Article

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Improving G×E Interaction Analysis Through Spatial and Non-Spatial Mixed Models in Multi-Environment Trials of Niger Seed Genotypes

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Abstract

Multi-environment trials (METs) are central to plant breeding programs for evaluating genotype performance and adaptation, yet spatial field variability and genotype × environment interaction (GEI) often reduce the precision of genotype assessment. This study aimed to improve genotype evaluation by integrating spatial linear mixed models, GGE biplot analysis, and parametric and non-parametric stability statistics. Grain yield data from seven environments were analysed using linear mixed models fitted by restricted maximum likelihood. Non-spatial randomized complete block design (RCBD) model was compared with two-dimensional first-order autoregressive spatial model on an environment-specific basis. Spatial model provided a superior fit in three environments, while non-spatial model was adequate in the remaining environments, demonstrating that spatial dependence was not uniform across environments. Genotypic differences for grain yield were detected in most environments, with BLUEs ranging from 0.75 to 0.95 t ha^{-1} and an overall mean of 0.84 t ha^{-1}. The average-environment coordination view identified Genotypes 3 and 5 as closest to the ideal genotype. Parametric and non-parametric stability analyses supported the GGE results. Overall, the study demonstrates that integrating spatial modelling, GGE biplots, and stability statistics provides a robust framework for accurate genotype evaluation and reliable varietal recommendation in plant breeding programs.

Keywords: genotype x environment interaction; multi-environment trials; linear mixed models; spatial analysis

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Introduction

Genotype × environment interaction (GEI) remains one of the major challenges in plant breeding and variety evaluation, particularly in the context of multi-environment trials (METs) (Amelework et al. 2023). In plant breeding programs, METs are conducted across multiple environments (locations, years, or location × year combinations) with the objective of identifying high-yielding and stable genotypes (Lee et al. 2023). However, the presence of GEI can mask true genotypic performance and complicate selection decisions, necessitating robust and flexible statistical modeling approaches for reliable inference (Malosetti et al. 2013; Behera et al. 2024; Argaw et al. 2025).

Traditionally, the design and analysis of METs have relied on classical analysis of variance (ANOVA) or linear mixed models that assume homogeneous variance–covariance structures across trials (Ramon 2002). Such assumptions are often unrealistic under field conditions, where spatial heterogeneity arising from variation in soil fertility, moisture availability, pH, and other edaphic factors is common. Failure to adequately model this heterogeneity may lead to biased estimates, reduced precision, and ultimately misleading varietal evaluation and recommendation decisions (Tarekegn and Berahnu 2022; Tadese et al. 2024; Argaw et al. 2025). Spatial linear mixed models provide a powerful framework for addressing these limitations by explicitly modeling local spatial variation within trials as well as residual heterogeneity between trials (Oberg et al. 2007; McIntosh 2015; Stefanova et al. 2023). Several spatial variance–covariance structures have been proposed for agricultural field experiments (VSN International 2015). The two-dimensional separable autoregressive model [AR(1) × AR(1)] is the most used spatial model in plant breeding (Velazco et al. 2017; Negash et al. 2014; Borges da Silva et al. 2021; Tarekegn and Berhanu 2022). This model captures correlation in both row and column directions, assuming that correlation decays exponentially with distance between plots (Marques et al. 2023).

Niger seed (*Guizotia abyssinica*), locally known as "Noug" is one of the most important indigenous oilseed crops in Ethiopia and is also cultivated in countries such as India (Geleta and Ortiz 2013; Gebeyehu et al. 2025). In Ethiopia, the crop is grown on approximately 191,766 ha, with an annual production of about 214,798 tons and an average productivity of 1.1 t ha^{-1} (CSA 2020/21). In addition to its economic importance, niger seed offers agronomic benefits, including weed suppression for subsequent crops, making it well suited for crop rotation systems (Getnet and Sharma 1996). Despite its importance, MET analyses conducted for niger seed to date have rarely accounted explicitly for GEI, potentially confounding varietal evaluation and recommendation efforts. More broadly, many GEI studies in other crops continue to rely on classical ANOVA-based approaches, which may lead to misleading interpretations and erroneous conclusions when spatial variability is not adequately modeled (Yu et al. 2024; Argaw et al. 2025). Widely used GEI analysis methods such as additive main effects and multiplicative interaction (AMMI), genotype and genotype × environment interaction (GGE) biplot analysis, Finlay–Wilkinson regression, and various parametric and non-parametric stability statistics are valuable tools, but their effectiveness depends strongly on the quality of the underlying model used to estimate genotypic effects (Reza and Ahmed 2008; Malosetti et al. 2013; Yue et al. 2022; Dang et al. 2024).

