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Genotype × Environment Interaction and Stability Analysis of Grain Yield of Emmer Wheat (*Triticum dicoccum*) Landraces Using AMMI and GGE Biplot Analyses

Zemariam Teferi[1] | Yemane Tsehaye[1] | Zewdie Bishaw[2] | Fetien Abera[3]

[1]Department of Horticultural and Crop Science, Mekelle University, Mekelle, Tigray, Ethiopia | [2]Emeritus Scientist and Consultant, International Center for Agricultural Research in the Dry Areas, Addis Ababa, Ethiopia | [3]Department Genetics & Genomics (CPBGG) Center of Plant Breeding, SC State University, Orangeburg, South Carolina, USA

Correspondence: Zemariam Teferi (zemariamtafere14@gmail.com)

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ABSTRACT

Emmer wheat (*Triticum dicoccum* Schrank) is an important traditional cereal crop in Ethiopia valued for its genetic diversity and adaptation to marginal environments. However, its productivity is constrained by strong genotype × environment interaction (GEI), limiting the identification of stable and high-yielding genotypes adapted to diverse agroecological conditions. This study aimed to evaluate GEI and identify both broadly and specifically adapted emmer wheat landraces using AMMI and GGE biplot analyses. A total of 270 emmer wheat landraces were evaluated, comprising 260 landraces obtained from the Ethiopian Biodiversity Institute and 10 landraces collected from emmer wheat-growing areas of the Tigray Region, during the 2023/24 and 2024/25 main rainy seasons using an alpha-lattice design with two replications. The trials were conducted across three locations in the first year, with two of these locations repeated in the second year, resulting in five test environments (location–year combinations). Combined analysis of variance revealed highly significant differences among genotypes and significant GEI ($p < 0.001$). Environmental effects contributed the largest proportion of the total variation (43.9%), followed by GEI (31.1%) and genotype (16.1%), demonstrating the strong influence of environmental conditions on grain yield. AMMI and GGE biplot analyses effectively characterized the GEI pattern. The first two AMMI interaction principal components explained 89.7% of the GEI variation, while the GGE biplot explained 79.32% of the total GGE variation and identified two distinct mega-environments. Genotype G207 exhibited specific adaptation to mega-environment II (E4-E5), whereas G158 was specifically adapted to mega-environment I (E1–E3). The discriminativeness versus representativeness biplot identified E2 as the most suitable test environment for selecting broadly adapted genotypes. Among the evaluated landraces, G59 showed the highest yield stability and potential for broad adaptation across environments, whereas G266, G196, and G56 exhibited relatively low stability. GGE analysis identified genotypes associated with specific mega-environments, indicating potential specific adaptation. Overall, the study revealed substantial genetic variability and strong GEI affecting grain yield in Ethiopian emmer wheat. Accordingly, G207 and G158 are recommended for further evaluation in their respective mega-environments, while G59 is recommended for wider evaluation as a promising, broadly adapted genotype for breeding programs aimed at improving yield stability and adaptation. Further multilocation and multiyear evaluation is recommended before release.

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1 | Introduction

1.1 | Back Ground of the Study

Emmer wheat (*Triticum dicoccum* Schrank) is one of the earliest domesticated cereal crops and an important ancestor of modern cultivated wheat. It is a tetraploid hulled wheat ($2n = 4x = 28$; AABB genome) derived from wild emmer (*Triticum dicoccoides*) in the Fertile Crescent approximately 10,000 years ago [1]. From its center of origin, emmer wheat spread widely to Europe, North Africa, West Asia, and the Horn of Africa, where it adapted to diverse agroecological conditions [2, 3]. Although it is global cultivation has declined due to the dominance of free-threshing bread wheat (*Triticum aestivum*) and durum wheat (*Triticum durum*), emmer wheat remains important in marginal environments because of its resilience, low input requirements, and nutritional value [4, 5].

Ethiopia is recognized as a secondary center of diversity for emmer wheat and maintains a wide range of genetically diverse landraces preserved by smallholder farmers [6]. These landraces represent valuable genetic resources for wheat improvement due to their adaptation to drought, poor soil fertility and high-altitude environments [7, 8].

Emmer wheat continues to be cultivated in Ethiopian highland regions such as Bale, Arsi, Shewa, Harerge, Wello, Gojam, Gondar, and Tigray. Although earlier estimates suggested that emmer wheat accounted for approximately 7% of Ethiopia's total wheat production, recent official agricultural statistics no longer report it separately from other wheat types. Nevertheless, available studies indicate that it remains an important traditional crop in smallholder farming systems due to its adaptation to marginal conditions and cultural importance [9, 10].

Beyond its agronomic significance, emmer wheat is valued for its superior nutritional quality, including higher levels of protein, dietary fiber, essential amino acids, and micronutrients such as iron and zinc compared to many modern wheat cultivars [11, 12]. Ethiopian emmer wheat landraces also exhibit considerable variability in grain quality traits, highlighting their potential for nutritional improvement and breeding. The crop plays an important role in traditional diets, where it is used in preparing bread, porridge, and cultural foods, particularly for vulnerable groups such as postpartum mothers [5, 13].

Despite its importance, emmer wheat production is constrained by several biotic, abiotic, and socio-economic factors. It generally has lower yield potential than modern wheat cultivars, is susceptible to lodging, and requires labor-intensive postharvest processing due to its hulled grains. Additional constraints include limited availability of improved varieties, inadequate seed systems, declining farmer preference, weak market demand, and replacement by high-yielding bread wheat. Environmental stresses such as drought, declining soil fertility, and diseases further reduce productivity. Nevertheless, the broad genetic diversity and adaptation of emmer wheat to marginal environments make it a valuable genetic resource for developing climate-resilient wheat cultivars [5, 10, 14, 15].

In multienvironment crop improvement programs, understanding genotype performance across diverse environments is essential for identifying stable and high-yielding genotypes [16–18]. In Ethiopia, emmer wheat is predominantly grown under rain-fed conditions across environments that vary in rainfall, temperature, soil type and management practices. As a result, genotype × environment interaction (GEI) plays a major role in determining grain yield (GY) performance, often causing changes in genotype ranking across environments. This complexity makes it difficult to recommend widely adapted varieties without multienvironment testing [18–20].

The Additive Main Effects and Multiplicative Interaction (AMMI) model and the genotype plus genotype × environment interaction (GGE) biplot are widely used approaches for analyzing GEI. The AMMI model combines analysis of variance (ANOVA) with principal component analysis (PCA) to separate additive main effects from multiplicative interaction effects, allowing better interpretation of genotype stability and environmental influence [19, 21]. In contrast, the GGE biplot focuses on genotype performance and GEI simultaneously, enabling visualization of mega-environments, identification of winning genotypes, and evaluation of test environments [18]. The complementary use of AMMI and GGE provides a robust framework for selecting stable and specifically adapted genotypes in plant breeding.

Despite several studies on Ethiopian emmer wheat, most have focused on morphological characterization, nutritional traits, or limited location trials [9, 10]. There remains a lack of comprehensive evaluation of large collections of emmer wheat landraces across multiple environments using combined AMMI and GGE approaches, particularly in the Tigray region. This limits the identification of broadly adapted and specifically adapted genotypes for targeted cultivation and breeding [17, 19].

