. Ranking Environments

deviation from the ideal center, signaling poor overall representativeness for broad selection purposes (Figure 6).

Correspondingly, among the evaluated hybrids, VMAH313 was located closest to the ideal genotype position, indicating the most desirable combination of mean performance and stability. VMAH 322, GAJA 031, and VMAH 303 follow in subsequent concentric rings, while VMAH 256 and VMAH 158 are penalized heavily for their deviation (instability) despite their varied yield

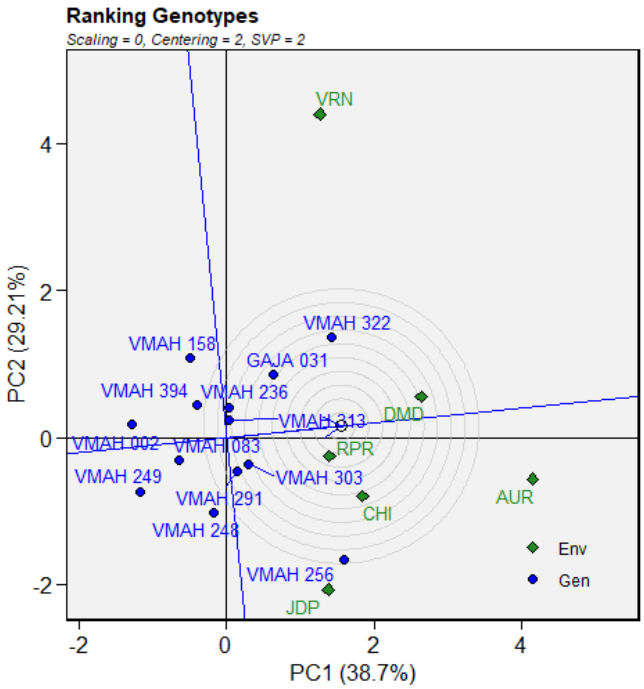


Figure 7. Ranking Genotypes

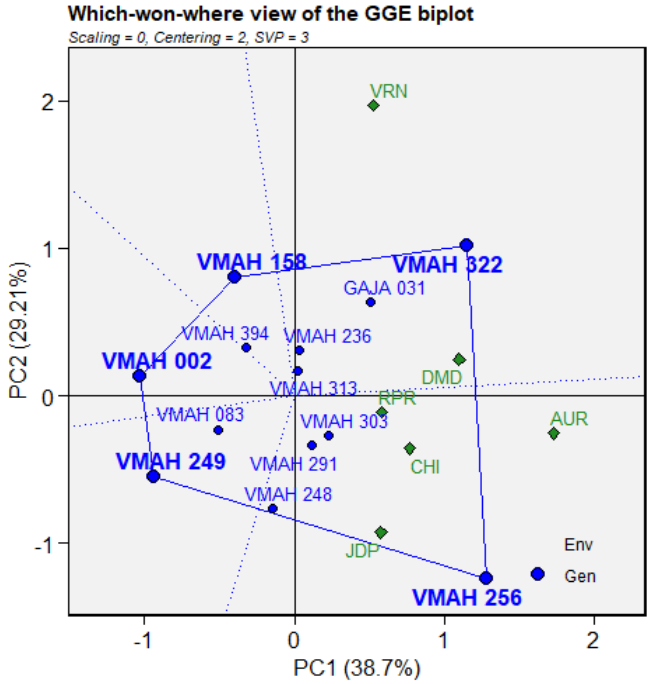


Figure 8. Which-won-where view of the GGE biplot

potentials (Figure 7). Finally, the which-won-where polygon visualization partitions the biplot into distinct sectors representing differential genotype adaptation across the evaluated environments.

This guides targeted selection by enabling precise hybrid recommendations based on regional dominance, maximizing yield gains in specific environmental belts during final release decisions (Figure 8).

Multi-trait stability index (MTSI) selection

The Multi-Trait Stability Index (MTSI) was utilized for simultaneous selection, integrating high grain yield (GYDTH), desirable agronomic performance (including lower plant and ear heights, alongside higher standability, ear number, field weight, and shelling percentage), and high cross-environment stability (low WAASB). The selection differential was applied to maximize beneficial traits, minimize undesirable traits, and minimize instability indices. The final ranking based on the MTSI score identified the optimal selection candidates (Table 6).

The hybrid VMAH 236 achieved Rank 1 with the lowest MTSI score (0.45), demonstrating the optimal overall combination of ideal mean multi-trait performance and supreme stability. GAJA 031 followed at Rank 2 (MTSI = 1.50), confirming strong trait balance and cross-environment stability. Hybrid VMAH 083 earned Rank 3 (MTSI = 1.68), presenting a high-yielding, broadly adapted selection candidate. VMAH 322 secured Rank 4 (MTSI = 1.78), rounding out the top-performing group. In contrast to the lowest-ranking hybrids such as VMAH 249 (MTSI = 4.52), these top four candidates exhibit the most favorable balance of yield, agronomic traits, and stability across the tested environments (Table 6).