In this study, we conducted a comparative analysis of spatial and non-spatial (RCBD-based) mixed models using multi-environment trial data of niger seed. The objective was to evaluate the extent to which spatial modeling improves model fit, precision, and the reliability of inference in MET analysis. Following model selection using information criteria and likelihood ratio tests, we applied complementary GEI assessment methods, including GGE biplot analysis, as well as parametric and non-parametric stability statistics, to assess genotypic performance and stability across environments. This integrated approach combines the strengths of spatial modeling with established GEI analysis techniques, providing practical insights for improving routine data analysis pipelines in plant breeding programs.

Methodology

Data Source

The national trials comprising 12 elite niger seed genotypes, including two (standard and local) checks, were carried out during the 2021/22-2024/25 main cropping seasons across seven locations such as Ambo, Ginchi, Holetta, ArsiRobe and Wolkite (Tables 1 and 2). The trials were laid out using randomized complete block design (RCBD) with four replications. Each plot had six rows with between rows spacing of 0.3m. Only the central four rows with a net area of 6 m^2 out of the gross area of 9 m^2 was used for data collection. A seed rate of 10 kg ha^{-1} and fertilizer rate of 60.5 kg $ha^{-1}$of NPS and 25 kg $ha^{-1}$of urea were used as recommended. The fertilizer was applied during planting time. All other cultural practices were followed as recommended for all trials across locations. Data on seed yield was measured as the total seed yield harvested from the net plot area, and then extrapolated to a per-hectare basis. Trials with poor data quality were removed.

Table 1. Description of the niger seed genotypes testing sites.

Location	Coordinates	Altitude(masl)	Average Rain fall(mm)	Soil type	Temperature(ºc)	
					Max	Min
Ambo	N08°58′05″ E37.51′34″	2175	1235	Vertisols	26.0	12.0
Ginchi	N09°1′60″ E38°9′0″	2200	1031	Vertisols	23.8	9.3
Holeta	N09°03′25″ E38°30′26″	2400	1044	Nitosols	22.0	6.0
ArsiRobe	N09°36′00″ E39°08′00″	2435	1435	Clay	22.0	7.0
Wolkite	N08°17′00″ E37°47′00″	1910	1100	Nitosols	24.6	10.2

Table 2. Code, name and sources of niger seed genotypes tested. .

Genotype code	Name	Source
1	15657	HARC
2	15671	HARC
3	15681	HARC
4	200428	HARC
5	225954	HARC
6	15528sps1	HARC
7	212731	HARC
8	15535	HARC
9	202262	HARC
10	202258	HARC
11	Ginchi-1 (Standard check)	HARC
12	Local check	LM

HARC: Holetta Agricultural Research Center, LM:local market.

Statistical Procedures

Linear Mixed Models and Spatial Analysis

Data from each trial (hereafter referred to as "environment") were first analysed using a baseline randomized complete block design (RCBD) linear mixed model fitted by restricted maximum likelihood (REML). In this initial model, genotype was treated as a fixed effect, while replication (block) was considered a random effect. The baseline RCBD model assumes that residual errors are independent and identically distributed, i.e. $\varepsilon \sim N(0, \sigma^2 I)$, with no explicit accounting for spatial dependence among experimental units.

To better accommodate within-environment field heterogeneity, spatial linear mixed model (SLMM) was subsequently fitted by extending the RCBD model to include spatial correlation in the residuals. This model relaxes the assumption of independent residuals by modelling spatial dependence across plot positions within each trial using alternative residual covariance structure. The general matrix form of the linear mixed model used is:

$$y = X\beta + Zu + \varepsilon,$$

Where, y is the vector of observed plot-level responses, β is the vector of fixed effects (genotypes), u is the vector of random effects (replications), X and Z are the corresponding design matrices, and ε is the vector of residual errors. For the spatial model, residuals were assumed to follow:

$$\varepsilon \sim N(0, R),$$

Where R represents a spatially structured covariance matrix.

In this study, a separable two-dimensional first-order autoregressive model [AR(1) × AR(1)] was used:

$$R = \sigma^2[AR(1)_{row} \otimes AR(1)_{column}],$$

which assumes that spatial correlation decays exponentially with increasing distance between plots in both row and column directions (Gilmour et al. 1997). The model estimates the correlation between adjacent rows [ϱ(row)] and adjacent columns [ϱ(column)].