Based on the diverse agroecological origins and genetic variability of Ethiopian emmer wheat landraces, it was hypothesized that GY would be significantly influenced by GEI, resulting in differential genotype responses across environments. Furthermore, it was hypothesized that some landraces would exhibit broad adaptation and stable performance across environments, whereas others would display specific adaptation to particular environmental conditions.

Therefore, the objectives of this study were to (i) evaluate the GY performance of Ethiopian emmer wheat landraces across five environments, (ii) assess the magnitude and structure of GEI using AMMI and GGE biplot analyses, (iii) identify high-yielding and stable genotypes with broad adaptation, (iv) detect specifically adapted genotypes for distinct mega-environments, and (v) provide information to support breeding, conservation, and targeted cultivar development.

2 | Materials and Methods

2.1 | Description of the Study Areas

The multienvironment trial (MET) was conducted over two consecutive main cropping seasons (2023/24 and 2024/25) at selected districts in the Southeastern zone, Eastern zone, and Mekelle zone of the Tigray Region in Northern Ethiopia. In the first season, experiments were carried out at three locations (*Hintalo Wajirat*, *Kilte Awulaelo*, and Mekelle Agriculture Research Center [MARC], *Illalla* farm).), while in the second season, two locations (*Kilte Awulaelo* and MARC, *Illalla* farm)

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were repeated (Figure 1). Each location–year combination was considered a distinct environment.

2.1.1 | Hintalo Wajirat

Hintalo Wajirat district is located in the Southeastern Zone of the Tigray Region, Ethiopia, approximately between 12°55′ and 13°20′ N latitude and 39°20′ and 39°55′ E longitude. The district is bordered by the Southern Zone to the south, *Saharti-Samre* to the west, *Inderta* to the north, and the Afar Region to the east. The area is characterized by rugged topography, with elevations ranging from approximately 1400 to 2850 m above sea level . It receives an annual rainfall of 350–700 mm and has a mean annual temperature of about 16.8°C. The dominant soils are Cambisols and Vertisols, generally alkaline with low organic matter, nitrogen, and available phosphorus, but relatively higher cation exchange capacity and potassium levels [22]. The experimental site was located at a Farmer Training Center (FTC) approximately 5 km from Adigudom town.

2.1.2 | Kilte Awulaelo

Kilte Awulaelo district lies in the Eastern Zone of the Tigray Region between 13°45′–14°00′ N latitude and 39°30′–39°45′ E longitude. It is bordered by Hawzien and Saesie Tsadamba to the north, Atsbi Womberta to the east, Degua Tembien to the west, and Mekelle to the south. The district is situated at an elevation of 1800–2300 m above sea level within a *Woina-dega* agroecological zone. The district experiences variable seasonal rainfall, with annual rainfall generally ranging from approximately 500 to 1200 mm and having a mean temperature of 15°C–28°C. Major soil groups reported in the area include Leptosols, Calcisols, Vertisols, and Cambisols [23, 24].

The soils show considerable spatial variation in soil reaction, ranging from slightly acidic to alkaline, depending on soil type and landscape position [25]. The experiment was conducted under farmers' field conditions at Ayanalem Tabiya, Kushet *Mai Tiwaru*, about 3 km west of Wukro town, on Vertisol soil.

2.1.3 | Illalla

The Illala research site is located in the vicinity of Mekelle, Tigray Region, Ethiopia, at approximately 13°30′ N latitude and 39°40′ E longitude. It is bordered by *Hintalo Wajirat* to the south, Degua Tembien to the west, Wukro and Atsbi Womberta to the north, and the Afar Region to the east. The area lies at an elevation of 1500–2000 m above sea level. It receives 400–799 mm annual rainfall and has a mean annual temperature of 15°C–20°C. The experiment was conducted at the MARC research farm. Soils are predominantly Vertisols, characterized by high clay content, alkaline reaction, and high water-holding capacity, but low organic matter, nitrogen, and available phosphorus, with relatively higher cation exchange capacity and moderate to high potassium levels [10].

2.2 | Plant Materials

A total of 270 emmer wheat (*Triticum dicoccum* Schrank) landraces were used in this study. Of these, 260 landraces were obtained from the Ethiopian Biodiversity Institute (EBI), representing diverse emmer wheat-growing regions of Ethiopia, while the remaining 10 landraces were collected from major emmer wheat-producing areas of the Tigray Region.

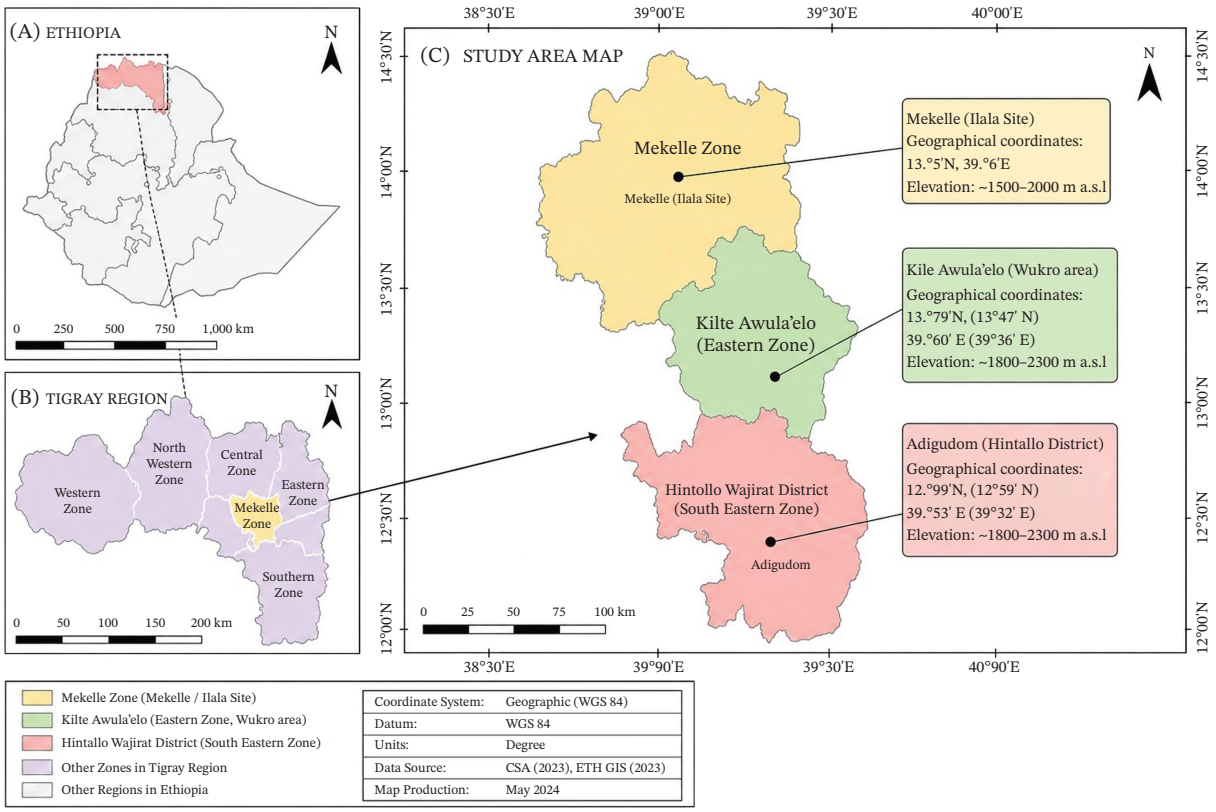


FIGURE 1 | Location map of the study area for the field trial experiment.