Discussion

Significance of G×E interaction and environmental effects

The significant effects observed for genotype (G) and environment (E), together with the non-significant

Table 6. Multi-trait stability Index

Genotype	Multi-Trait Stability Index
VMAH 236	0.45
GAJA 031	1.50
VMAH 083	1.68
VMAH 322	1.78
VMAH 256	1.81
VMAH 291	2.36
VMAH 394	2.40
VMAH 158	2.63
VMAH 248	2.87
VMAH 303	3.02
VMAH 002	3.18
VMAH 313	3.82
VMAH 249	4.52

genotype × environment (G×E) interaction, indicate that environmental differences had a much greater influence on grain yield than differential genotype responses across environments. Nevertheless, exploratory multivariate analyses (AMMI and GGE biplots) were useful for visualizing genotype adaptation patterns and identifying stable hybrids (Van Eeuwijk *et al.*, 2024; Rameez *et al.*, 2023). The magnitude of the error sum of squares (ESS), accounting for approximately 9.1% of the total variation, confirms that environmental heterogeneity is the primary driver of phenotypic variance, an observation consistently reported in multi-environment trials (METs) across diverse agro-climatic zones (Tadesse *et al.*, 2023; Wang *et al.*, 2023). The extreme range in mean grain yield, from 11.66 t/ha at Aurangabad (AUR) to 5.42 t/ha at Varanasi (VRN), starkly illustrates the differential influence of non-controllable factors such as soil type, rainfall, and temperature (Setiyono *et al.*, 2022; Jaiswal and Kumar, 2023).

Although the G×E interaction sum of squares was not statistically significant, partitioning the interaction using AMMI and GGE analyses provided useful graphical insight into genotype adaptation and environmental relationships (Piepho *et al.*, 2024; Yan, 2021). Environments like AUR and Raipur (RPR), which exhibited high mean yields and moderate to high heritability estimates (0.589 and 0.596, respectively), are valuable as discriminating environments where genetic differences are reliably expressed, making them optimal for primary yield selection (Ma *et al.*, 2024; Setiyono *et al.*, 2022). Conversely, the critically low heritability observed in Dhamnod (DMD) (0.032), despite its high mean yield, suggests that selection based on simple phenotypic mean in such environments would be highly unreliable due to overwhelming environmental noise (Shrestha *et al.*, 2024). Furthermore, the low yield and high coefficient of variation (CV = 34.33%) in VRN confirm its status as a high-stress, low-potential mega-environment, likely characterized by combined stresses such as waterlogging and heat during critical reproductive phases (Rai *et al.*, 2023; Vannozzi *et al.*, 2023). These environmental characterizations are crucial for defining targeted breeding strategies (Moges *et al.,* 2022).

Dissection of G×E via AMMI and GGE biplot models

The application of the additive main effects and multiplicative interaction (AMMI) model proved effective, with the first two interaction principal component axes (IPCA1 and IPCA2) cumulatively explaining 79.2% of the G×E sum of squares. The first two IPCAs adequately summarized the observed interaction pattern (Gauch *et al.*, 2024; Gauch, 2022). Highlighting the first two IPCA axes is essential for capturing the biological reality of differential hybrid responses (Hailu *et al.*, 2021).

The genotype and genotype-by-environment (GGE) biplot analysis provided crucial visual and interpretive context for hybrid deployment and suggested three putative mega-environments. The clustering of AUR, RPR, and DMD into a single high-potential mega-environment, contrasting sharply with the marginal stress zone of Varanasi (VRN), provides clear guidance for selection and resource allocation (Yan and Kang, 2020; Yan *et al.*, 2023). The 'Which-Won-Where' pattern suggested hybrid VMAH 256 as the specifically adapted "winner" in the favorable mega-environment (AUR/RPR), reinforcing the need to select responsive genotypes for high-input agricultural systems (Sleper and Pohler, 2024; Ali *et al.*, 2022). In contrast, hybrids positioned near the biplot origin, such as VMAH 322, are considered stable and broadly adapted (Amira and Abo El-Khair, 2021; Moges *et al.*, 2022). This delineation underscores the importance of multivariate visualization techniques over univariate means for complex MET data (Yan, 2021).