Models Evaluation

To determine the better fitting model for each environment, the model selection criteria such as Akaike Information Criterion (AIC) and Bayesian Information Criterion (BIC) were employed as follows:

$$AIC = -2 \times logL + 2k$$

$$BIC = -2 \times logL + k \times \log(n)$$

Where $logL$ is the log-likelihood of the fitted model, k is the number of estimated parameters in the model, and n is the number of observations.

Lower AIC and BIC values indicate a better model fit. Once the optimal model (spatial or non-spatial) was selected per environment, Best Linear Unbiased Estimators (BLUEs) of genotypic performance were extracted for further G×E and stability analyses.

GGE Biplot Analysis

GGE biplot analysis was conducted using genotype BLUEs to visualize and interpret genotype performance across environments. The GGE biplot was used to generate which-won-where and genotype ranking biplots, facilitating the identification of high-yielding and stable genotypes. The GGE biplot model (Yan and Tinker 2006) can be expressed as:

$$Y_{ij} - \mu - \beta_j = \sum_{k=1}^{t} \lambda_k \xi_{ik} \eta_{jk} + \varepsilon_{ij},$$

where Y_{ij} is the mean performance of genotype i in environment j, μ is the grand mean, β_j is the environment main effect, λ_k is the singular value for principal component k, ξ_{ik} and η_{jk} are genotype and environment scores for component k, and ε_{ij} is the residual term.

Parametric and Non-Parametric Stability Statistics

Both parametric and non-parametric stability statistics were computed to further assess genotype stability across environments. These included cultivar superiority, static stability variance, Wricke’s ecovalence, mean rank, rank variance, mean absolute differences of pairwise ranks, and variance of ranks (VSN International 2015). The performance and stability of the genotypes were also shown using the mean-CV plot (Francis and Kannenberg 1978). These complementary measures allowed for a comprehensive evaluation of yield performance and stability from different statistical perspectives.

Software

Spatial and non-spatial mixed model analyses were conducted using Genstat software 18th edition. GGE biplots were generated using Genotype x Environment Analysis with R for Windows (GEA-R) version 4.1, while relationships among environments were explored using heatmaps produced with the seaborn package in Python version 3.14.

Result

Linear Mixed Models Comparison and Spatial Analysis

A first-order autoregressive correlation in two-dimensions was evaluated separately for each test environment against the classical RCBD (non-spatial model) which assumed independent and identically distributed residuals. This spatial mixed modelling markedly improved model fit, with a large reduction in −2LL and substantially lower AIC and BIC values for E1 (Ambo 2021/22). Residual variance decreased from 0.0737 to 0.0646, and strong spatial correlations were detected in both rows (ϱ = 0.72) and columns (ϱ = 0.67) in this environment. Similarly, this modelling substantially improved goodness-of-fit for E2 (Ginchi 2021/22), as indicated by a notable reduction in −2LL and lower AIC and BIC values. The residual variance decreased from 0.0933 to 0.0878, and moderate spatial correlations were detected in rows (ϱ = 0.33) and columns (ϱ = 0.49) in this environment. Besides, for E3 (Holetta 2021/22), spatial modelling improved model fit as indicated by a notable reduction in −2LL and lower AIC and BIC values compared with the non-spatial model. The residual variance slightly decreased (0.0124 to 0.0123), and moderate spatial correlations were detected, particularly across rows (ϱ = 0.43) in this environment. These results indicate meaningful spatial dependence; therefore, the spatial model was retained for environments E1 (Ambo 2021), E2 (Ginchi 2021/22) and E3 (Holetta 2021/22) (Tables 1 and 2).

On the other hand, the spatial model produced a slightly smaller −2LL in environment E5 (Wolkite 2022/23); however, the improvement was negligible and resulted in higher AIC and BIC values relative to the non-spatial model. In this environment, the spatial correlation estimates for rows and columns were near zero, and residual variance did not decrease. In environment E6 (Wolkite 2023/24), although the spatial model produced a slightly smaller −2LL, the improvement was negligible and resulted in higher AIC and BIC values relative to the non-spatial model. Residual variance remained unchanged and estimated row and column correlations were weak in this environment. Although the spatial model slightly improved −2LL and marginally reduced the residual variance in environment E7 (Wolkite 2024/25) too, the improvement was insufficient to offset the penalty for additional parameters, resulting in higher AIC and BIC values. Estimated spatial correlation was weak (ϱrow ≈ 0.25; ϱcol ≈ 0.00) in this environment. There is weak-to-moderate spatial correlation at E4 (ArsiRobe 2022/23); incorporating spatial structure improves model fit slightly, but the improvement is marginal, as indicated by unchanged residual variance and BIC not supporting it strongly in this environment. Therefore, spatial modelling was not warranted and the non-spatial (RCBD) model was retained for environments E4 (ArsiRobe 2021/22), E5 (Wolkite 2022/23), E6 (Wolkite 2023/24), and E7 (Wolkite 2024/25) (Tables 1 and 2).