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2.3 | Experimental Design and Field Management

The experiment was conducted using an alpha lattice design with two replications. Prior to sowing, seeds of each landrace were prepared according to plot requirements, assigned randomized plot numbers, and arranged according to the field layout. Each plot consisted of a single 1.5 m row, with 0.40 m spacing between rows and 0.10 m spacing between plants. Each replication comprised six incomplete blocks, resulting in 12 blocks in total, with 45 landraces per block. The spacing between blocks and replications was 1.0 and 2.0 m, respectively. A seed rate of 100 kg ha^{-1} was used. Fertilizers were applied at rates of 100 kg P_2O_5 ha^{-1} and 100 kg N ha^{-1} in accordance with standard agronomic recommendations for the study area.

2.4 | Collected Data

During the field experiments, agronomic, phenological, and yield-related traits were recorded following standard procedures. However, for the present study, only GY (q ha^{-1}) data were considered for the GEI and stability analyses. GY was measured on a plot basis from the net harvested area and converted to q ha^{-1} for statistical analysis.

2.5 | Statistical Data Analysis

MET data were analyzed using a sequential analytical framework. First, a combined ANOVA was performed to partition the total phenotypic variation into genotype (G), environment (E), and GEI effects and to quantify their relative contributions to total variation. Second, variance components were estimated using restricted maximum likelihood (REML), and genotype performance was predicted using best linear unbiased prediction (BLUP). Third, significant GEI was further investigated using the AMMI model, and genotypic stability was assessed using the Modified AMMI Stability Value (MASV). Finally, GGE biplot analysis was conducted to evaluate genotype performance, stability, adaptability, and the discriminating ability and representativeness of test environments.

All statistical analyses were performed in R version 4.2.3 [26], except AMMI biplot analysis, which was conducted using GenStat Version 18 [27]. GGE biplot analysis was performed using the GGEBiplotGUI package [8]. For variance component estimation and genotype prediction, a linear mixed model was fitted in which genotype, environment, GEI, and replication nested within environment were treated as random effects, while the overall mean was considered fixed.

The combined linear model was as follows:

$$Yijk = \mu + Gi + Ej + (GE)ij + Rk(j) + \varepsilon ijk, \quad (1)$$

where *Yijk* is the observed GY of genotype *i* in replication *k* within environment *j*; μ is the overall mean; *Gi* is the genotype effect; *Ej* is the environment effect; (GE) *ij* is the GEI effect; *Rk*(*j*) is the replication effect nested within environment; and εijk is the residual error.

2.5.1 | AMMI Analysis

The AMMI model was used to analyze GEI for GY. The model combines ANOVA for the additive effects of genotypes and environments with PCA of the interaction matrix to describe multiplicative GEI effects [21]. Following the combined ANOVA, the GEI sum of squares was partitioned into interaction principal component axes (IPCAs), and significant IPCAs were used to interpret interaction patterns.

An AMMI biplot with symmetric scaling was generated to visualize the relationships among genotypes, environments, and their interactions. In addition, an AMMI mega-environment delineation biplot was constructed to identify groups of environments with similar genotype responses and to determine specifically adapted and broadly adapted genotypes.

The AMMI model was expressed as follows:

$$Yij = \mu + Gi + Ej + \Sigma\lambda n\alpha in\gamma jn + \varepsilon ij, \quad (2)$$

where *Yij* is the mean GY of genotype *i* in environment *j*; μ is the grand mean; *Gi* is the genotype deviation from the grand mean; *Ej* is the environment deviation from the grand mean; λn is the singular value of the *n*th IPCA; αin is the genotype eigenvector score for the *n*th IPCA; γjn is the environment eigenvector score for the *n*th IPCA; and εij is the residual error.

2.5.2 | Stability Index (MASV)

Genotypic stability was assessed using the MASV, which was calculated from the IPCA scores obtained from the AMMI model. Lower MASV values indicate greater stability across environments. The stability statistic was computed following [28].

$$\mathrm{MASV} = \Sigma\sqrt{(\lambda k \times \mathrm{IPCAk}^2)}, \quad (3)$$

where λk is the eigenvalue of the *k*th IPCA and IPCAk is the genotype score on the *k*th IPCA.

2.5.3 | GGE Biplot Analysis

GGE biplot analysis was employed to evaluate genotype performance and stability across environments and to visualize GEI patterns for GY [18].

The GGE biplot was used to identify high-yielding and stable genotypes, visualize the "which-won-where" pattern for mega-environment identification, assess genotype stability using the Average Environment Coordinate (AEC) method, and evaluate the discriminating ability and representativeness of test environments. Genotypes with high mean yield and low projection onto the AEC ordinate were considered more stable [18]. Environments with longer vectors were regarded as more discriminating, whereas environments located closer to the average environment axis (AEA) were considered more representative. The analysis was based on the decomposition of genotype main effects and GEI effects after environment centering. Singular value decomposition was performed as follows:

$$Yij - \overline{Y}.j = \Sigma\lambda k\xi ik\eta jk, \quad (4)$$

where *Yij* is the mean GY of genotype *i* in environment *j*; $\overline{Y}.j$ is the mean yield of all genotypes in environment *j*; λk is the singular value of the *k*th principal component; ξik is the genotype score for the *k*th principal component; ηjk is the environment score for the *k*th principal component; and *k* is the number of retained principal components.

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3 | Result of the Study

3.1 | Combined ANOVA for GY of Emmer Wheat Landraces Across Five Environments

The combined ANOVA revealed highly significant ($p < 0.001$) effects of environment (E), genotype (G), and GEI on GY, indicating substantial variation among test environments and genotypes as well as differential genotype responses across environments (Table 1). The environment effect accounted for the largest proportion of the total variation, with a sum of squares of 18,532.4, representing approximately 43.9% of the total treatment variation. The highly significant environmental effect ($F = 135.24$, $p < 0.001$) indicates that the testing environments differed considerably in their capacity to support GY, reflecting variations in climatic and edaphic conditions among location-year combinations.

Genotypic differences were also highly significant ($F = 9.27$, $p < 0.001$), with a sum of squares of 6863.2, accounting for approximately 16.3% of the total variation. This result demonstrates the existence of substantial genetic variability among the evaluated genotypes and suggests opportunities for selection and genetic improvement. The GEI was highly significant ($F = 4.50$, $p < 0.001$), contributing 13020.2 units of sum of squares, equivalent to approximately 30.9% of the total variation. The magnitude and significance of GEI indicate that genotype performance was not consistent across environments, with some genotypes performing relatively better in specific environments than in others. This crossover response complicates genotype selection and highlights the importance of evaluating genotypes across multiple environments. The replication effect within environments was also significant ($F = 12.78$, $p < 0.001$), suggesting measurable variation among experimental blocks and supporting the effectiveness of including replication in the experimental design.