Integration of stability metrics

A comprehensive assessment of stability requires integrating multiple biometric approaches (Eeuwijk *et al.*, 2023). The traditional Eberhart and Russell regression analysis effectively quantified the responsiveness and predictability of the hybrids (Eberhart and Russell, 1966). Hybrid VMAH 256 exhibited a regression coefficient significantly greater than unity (> 1.0), confirming its classification as a highly responsive genotype with specific adaptation to optimal environments, maximizing returns on favorable inputs (Shrestha *et al.*, 2024). Conversely, VMAH 236 displayed a coefficient less than unity and a low deviation from regression, characterizing it as a stable, unreactive hybrid ideally suited for low-input or marginal conditions where risk aversion is paramount (Balakrishnan *et al.*, 2024; Dehnavi and Akbari, 2023). VMAH 322 registered a b_i value approximating unity, coupled with low deviation, establishing it as a highly predictable,

broadly adapted candidate (Tadesse *et al.*, 2023; Hassanein and Al-Tawaf, 2024).

The WAASB, a modern non-parametric index derived from AMMI, provided a consolidated, robust measure of static stability by incorporating all significant IPCA effects (Olivoto *et al.*, 2023; Oliveira *et al.*, 2023). The lowest WAASB score recorded by VMAH 236 validated its superior stability, independently confirming the regression findings and its suitability as a choice for unfavorable environments (Oladosu *et al.*, 2021; Wolde and Dagne, 2022). The WAASB index offers a key advantage over simple deviation from regression as it considers all axes of interaction variance, leading to a more accurate representation of genotypic stability (Dhakal *et al.*, 2024).

Multi-trait stability index (MTSI) and selection strategy

The ultimate objective of breeding is the simultaneous selection for multiple desirable traits, specifically high yield and enhanced stability (Yan and Kang, 2020; Bhandari *et al.*, 2022). The MTSI, successfully addressed this challenge by integrating mean yield (maximization target) and stability indices (WAASB, minimization targets) into a single objective ranking criterion (Olivoto and Nardino, 2020; Olivoto *et al.*, 2023). This integrated approach is crucial, as relying solely on yield or a single stability parameter can lead to the selection of unstable high-yielders or low-yield, overly stable genotypes, compromising overall genetic gain (Yan *et al.*, 2023; Sharma and Singh, 2023).

The MTSI suggested VMAH 236 as the premier candidate (Rank 1) (Table 6), achieving an optimal balance between mean productivity and minimal performance variation across environments (Abhinandan *et al.*, 2024; Tarekegne and Mengistu, 2023). GAJA 031 (Rank 2) and VMAH 083 (Rank 3) were identified as secondary selections, confirming their broad adaptability across the tested agro-ecologies (Girma *et al.*, 2023).

Although VMAH 256 demonstrated high yield potential in favorable environments like AUR, its lower MTSI rank (Rank 5) highlights significant stability penalties, justifying its recommendation specifically for high-input, responsive zones rather than broad commercial release. Previous workers have also discussed their selection strategy similarly (Rai *et al.*, 2023; Kambiranda *et al.*, 2024; Singh and Kumar, 2024; Attia *et al.*, 2022).

Future perspectives and limitations

While this study provides robust empirical evidence based on advanced statistical modeling, an inherent limitation is the lack of detailed physiological and molecular characterization (Crossa *et al.*, 2021; Zhu *et al.*, 2024). Future efforts must focus on validating these MTSI-based recommendations by integrating high-throughput phenotyping data and linking the performance of VMAH 322 and VMAH 236 to specific molecular markers or quantitative trait loci (QTLs) for stability (Perez-Rodríguez *et al.*, 2024). The integration of these findings with genomic selection (GS) models, especially those that explicitly account for G×E effects, will be instrumental in accelerating the selection cycle and enhancing the predictive accuracy for grain yield stability (Van Eeuwijk *et al.*, 2024; Farahani and Arshad, 2021). The strategic deployment of hybrids based on these MTSI findings represents a necessary and highly effective approach toward mitigating the adverse effects of climatic variability and achieving sustained genetic gain in maize production (Piepho *et al.*, 2024; Memon and Bakhsh, 2021).

Conclusion

The present study demonstrated significant genotype and environmental effects on maize grain yield, whereas the genotype × environment interaction was not statistically significant in the combined ANOVA. Nevertheless, AMMI, GGE biplot, Eberhart–Russell regression, WAASB, and MTSI analyses provided valuable complementary information for identifying stable and high-performing hybrids across environments. Hybrid VMAH 236 was suggested by the MTSI as the top candidate (Rank 1) for advanced multilocation testing and subsequent commercial deployment, combining consistent high yield with superior overall stability. GAJA 031 and VMAH 322 were established as the next most desirable hybrids, offering strong yield predictability across diverse environments. Conversely, VMAH 256 is recommended specifically for high-potential, high-input environments (e.g., AUR) due to its highly responsive, specifically adapted nature. These findings provide actionable, data-driven recommendations that will guide the national maize breeding program in strategically deploying superior genetics tailored to specific agro-climatic conditions,

thereby potentially improving yield consistency and farmer profitability in the face of climatic uncertainty.

Declarations

The authors have no competing interests to declare that are relevant to the content of this article.

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