Table 3. Comparison of non-spatial (RCBD) and spatial mixed models for each environment.

Environment	Model	−2LL	AIC	BIC	Residual variance	Best fit
E1	Non-spatial (RCBD)	-41.240	-39.240	-37.660	0.074	
E1	Spatial (AR1×AR1)	-80.600	-74.600	-69.850	0.065	Spatial
E2	Non-spatial (RCBD)	-32.740	-30.740	-29.160	0.093	
E2	Spatial (AR1×AR1)	-43.800	-37.800	-33.050	0.088	Spatial
E3	Non-spatial (RCBD)	-105.380	-103.380	-101.800	0.012	
E3	Spatial (AR1×AR1)	-112.660	-106.660	-101.910	0.012	Spatial
E4	Non-spatial (RCBD)	-109.360	-107.360	-105.770	0.011	
E4	Spatial (AR1×AR1)	-115.620	-109.620	-104.870	0.011	Non-spatial
E5	Non-spatial (RCBD)	-145.120	-143.120	-141.540	0.004	
E5	Spatial (AR1×AR1)	-145.450	-139.450	-134.700	0.004	Non-spatial
E6	Non-spatial (RCBD)	-112.280	-110.280	-108.690	0.010	
E6	Spatial (AR1×AR1)	-113.910	-107.910	-103.160	0.010	Non-Spatial

E7	Non-spatial (RCBD)	-111.910	-109.910	-108.330	0.010	Non-spatial
E7	Spatial (AR1×AR1)	-114.200	-108.200	-103.450	0.010	

E 1: Ambo 2021/22, E2: Ginchi 2021/22, E3: Holetta 2021/22, E4: ArsiRobe 2022/23, E5: Wolkite 2022/23, E6: Wolkite 2023/24, E7: Wolkite 2024/25, LL= loglikelihood.

Table 4. Estimated spatial autocorrelation parameters.

Environment	ϱ(row)	ϱ(col)
E1	0.7198	0.6734
E2	0.3295	0.4942
E3	0.4251	0.2339
E4	0.3955	0.2070
E5	-0.1319	0.0238
E6	-0.1146	0.2560
E7	0.2514	0.0041

ϱ(row): correlation between adjacent rows, ϱ(column): correlation between adjacent columns, for designation of each environment, see Table 3.

Best Linear Unbiased Estimates (BLUEs) and Environment Relationships

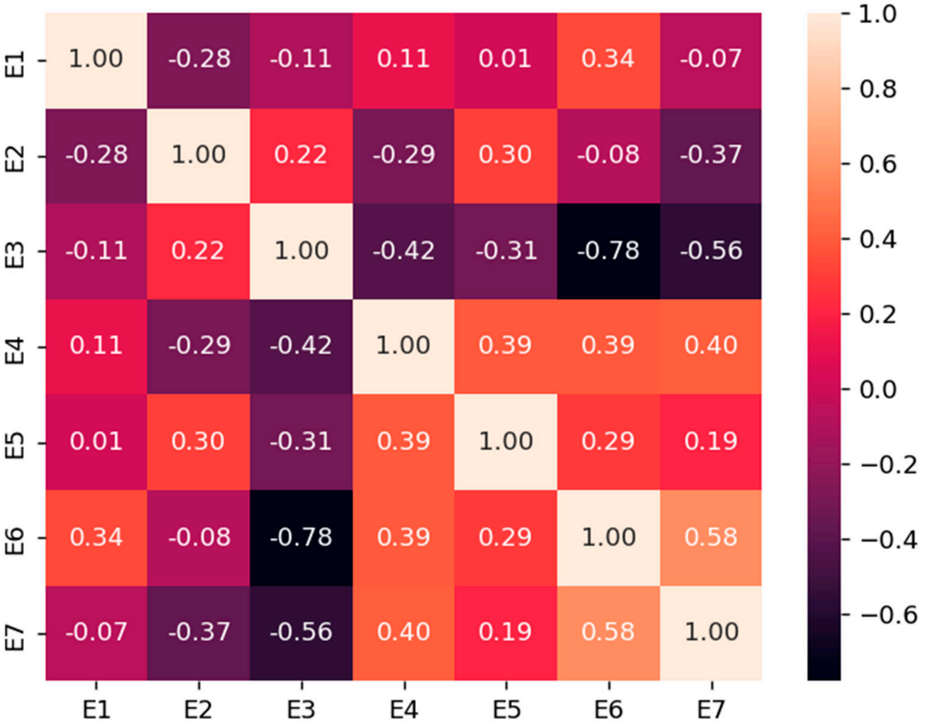
The Best Linear Unbiased Estimates (BLUEs) for grain yield of the test genotypes across environments are presented in Table 5. The Wald F-test indicated significant differences among genotypes in all trials, with the exception of environment E2, where genotypic effects were not statistically significant. Across environments, grain yield of the test genotypes ranged from 0.75 to 0.95 t ha^{-1}, with an overall mean of 0.84 t ha^{-1}. Genotype 3 was the highest-yielding genotype (0.95 t ha^{-1}), followed by Genotype 5 (0.92 t ha^{-1}). Marked differences in environmental productivity were observed. Environment E1 recorded the highest mean yield (1.14 t ha^{-1}), closely followed by E7 (1.13 t ha^{-1}), indicating more favourable growing conditions in these environments. Relationships among test environments are illustrated in Figure 1. The environment correlation analysis revealed distinct patterns of genotype response. Environments E4 (ArsiRobe 2022/23), E5 (Wolkite 2022/23), E6 (Wolkite 2023/24), and E7 (Wolkite 2024/25) were positively correlated, suggesting similar genotype rankings and comparable discriminating ability. In contrast, environment E3 (Holetta 2021/22) exhibited strong negative correlations with several other environments, indicating crossover genotype × environment interaction. Consistent changes in genotype rankings across environments (Table 5) further confirm the presence of differential genotype responses to environmental conditions.