Among the treatment sources of variation (G, E, and GEI), the environment effect was approximately 2.7 times larger than the genotype effect and 1.4 times larger than the GEI effect, indicating that environmental factors were the dominant source of yield variation. Nevertheless, the substantial contribution of GEI relative to genotype main effects emphasizes the need for stability and adaptability analyses. Therefore, AMMI, MASV, and GGE biplot analyses were subsequently conducted to investigate the interaction structure, identify stable genotypes, and determine superior genotypes across environments.

3.2 | REML Variance Components and BLUP Analysis

3.2.1 | REML Variance Component Analysis

Variance components estimated using REML revealed substantial variation among the sources of variation for GY. Environmental variance ($\sigma^2 e = 8.487$) was the largest component, indicating a strong influence of environmental conditions on trait expression. This was followed by GEI variance ($\sigma^2 ge = 4.705$), demonstrating that genotypes responded differently across environments. Genotypic variance ($\sigma^2 g = 1.318$) was relatively lower compared to environmental and interaction effects, suggesting that environmental factors played a dominant role in determining phenotypic performance (Table 2). The coefficient of variation (CV = 13.5%) and grand mean (12.1) indicated acceptable experimental precision and reliability of the data.

3.2.2 | BLUP-Based Genotypic Performance

BLUP analysis was used to estimate the adjusted genotypic performance of the evaluated genotypes for GY while accounting for environmental and genotype × environment (G × E) effects. The BLUP values showed considerable variation among genotypes, ranging from −1.85 to 3.05, indicating substantial differences in predicted genotypic performance for GY (Table 3). Genotype G155 exhibited the highest BLUP value (3.046), followed by G96 (2.544), G177 (1.974), G78 (1.933), and G114 (1.661), indicating superior predicted genotypic performance for GY. In contrast, G247 showed the lowest BLUP value (−1.849), followed by G197 (−1.834), G97 (−1.824), G225 (−1.699), and G241 (−1.611), indicating relatively lower predicted genotypic performance. Overall, the BLUP analysis identified genotypes with contrasting levels of predicted genetic performance for GY. The BLUP estimates were interpreted as indicators of predicted genotypic performance, while stability, broad adaptation, and specific adaptation were assessed separately using AMMI- and GGE-based analyses.

3.3 | AMMI ANOVA and PCA of GEI

The AMMI analysis (Table 4), revealed that environmental effects were highly significant ($F = 142.71$, $p = 2.44 \times 10^{-5}$), indicating strong variability among test environments and their major contribution to the total phenotypic variation. Genotypic effects ($F = 9.43$, $p < 0.001$) and G × E interaction ($F = 4.55$,

TABLE 1 | Combined analysis of variance (ANOVA) for grain yield across five environments.

Source of variation	DF	Sum of squares	Mean square	*F* value	Pr (> *F*)
Environment (E)	4	18532.4	4633.1	135.24	< 0.001***
Replication (Env)	5	171.3	34.3	12.78	< 0.001***
Genotype (G)	269	6863.2	24.9	9.27	< 0.001***
Genotype × Environment	1076	13020.2	12.1	4.50	< 0.001***
Error	1345	3577.1	2.66	—	—
Total	2699	42164.2	—	—	—

Note: Environment refers to the five location–year combinations evaluated in the study. Replication (Env) denotes replication nested within environment. Genotype × environment (G × E) represents the interaction between genotypes and environments. Error variance was obtained from the lattice-adjusted analysis.
Abbreviations: DF, degrees of freedom; MS, mean square; SS, sum of squares.
***Significant at $p < 0.001$.

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TABLE 2 | Variance components estimated using REML for grain yield (GY).

Statistic	GY
Genotypic variance (σ^2g)	1.318
Genotype × environment variance (σ^2ge)	4.705
Environmental variance (σ^2e)	8.487
Residual variance	2.667
Grand mean	12.10
Coefficient of variation (CV %)	13.5

Note: GY = grain yield (q ha^{-1}); σ^2g = genotypic variance; σ^2ge = genotype × environment interaction variance; σ^2e = environmental variance; residual variance = experimental error variance; grand mean = overall mean grain yield across environments; CV (%) = coefficient of variation, calculated as the ratio of the standard deviation to the mean and expressed as a percentage.

TABLE 3 | Selected (top 20 and bottom 5) genotypes based on BLUP estimates for grain yield (GY).

Category	Rank	Genotype	BLUP
Top	1	G155	3.045990
Top	2	G96	2.543710
Top	3	G177	1.974104
Top	4	G78	1.932712
Top	5	G114	1.660836
Top	6	G145	1.592761
Top	7	G59	1.572899
Top	8	G15	1.552636
Top	9	G166	1.551341
Top	10	G126	1.482245
Top	11	G92	1.470987
Top	12	G116	1.470314
Top	13	G137	1.458418
Top	14	G207	1.410464
Top	15	G67	1.364441
Top	16	G77	1.351276
Top	17	G167	1.351271
Top	18	G176	1.310235
Top	19	G175	1.296953
Top	20	G262	1.272371
Bottom	1	G247	−1.848529
Bottom	2	G197	−1.833601
Bottom	3	G97	−1.824349
Bottom	4	G225	−1.699393
Bottom	5	G241	−1.610546

$p < 0.001$) were also highly significant, confirming the presence of substantial genetic variability and differential genotype responses across environments. Partitioning of the G × E interaction through PCA showed that the first IPCA (IPCA1) accounted for 69.2% of the interaction sum of squares and was highly significant, while IPCA2 and IPCA3 explained an additional 20.5% and 8.5%, respectively, bringing the cumulative explanation of the interaction to 98.2%. The fourth (IPCA4) contributed only 1.8% and was not significant, indicating that higher-order interaction effects were negligible. Overall, the results demonstrate that the G × E interaction structure is effectively captured by the first two IPCAs, suggesting a relatively simple interaction pattern and supporting the use of AMMI1 or AMMI2 models for the identification of stable and specifically adapted genotypes across environments.

3.4 | Stability Analysis

The stability analysis revealed differences in GY stability among emmer wheat landraces across environments (Table 5). Landrace G59 emerged as the most stable genotype, exhibiting the lowest MASV value (9.5), indicating relatively low GEI and greater stability across the test environments, with a mean GY of 15 q ha^{-1}. The MASV is a stability index derived from the AMMI model that incorporates multiple interaction principal components to quantify the stability of genotypes across environments. G145 and G262 also showed relatively favorable stability, with low MASV values and mean GYs, indicating their potential for consistent performance across environments. G96 recorded the highest mean GY (16.97 q ha^{-1}) and a relatively favorable MASV value (25), indicating high GY combined with comparatively favorable stability based on the MASV measure. Landraces G92, G137, G175, and G141 showed intermediate levels of stability, with MASV values ranging from 51 to 87 and mean GYs of 14–15 q ha^{-1}. In contrast, G117, G196, and G56 exhibited relatively high MASV values (106–115), indicating lower stability and relatively lower mean GYs (12 q ha^{-1}).

3.5 | Stability and Yield Performance of Ethiopian Emmer Wheat Landraces Across METs From AMMI Biplot Analysis

The AMMI biplot based on the first two IPCAs (IPCA1 and IPCA2) explained 89.8% of the GEI sum of squares, with IPCA1 and IPCA2 accounting for 69.24% and 20.52%, respectively (Figure 2). The distribution of environments revealed contrasting interaction patterns, with E1, E2, and E3 positioned on the positive side of IPCA1, whereas E4 and E5 were located on the negative side, indicating differences in environmental conditions and the presence of crossover GEI. The close association among E1 and E3 suggests a similar genotype ranking pattern, while E4 and E5 represented contrasting environmental conditions. Genotypes positioned near the origin exhibited small interaction effects and were considered more stable across environments, whereas genotypes farther from the origin showed stronger specific adaptation to particular environments. Genotypes located in the direction of E1–E3 showed positive interaction and potential adaptation to these environments, while those associated with E4 and E5 displayed specific adaptation to the contrasting environmental conditions. Overall, the AMMI analysis revealed considerable GEI and identified distinct patterns of genotype adaptation, providing insights into environmental grouping and the selection of stable and specifically adapted genotypes.

3.6 | Mega-Environment Delineation and Genotypic Performance of Emmer Wheat Using AMMI Biplots

The AMMI scatter plot based on the first two IPACs explained 79.89% of the total GEI, with IPCA1 and IPCA2 accounting for

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TABLE 4 | AMMI analysis of variance and principal component decomposition for grain yield of emmer wheat landraces.

Source	DF	SS	MS	*F*-	Pr (> *F*)	Proportion	Accumulated
Env	4	18,487	4621.82	142.71	2.44E − 05	NA	NA
Rep (Env)	5	162	32.39	12.11	1.69E − 11	NA	NA
Gen	269	6782	25.21	9.43	3.57E − 179	NA	NA
Gen ∗ Env	1076	13,088	12.16	4.55	2.90E − 146	NA	NA
PC1	272	9061	33.31	12.46	0.00E + 00	69.2	69.2
PC2	270	2686	9.95	3.72	0.00E + 00	20.5	89.8
PC3	268	1107	4.13	1.55	0.00E + 00	8.5	98.2
PC4	266	233	0.88	0.33	1.00E + 00	1.8	100
Residuals	1345	3596	2.674	NA	NA	NA	NA
Total	3775	55,203	14.62	NA	NA	NA	NA

Note: Pr (> *F*) = probability associated with the F-test; PC1–PC4 = first to fourth interaction principal component axes (IPCAs) derived from the genotype × environment interaction; Proportion (%) = percentage of genotype × environment interaction sum of squares explained by each IPCA; Accumulated (%) = cumulative proportion of genotype × environment interaction explained. Rep (Env) indicates replications nested within environments.
Abbreviations: DF, degrees of freedom; MS, mean square; NA, not applicable; SS, sum of squares.

TABLE 5 | Yield performance and MASV stability ranking of the top 20 genotypes selected from a panel of 270 genotypes.

Genotype	GY (Q ha^{-1})	MASV	MASV rank
G59	15.08	9.5	1
G262	15.08	21.5	2
G145	15.14	32	4
G96	16.97	25	3
G92	14.90	51	5
G137	14.88	58	6
G141	14.26	84	11
G175	14.57	87	13
G167	14.67	67	7
G108	13.43	72.5	9
G74	13.48	96	16
G65	13.05	94	14
G12	14.47	98	17
G8	13.70	86	12
G123	14.10	73	10
G77	14.69	71	8
G196	12.39	109	19
G84	14.06	95.5	15
G117	15.88	106	18
G56	12.33	115	20

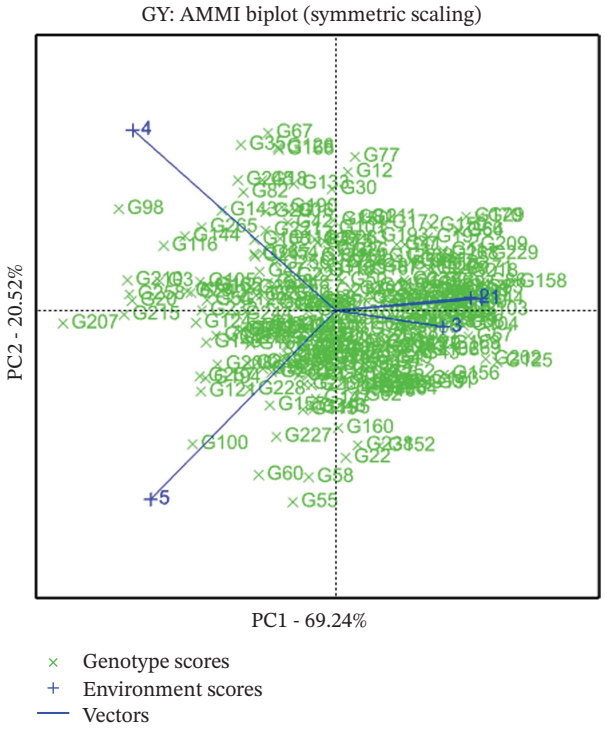


FIGURE 2 | AMMI biplot (symmetric scaling) for grain yield of 270 emmer wheat landraces across five environments.

54.79% and 25.09% of the interaction variation, respectively (Figure 3). The environments were separated into two distinct groups, with E1, E2, and E3 positioned on the positive side of IPCA1 and E4 and E5 located on the negative side, indicating contrasting environmental responses and substantial G × E interaction. The close proximity of E1, E2, and E3 suggests similar genotype discrimination patterns, whereas E4 and E5 formed a separate environmental group. Most genotypes were clustered around the origin, indicating low interaction effects and broad adaptation across environments. In contrast, genotypes such as G155, G96, G207, G98, and G112 were located farther from the origin and exhibited stronger interactions with specific environments. The association of G158 with E1–E3 and of G207 with E4-E5 suggests differential adaptation of genotypes across environments, highlighting the importance of considering G × E interaction in genotype evaluation and selection.

3.7 | Assessment of Mean Performance and Stability

3.7.1 | Basic View of GGE Biplot

The GGE biplot analysis explained a cumulative 79.32%, with PC1 and PC2 explaining 59.71% and 19.61%, respectively (Figure 4). The environment vectors (blue lines) revealed two distinct environmental clusters based on their spatial orientation and the

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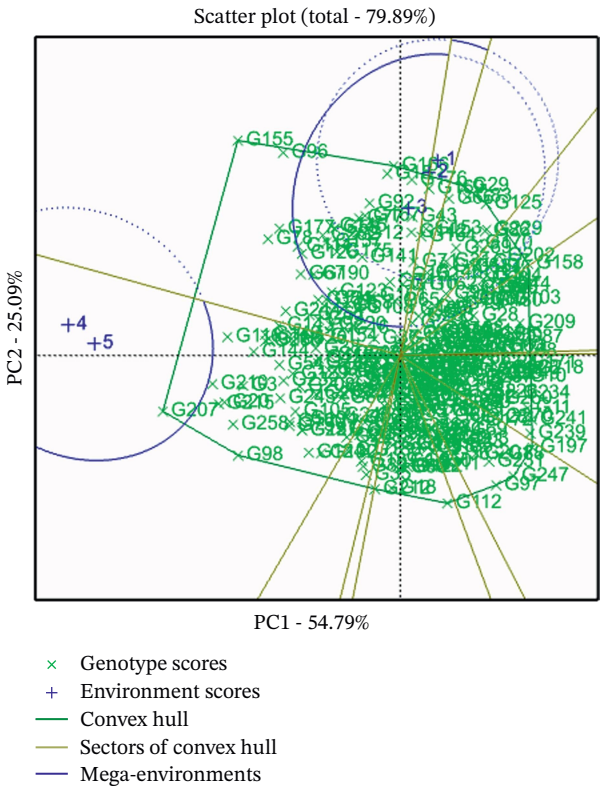


FIGURE 3 | AMMI biplot showing mega-environment delineation for grain yield of 270 emmer wheat landraces across five environments.

acute angles between them. Environments E1, E2, and E3 formed a primary cluster in the upper-right quadrant, indicating strong positive correlation and similar genotype ranking within these sites. Conversely, E4 and E5 clustered together along the negative horizontal axis, demonstrating a separate mega-environment that provides a different set of selective pressures compared to the E1–E3 group.