Table 5. Best Linear Unbiased Estimates (BLUEs) of the test genotypes.

Genotype	Environment														Mean	R
	E1	R	E2	R	E3	R	E4	R	E5	R	E6	R	E7	R		
1	1.14	5	0.70	12	0.48	8	0.68	1	0.51	9	1.21	3	1.32	1	0.87	3
2	1.43	1	0.72	11	0.55	5	0.61	4	0.6	5	0.88	7	1.08	7	0.83	5
3	1.22	3	1.02	4	0.56	4	0.62	3	0.69	2	1.21	3	1.25	2	0.95	1
4	1.13	6	0.96	6	0.49	7	0.66	2	0.67	3	1.11	4	1.07	8	0.87	3
5	1.20	4	1.05	2	0.49	7	0.66	2	0.72	1	1.23	2	1.1	5	0.92	2
6	1.14	5	0.91	7	0.45	9	0.52	6	0.57	6	1.05	5	1.19	3	0.84	4
7	1.01	9	1.00	5	0.62	3	0.68	1	0.53	8	0.74	9	1.08	7	0.81	6
8	1.27	2	0.89	8	0.51	6	0.51	7	0.49	10	1.34	1	1.13	4	0.87	3

9	1.04	8	1.04	3	0.49	7	0.51	7	0.53	8	1.04	6	1.09	6	0.83	5
10	0.86	10	0.88	9	0.55	5	0.53	5	0.66	4	0.85	8	1.19	3	0.8	7
11	1.12	7	0.82	10	0.66	2	0.51	7	0.46	11	0.73	10	1.01	9	0.75	8
12	1.14	5	1.12	1	0.69	1	0.37	8	0.54	7	0.68	11	1.01	9	0.8	7
Mean	1.1		0.9		0.6		0.57		0.58		1.01		1.13		0.84	
SE	0.1		0.1		0		0.02		0.01		0.01		0.01		0.03	
Wald F test	**		ns		*		***		***		***		**		***	

*,** and ***: significant at p<0.05,0.01 and 0.001 level, respectively, R: rank, for designation of each environment and genotype, see Tables 2 and 3.



	E1	E2	E3	E4	E5	E6	E7
E1	1.00	-0.28	-0.11	0.11	0.01	0.34	-0.07
E2	-0.28	1.00	0.22	-0.29	0.30	-0.08	-0.37
E3	-0.11	0.22	1.00	-0.42	-0.31	-0.78	-0.56
E4	0.11	-0.29	-0.42	1.00	0.39	0.39	0.40
E5	0.01	0.30	-0.31	0.39	1.00	0.29	0.19
E6	0.34	-0.08	-0.78	0.39	0.29	1.00	0.58
E7	-0.07	-0.37	-0.56	0.40	0.19	0.58	1.00

Figure 1. Heatmap showing the relationship of test environments, for designation of each environment, see Table 3.