The distribution of genotypes (green labels) relative to these environmental vectors identifies specific adaptations and performance trends. Genotypes G155 and G96 exhibited high PC2 scores, suggesting specific adaptation to the E1, E2, and E3 environments. In contrast, the dense concentration of genotypes near the origin indicates a large group with average performance and lower sensitivity to environmental fluctuations. Genotypes located further from the origin along the PC1 axis represent those with higher potential yields, while their proximity to the horizontal abscissa suggests greater stability across the tested locations. This spatial arrangement indicates that the testing environments effectively discriminated between genotypes, identifying those with broad versus specific adaptation.

3.7.2 | Which-Won-Where Biplot Analysis of Emmer Wheat Landraces Across Five Environments

The which-won-where feature of the GGE biplot was used to visualize genotype performance across environments and to identify potential mega-environments. The polygon was constructed by connecting the vertex genotypes G158, G96, G155, G112, and G207, which were located farthest from the biplot origin in different directions. Perpendicular lines drawn from the origin divided the biplot into several sectors, each representing a group of environments and their corresponding winning genotype (Figure 5).

Environments E1, E2, and E3 were grouped within the same sector on the positive side of PC1 and were associated with the vertex genotype G158, indicating that G158 was the winning genotype in this group of environments. In contrast, environments E4 and E5 were located in a different sector on the negative side of PC1 and were associated with G207, identifying G207 as the winning genotype in these environments. According to GGE biplot theory, environments that fall within the same sector and share the same winning genotype are considered a mega-environment. Therefore, the five test environments were classified into two mega-environments: Mega-environment I (E1, E2, and E3), where G158 was the winning genotype, and Mega-environment II (E4 and E5), where G207 was the winning genotype. This grouping indicates the presence of crossover GEI.

The remaining vertex genotypes (G96, G112, and G155) formed sectors that did not contain any test environments. Although these genotypes contributed to the overall structure of the GGE biplot, they were not identified as winning genotypes in any of the evaluated environments.

3.7.3 | Biplot Analysis of Environmental Discriminativeness and Representativeness

The discriminativeness and representativeness of the testing environments were evaluated using the GGE biplot based on the AEA (Figure 6). The vector length of each environment indicated its discriminating ability, while the angle between each environment vector and the AEA reflected its representativeness. Environments E4 and E5 exhibited the longest vectors and were located farthest from the origin along the negative side of Axis 1, indicating high discriminating ability but low representativeness. In contrast, E2 showed a relatively short vector and the smallest angle with the AEA, indicating that it was the most representative environment of the overall testing conditions.

Environments E1 and E3 showed intermediate vector lengths and moderate proximity to the AEA, suggesting that they provided a balance between discriminating ability and representativeness. The close clustering of E1, E2, and E3 on the positive side of Axis 1 indicates that these environments are positively correlated and represent a similar environmental pattern. In contrast, E4 and E5 formed a distinct group on the opposite side of Axis 1, indicating a contrasting environmental structure and low correlation with the first group.

From a selection perspective, E2 is identified as the most suitable environment for general genotype evaluation due to its high representativeness and proximity to the AEA, ensuring that genotype performance in this environment closely reflects the overall mean performance across environments. Conversely, E4 and E5 are more suitable for genotype discrimination and identification of specifically adapted genotypes due to their high discriminating power and contrasting environmental effects.

3.7.4 | Mean Versus Stability View of Biplot

The mean performance and genotype stability were evaluated using the AEC method (Figure 7). The AEC abscissa (the green line with a single-headed arrow) indicates the direction of higher mean performance across all environments. Genotypes located

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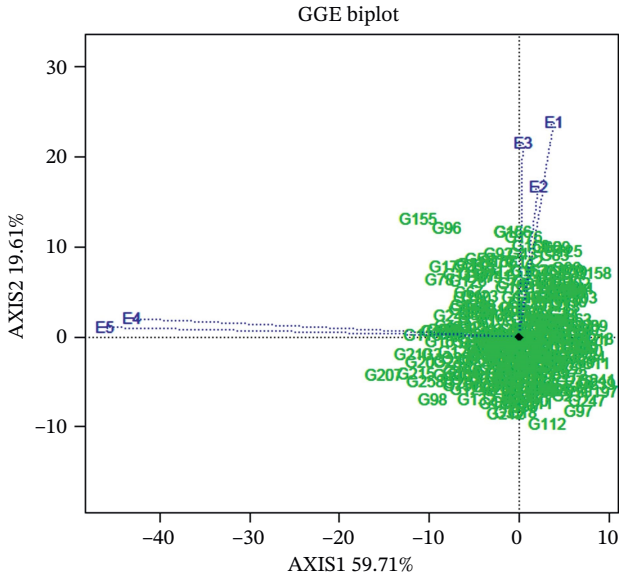


FIGURE 4 | GGE biplot (basic view) of 270 emmer wheat landraces tested across five environments.

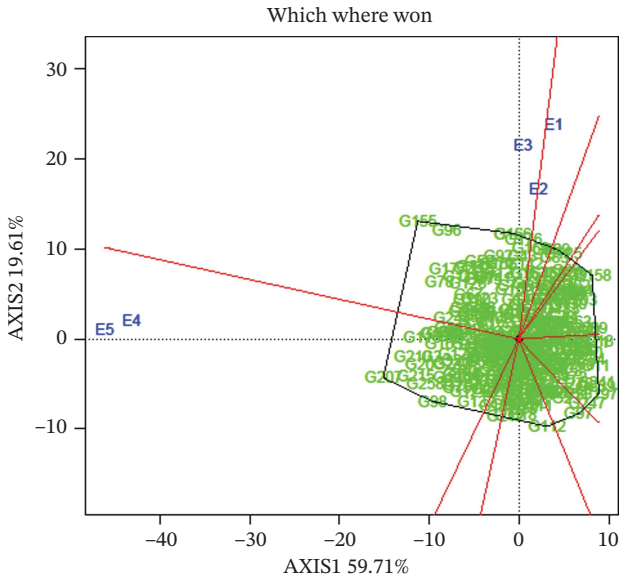


FIGURE 5 | Which-won-where biplot of 270 emmer wheat landraces tested across five environments.

extending along this axis toward the arrow direction, such as G155, G96, and G176, exhibited the highest mean performance. Conversely, genotypes positioned at the opposite end of the abscissa, such as those in the lower-right quadrant like G112, demonstrated the lowest mean performance.

Genotype stability is shown by the perpendicular distance (projections) from each genotype to the AEC abscissa. A shorter projection indicates greater stability across environments, while a longer projection denotes lower stability and higher genotype-by-environment (GE) interaction. In this biplot, a large group of genotypes clustered near the origin showed short projections, suggesting high stability but average performance. Genotypes G155 and G96 exhibited the longest projections relative to the AEC abscissa, indicating significant instability and highly specific performance across the testing environments. In contrast,

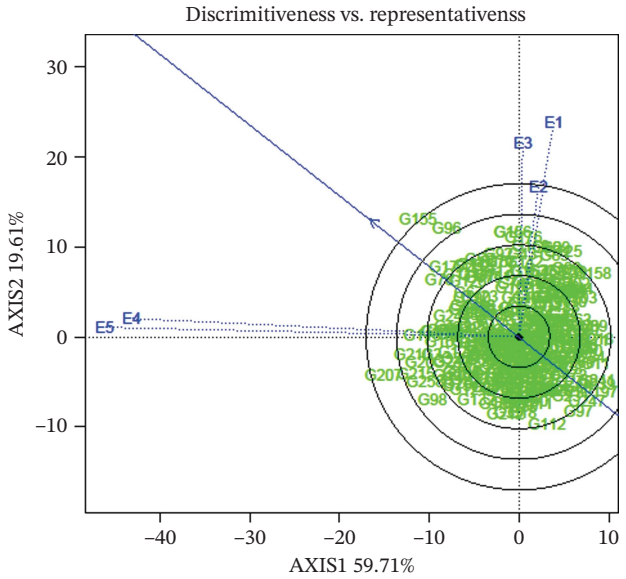


FIGURE 6 | Discriminativeness and representativeness of environments biplot view of 270 emmer wheat landraces tested across five environments.

genotypes positioned closer to the horizontal axis while maintaining a high coordinate on the AEC abscissa represent the most desirable candidates for broad adaptation, as they combine high mean performance with minimal environmental sensitivity.

3.7.5 | Relationship Among Environments: Biplot of Emmer Wheat Landraces Across Five Environments

The GGE biplot explained a cumulative 79.32% of the total phenotypic variation, with Axis 1 and Axis 2 accounting for 59.71% and 19.61%, respectively (Figure 8). The relationships among the five testing environments were assessed based on the magnitude and orientation of their vectors relative to the biplot origin. Environments E1, E2, and E3 clustered in the upper-right quadrant and formed acute angles with each other, indicating a strong positive correlation and similar genotype ranking across these environments. In contrast, environments E4 and E5 exhibited relatively long vectors extending toward the negative side of Axis 1, suggesting a greater discriminating ability in differentiating among genotypes. The wide angular separation between the E1–E3 cluster and the E4-E5 group, approaching an obtuse angle, indicates contrasting genotype responses across these environment groups. Most genotypes were clustered around the biplot's origin, reflecting average performance across environments. However, genotypes such as G155 and G96 showed higher positive scores along Axis 2 and were oriented toward the direction of the E1, E2, and E3 vectors, suggesting a closer association with these environments.

4 | Discussion

4.1 | Magnitude of Variation and GEI

The combined ANOVA across five environments revealed highly significant ($p < 0.001$) effects of genotype, environment, and G × E interaction for GY, indicating substantial genetic

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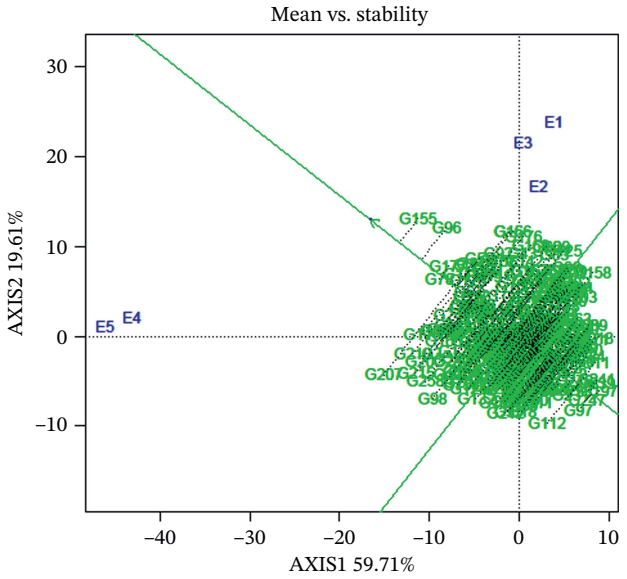


FIGURE 7 | Biplot analysis mean performance vs stability view of 270 emmer wheat landraces tested across the five environments.

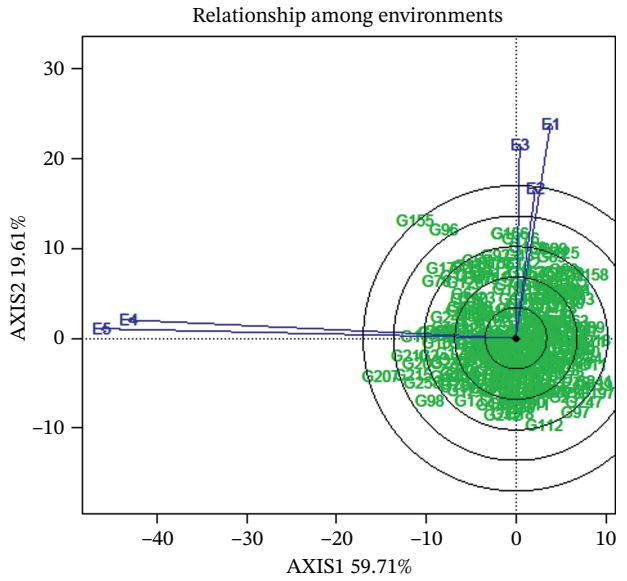


FIGURE 8 | Relationship among environments: biplot of 270 emmer wheat landraces tested across five environments.

variability among emmer wheat landraces and strong environmental control of phenotypic expression. The large environmental effect indicates that yield performance was primarily influenced by site conditions, while the significant G × E interaction confirms differential genotype responses across environments, resulting in genotype re-ranking. Such crossover interactions reduce the reliability of selection based on single environments and highlight the necessity of multienvironment testing for effective genotype evaluation. Similar patterns have been widely reported in wheat, where environmental heterogeneity is the primary driver of yield variability and stability challenges in breeding programs [2, 19, 29].

The REML variance component analysis further supported the ANOVA results by showing that environmental variance constituted the largest proportion of total variation, followed by GEI and genotypic variance. The predominance of environmental and interaction variances indicates that GY expression in emmer wheat is highly sensitive to environmental conditions and that genotype performance cannot be reliably predicted from a single testing environment. Similar patterns have been reported in bread and durum wheat, where environmental effects and G × E interaction account for a major proportion of yield variability under multienvironment testing [2, 19, 30]. The relatively lower genotypic variance observed in this study further emphasizes the importance of evaluating genotypes across diverse environments to accurately identify superior and stable materials for breeding.