GGE Biplot Analysis

The which-won-where pattern and genotype ranking based on the GGE biplot are presented in Figure 2 a and b. The first two principal components of the GGE biplot explained 72.2% of the total genotype (G) plus genotype × environment (GE) variation, indicating an adequate representation of the multi-environment data. Based on the polygon view (which-won-where), the test environments were grouped into five mega-environments (Figure 2a). Environments E1 (Ambo 2021/22), E2 (Ginchi 2021/22), E3 (Holetta 2021/22), and E5 (Wolkite 2022/23) each formed a distinct mega-environment, with genotypes 2, 9, 12, and 5 identified as the respective winning genotypes. Another mega-environment comprised environments E4 (ArsiRobe 2022/23) and E7 (Wolkite 2024/25), in which genotype 8 was the best-performing genotype. The average-environment coordination (AEC) view (Figure 2b) was used to assess genotype mean performance and stability. Genotypes 3 and 5 were located closest to the ideal genotype, indicating high mean grain yield combined with greater stability across environments. In contrast, genotypes 2, 10, and 12 exhibited below-average yield and high instability. Genotype 11 was the lowest-yielding genotype but showed relatively stable performance across environments.

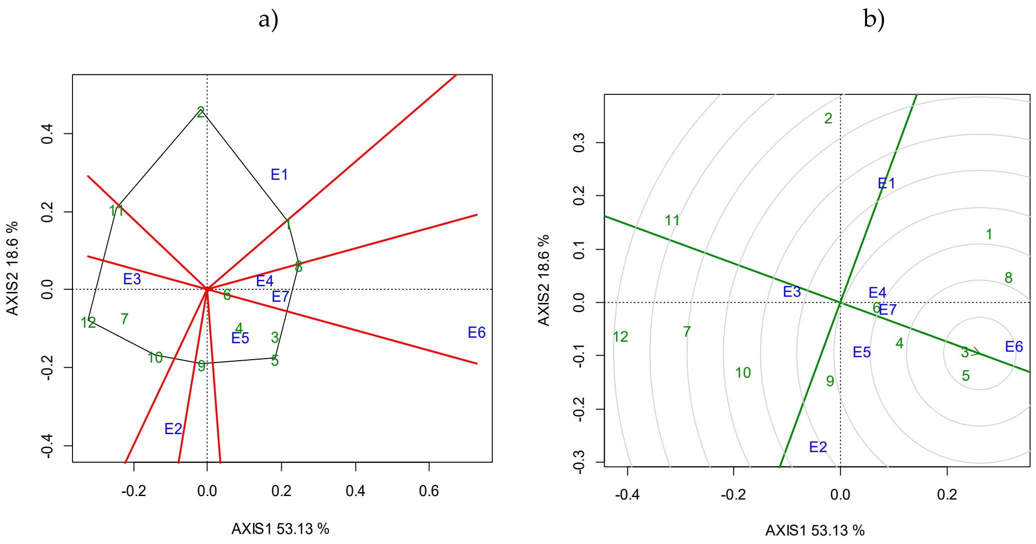


Figure 2. a) The which-won-where pattern of genotypes and selected test environments; b) Ranking genotypes relative to an ideal genotype (located at the center of the concentric circles), for designation of each environment and genotype, see Tables 2 and 3.

Stability Assessment Using Parametric and Non-Parametric Statistics

After mixed model adjustment, parametric and non-parametric stability statistics of the genotype performance were computed as shown in Table 6. To complement the GGE biplot analysis, stability parameters based on BLUEs of genotype means were computed to quantify yield stability across environments. Using adjusted means from LMM account for spatial correlation and heterogeneous error variance, which result in more accurate and less biased estimates of stability indices and thereby reliable evaluation of genotypes. According to the parametric statistics, the lowest cultivar superiority value (0.008) was recorded by genotype 3 ranked 1st followed by genotypes 5 and 8, which recorded cultivar superiority values of 0.013 and 0.018, and ranked 2nd and 3rd, respectively. The lowest static stability value (0.046) was recorded by genotype 7 ranked 1st, followed by genotypes 10 and 11, having values of 0.054 and 0.059 ranked 2nd and 3rd, in that order. Genotypes 6, 3 and 4 recorded the Wricke's ecovalence values of 0.015, 0.025 and 0.026, ranked 1st, 2nd, and 3rd, respectively. According to the non-parametric statistics, Genotypes 3, 5 and 4 had mean ranks of 3.286, 4.000 and 6.143 which ranked 1st, 2nd and 3rd, respectively. Means absolute differences of pairs of ranks ranked genotypes 3, 9 and 6 as 1st, 2nd, and 3rd with values of 1.333, 2.667 and 2.762, respectively. The lowest variances of ranks was recorded by genotype 3 with a value of 1.240 followed by genotype 9 with a value of 5.620 and genotype 6 with a value of 6.330. Static stability gave rankings that differ from other stability statistics. The mean- CV plot revealed genotypes 3, 5 and 4 as good performer and stable. Stability analysis based on adjusted genotype means (BLUEs) supported the GGE results, identifying genotype 3 as high-yielding and stable across environments. Genotype 5 was relatively good based on these stability indices. Other genotypes showed variable rankings across stability parameters, indicating either specific adaptation or unstable performance.

Table 6. Genotype stability using cultivar parametric and non-parametric indices.

GEN	CS	R	SS	R	W	R	MR	R	MADPR	R	VR	R
1	0.028	(6)	0.121	(11)	0.157	(11)	6.857	(6)	5.619	(11)	22.480	(11)
2	0.034	(8)	0.106	(10)	0.154	(10)	6.286	(4)	3.714	(6)	9.900	(6)
3	0.008	(1)	0.095	(8)	0.025	(2)	3.286	(1)	1.333	(1)	1.240	(1)
4	0.021	(4)	0.067	(4)	0.026	(3)	6.143	(3)	3.238	(4.5)	7.140	(4)

5	0.013	(2)	0.088	(7)	0.055	(5)	4.000	(2)	3.238	(4.5)	7.670	(5)
6	0.025	(5)	0.096	(9)	0.015	(1)	7.000	(7.5)	2.762	(3)	6.330	(3)
7	0.049	(9)	0.046	(1)	0.113	(8)	7.000	(7.5)	4.286	(9)	13.000	(9)
8	0.018	(3)	0.144	(12)	0.139	(9)	6.429	(5)	4.857	(10)	15.950	(10)
9	0.030	(7)	0.081	(5)	0.027	(4)	7.429	(10)	2.667	(2)	5.620	(2)
10	0.053	(10)	0.054	(2)	0.103	(7)	7.571	(11)	4.000	(8)	10.950	(7)
11	0.055	(12)	0.059	(3)	0.086	(6)	8.857	(12)	3.810	(7)	11.810	(8)
12	0.054	(11)	0.087	(6)	0.198	(12)	7.143	(9)	5.905	(12)	25.140	(12)

CS: Cultivar superiority, R: Rank, SS: Static stability, We: Wricke's ecovalence, MR: Mean ranks, MADPR: Means absolute differences of pairs of ranks, VR: Variances of ranks, for designation of each genotype, see Table 2.

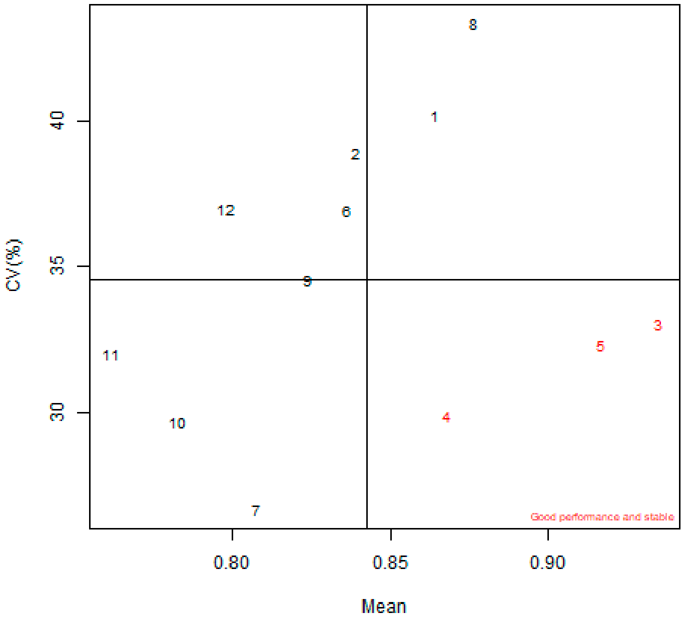


Figure 3. The Mean-CV plot, for designation of each genotype, see Table 2.