4.2 | G × E Structure and Mega-Environment Differentiation

The GGE biplot analysis revealed two distinct mega-environments, with E1–E3 clustering together and E4-E5 forming a separate group. This pattern indicates the presence of contrasting agroecological conditions and differential genotype performance across locations. The "which-won-where" pattern further confirmed crossover interaction and identified specifically adapted genotypes within each mega-environment. These results demonstrate that emmer wheat adaptation is environment-dependent and support the need for location-targeted breeding strategies. Similar mega-environment structures have been widely reported in wheat and other cereals using GGE biplot analysis [18, 31].

4.3 | Identification of High-Yielding and Stable Genotypes

Integration of AMMI-based stability parameters and the MASV identified genotypes with contrasting levels of GY performance and stability. Among them, G59 and G145 emerged as promising genotypes, combining relatively high GY with favorable stability across environments. G262 also showed favorable stability and yield performance, whereas G96 recorded the highest GY but exhibited relatively greater GEI, as reflected by its longer projection in the AEC biplot. The consistency of stability rankings across AMMI-based parameters supports the identification of promising genotypes for further evaluation and potential use in breeding programs. Similar findings have been widely reported in wheat METs, where AMMI-based approaches effectively distinguished stable and high-yielding genotypes under variable environments. Studies in bread wheat have confirmed significant GEI and the effectiveness of AMMI models in identifying superior genotypes across locations [28, 32]. In Ethiopia, AMMI and related stability analyses have been successfully applied in durum and bread wheat to identify stable cultivars adapted to diverse agroecologies, further supporting the reliability of IPCA-based stability measures in selection decisions [33, 34]. These findings are consistent with the present study, where MASV effectively discriminated stable genotypes and supported selection of high-performing entries for breeding advancement.

The BLUP analysis further supported the identification of superior genotypes by providing adjusted estimates of genotypic performance while accounting for environmental and G × E effects. The wide range of BLUP values observed among

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genotypes confirmed substantial genetic variability for GY. Genotypes G155, G96, and G177 exhibited the highest BLUP values, indicating higher predicted genotypic performance for GY. However, their stability varied across environments, as indicated by the AEC and AMMI-based stability analyses. Thus, high predicted genotypic performance based on BLUP was considered separately from stability and adaptation when identifying promising genotypes.

The consistency between BLUP-based rankings and stability analyses reinforces the reliability of these genotypes for selection and breeding advancement. Similar studies in wheat have demonstrated that BLUP-based prediction improves selection accuracy by minimizing environmental bias and providing more precise estimates of genotypic performance under multi-environment testing conditions [35, 36].

4.4 | Yield Stability Trade Off and Adaptation Pattern

A clear trade-off was observed between yield potential and stability, where high-yielding genotypes tended to show greater sensitivity to environmental variation, while more stable genotypes exhibited moderate but consistent performance across environments. This pattern reflects the classical challenge in cereal breeding of balancing productivity with adaptation stability under variable environments. Such trade-offs are well documented in wheat breeding systems and highlight the importance of defining breeding targets based on environmental context rather than uniform selection criteria [9, 19, 33].

4.5 | Breeding Implications for Broad and Specific Adaptation

The combined evidence from ANOVA, AMMI, stability indices, and GGE biplot analysis supports a dual breeding strategy in emmer wheat. Genotypes G59 and G145, characterized by high yield and stability, are strong candidates for broad adaptation and should be advanced to multilocation variety trials. In contrast, genotypes identified through the GGE "which-won-where" pattern demonstrate specific adaptation to particular mega-environments and can be exploited for targeted breeding in defined agroecological zones. This GE matching strategy enhances selection efficiency and genetic gain in heterogeneous production systems [18].

4.6 | Implications for Farmers and Target Environments

From a production perspective, the identified mega-environments provide a practical framework for cultivar deployment. Environments E1 and E2, which showed greater similarity and stability, are suitable for broadly adapted genotypes such as G59 and G145, ensuring consistent yield performance and reduced production risk. In contrast, environments E3, E4, and E5, characterized by stronger environmental variability, are better suited for specifically adapted genotypes capable of exploiting local conditions. This targeted deployment strategy improves productivity while reducing yield uncertainty for farmers in stress-prone and heterogeneous agroecologies [18, 29].

5 | Conclusions

This study evaluated 270 emmer wheat landraces across five environments in the Tigray region using integrated multi-environment analytical approaches, including ANOVA, AMMI, MASV, and GGE biplot analyses. The results revealed substantial genetic variability among the evaluated landraces and highly significant GEI, indicating that GY performance of emmer wheat is strongly influenced by environmental conditions. The significant crossover interaction observed among environments demonstrates that genotype ranking varied across test locations, emphasizing the importance of multienvironment testing for effective selection decisions and reliable identification of stable and well-adapted genotypes.

The AMMI and GGE biplot models explained 79.32%–89.8% of the total G × E interaction variation, indicating that these models adequately captured the major interaction patterns and provided a reliable basis for evaluating genotype performance and stability. Both analyses consistently identified two major mega-environments, confirming the existence of both broadly and specifically adapted genotypes. Based on combined yield performance and stability parameters, genotypes G59, G262, and G145 were identified as promising candidates for broad adaptation across the tested environments. In contrast, G117, G196, and G56 exhibited relatively low yield stability based on their high MASV values. The GGE analysis identified G158 as the winning genotype across E1–E3 and G207 as the winning genotype across E4-E5, indicating their specific adaptation to the respective mega-environments and their potential value for targeted breeding and location-specific deployment.

The dominant contribution of environmental effects to GY variation highlights the strong influence of agroecological conditions on emmer wheat productivity and underscores the need for environment-specific breeding strategies, variety evaluation, and recommendation systems. These findings provide valuable information for developing both broadly adapted and specifically adapted emmer wheat cultivars suitable for diverse production environments.

5.1 | Study Limitations

Despite the robust multienvironment evaluation, this study was limited to five testing environments within a single regional agroecological zone and two growing seasons. Consequently, the environmental range may not fully represent long-term climatic variability or broader national and international adaptation potential. Furthermore, the study focused primarily on GY performance, while other important agronomic, physiological, quality, and stress-tolerance traits were not comprehensively integrated into the stability assessment.

6 | Recommendations

Future research should expand multienvironment testing across a wider range of agroecological zones and multiple years to better capture temporal and spatial variability in genotype performance and adaptation. Integrating physiological, grain quality, and stress-tolerance traits with yield stability analyses is also recommended to facilitate comprehensive selection of superior emmer wheat genotypes.

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For breeding programs, genotypes showing favorable yield performance and stability, such as G59, G145, and G262, should be advanced to multilocation variety trials for further validation and potential release. Specifically adapted genotypes identified through the GGE analysis, particularly G158 for E1–E3 and G207 for E4-E5, should be considered for targeted breeding and further evaluation within their respective mega-environments. For emmer wheat production in Tigray, G59, G145, and G262 warrant further validation across major production environments, while G158 and G207 may be evaluated in their respective mega-environments to assess their yield performance and adaptation. Overall, the integration of ANOVA, AMMI, stability indices, and GGE biplot analyses provides a robust framework for identifying high-yielding and stable emmer wheat genotypes and supports the development of both broadly and specifically adapted cultivars for diverse agroecological conditions.

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Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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