Discussion

Accounting for spatial variability and field heterogeneity in multi-environment trials (METs) is essential for accurate genotype evaluation and reliable varietal recommendation in plant breeding programs (Gilmour et al. 1997; Coelho et al. 2021). Field trials are inherently heterogeneous, and ignoring spatial dependence can inflate experimental error and obscure true genotypic differences (Ishimori et al. 2021; Yamamoto et al. 2022). Linear mixed models (LMMs) provide a flexible analytical framework for MET data by explicitly modelling spatial correlation and heterogeneous error variances, thereby improving the precision of genotype effect estimates and supporting informed selection decisions (Argaw et al. 2025). In this study, a two-dimensional first-order autoregressive spatial model was compared with a non-spatial randomized complete block design (RCBD) mixed model on an environment-specific basis. The spatial model provided a superior fit for environments E1 (Ambo 2012/22), E2 (Ginchi 2021/22), and E3 (Holetta 2021/22), whereas the non-spatial model was adequate for E4 (ArsiRobe 2022/23), E5 (Wolkite 2022/23), E6 (Wolkite 2023/24), and E7 (Wolkite 2024/25). This demonstrates that spatial dependence is not uniform across trials and that environment-specific model selection enhances the accuracy of genotype evaluation. Such findings are consistent with previous MET studies emphasizing the importance of flexible modelling strategies in heterogeneous fields (Duarte and Vencovsky 2005; Rodr´ıguez - ´Alvarez et al. 2016; Selle et al. 2019; Tarekegn and Berhanu, 2022).

Significant genotypic differences for grain yield were detected in most environments, although caution is required when interpreting Wald F-tests due to their potential anti-conservative behaviour, particularly with small number of observation (Luke 2017). The BLUEs revealed moderate yield variation among genotypes, with Genotype 3 and Genotype 5 exhibiting superior mean performance. Environment correlation analysis indicated both positively associated environments and strong crossover genotype × environment interaction, highlighting the complexity of genotype responses across environments.

The GGE biplot analysis complemented these results by providing insight into genotype performance, stability, and environment structure. The first two principal components explained 72.2% of the total G plus GE variation. The which-won-where view identified five mega-environments with distinct winning genotypes, indicating the presence of both broadly and specifically adapted genotypes. The average-environment coordination view further identified Genotypes 3 and 5 as closest to the ideal genotype, combining high mean yield with greater stability.

To complement the graphical GGE analysis, parametric and non-parametric stability statistics were computed using BLUEs adjusted for spatial correlation. The use of adjusted means resulted in more accurate and less biased estimates of stability indices. Parametric statistics such as cultivar superiority, Wricke's ecovalence, and static stability revealed differences in genotype ranking depending on the underlying stability concept. Genotype 3 consistently ranked among the most stable and high-performing genotypes across cultivar superiority and ecovalence measures, while Genotype 5 also showed favourable performance. Static stability rankings differed from other indices, reflecting the Type I (biological) stability concept, which favours minimal variance across environments, often at the expense of higher yield. In contrast, most other stability measures followed the dynamic (agronomic) stability concept, rewarding genotypes that combine high yield with acceptable stability (Elakhdar et al. 2025; Pour-Aboughadareh et al. 2025). Non-parametric stability statistics further supported these findings, with Genotype 3 ranking first or among the top genotypes across multiple indices, followed by Genotypes 5 and 6. The mean–CV plot also identified Genotypes 3, 5, and 4 as desirable for both yield and stability. Overall, the consistency between stability statistics and GGE biplot results strengthens confidence in the identification of Genotype 3 as broadly adapted, high-yielding, and stable, while Genotype 5 also showed good overall performance. Variable rankings of other genotypes suggest either specific adaptation or unstable performance across environments.

Conclusions

This study demonstrates that integrating spatial linear mixed models, GGE biplot analysis, and stability statistics provides a robust and comprehensive framework for genotype evaluation in plant breeding programs. Environment-specific modelling of spatial heterogeneity improved model fit and enhanced the precision of genotype ranking, leading to more reliable selection decisions. The presence of substantial genotype × environment interaction, including crossover responses, highlights the necessity of MET-based evaluation. The GGE biplot identified mega-environments, winning genotypes, and broadly adapted candidates, while parametric and non-parametric stability statistics quantified genotype stability using adjusted means. The strong agreement among BLUEs, GGE biplot results, and stability indices consistently identified Genotype 3 as high-yielding and stable across environments, with Genotype 5 also showing favourable performance. Differences among stability measures further emphasize the importance of considering both biological and agronomic stability concepts when making selection decisions. Overall, adoption of integrated analytical approach can enhance selection efficiency, improve varietal recommendation, and ultimately contribute to increased genetic gain in plant breeding programs operating under diverse and heterogeneous environments.

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