American Journal of Bioscience and Bioengineering
2026, Vol. 14, No. 4, pp. 67–74
https://doi.org/10.11648/j.bio.20261404.13

Research Article

# AMMI Analysis for Grain Yield Stability of Early Maturing Sorghum Genotypes in East Hararghe, Ethiopia

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## Abstract

Sorghum (Sorghum bicolor (L.) Moench) is a critical staple cereal in semi-arid tropics, yet its productivity is highly constrained by genotype × environment interaction (GEI), which complicates variety selection and recommendation. This study aimed to estimate the magnitude of GEI, evaluate grain yield performance, and identify stable, high-yielding and early-maturing sorghum genotypes for potential release in East Hararghe, Ethiopia. Fourteen sorghum genotypes alongside two standard checks (Fadis 01 and Melkam) were tested across six environments, combining two locations (Fadis and Erer) over three consecutive main cropping seasons (2022–2024) using a randomized complete block design with three replications. Data on grain yield and agronomic traits were subjected to combined analysis of variance, Additive Main Effects and Multiplicative Interaction (AMMI) analysis, and Genotype Main Effect plus GEI (GGE) biplot analysis. Combined ANOVA revealed highly significant ($P < 0.001$) effects for genotype, environment, and GEI, confirming differential genotypic responses across testing environments. AMMI analysis partitioned the total grain yield variation, attributing 18.54% to genotype, 25.15% to environment, and 28.86% to GEI, indicating that environmental factors and their interaction with genotypes were the dominant sources of variation. The first two interaction principal component axes (IPCA1 and IPCA2) jointly explained 75.56% of the GEI variation, with IPCA1 contributing 52.6% and IPCA2 contributing 22.96%. Genotype G6 (ETSC14576-5-1) recorded the highest mean grain yield (4265 kg $ha^{-1}$) and demonstrated exceptional stability across environments, as evidenced by its proximity to the IPCA zero line in the AMMI1 biplot, favorable AMMI stability value, and low genotype selection index. GGE biplot analysis further ranked G6 closest to the ideal genotype, confirming its superior mean performance and stability. Polygon view identified three mega-environments, with G6 emerging as the winning genotype in one of them. Based on the integrated assessment using mean yield, AMMI parameters, and GGE biplot outputs, genotype ETSC14576-5-1 (G6) is identified as the most stable and high-yielding genotype across the tested environments. Therefore, this genotype is recommended for variety verification and subsequent release for cultivation in East Hararghe and similar agro-ecologies.

## Keywords

AMMI, GGE, Genotypes, Grain Yield, Sorghum, Stability

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**Received:** 12 June 2026; **Accepted:** 1 July 2026; **Published:** 30 July 2026

## 1. Introduction

Sorghum (*Sorghum bicolor* (L.) Moench) ranks among the top five cereal crops globally after wheat, maize, rice, and barley [5] and is widely grown in areas with abiotic stresses due to its excellent stress resistance [1]. It is the second most important cereal after maize in Sub-Saharan Africa [9] and serves as a staple food for food-insecure populations [3]. Sorghum contains significant minerals (P, K, Ca, Zn, Mg, Fe, Na) and vitamins (A, B, D, E, K, β-carotene) [2, 11].

In Ethiopia, sorghum is widely grown for food and forage [13], particularly in lowland areas due to drought tolerance [8]. Major production regions include Oromia, Amhara, Tigray, and SNNPR. Despite its significance, Ethiopia's sorghum yield increment is insufficient, with drought being a primary limiting factor.

GEI analysis helps breeders develop improved genotypes with superior performance across diverse environments. AMMI (Additive Main Effects and Multiplicative Interaction) analysis investigates GEI in crop breeding. This study evaluated GEI, identified high-yielding genotypes for grain yield and agronomic traits, and assessed stability across testing environments.

## 2. Materials and Methods

### 2.1. Experimental Sites and Genotypes

Sixteen early maturing sorghum genotypes (including checks Fadis 01 and Melkam) were evaluated at Fadis and Erer research stations over three consecutive cropping seasons (2022-2024). The areas possess bimodal rainfall patterns suitable for early maturing sorghum.

***Table 1.*** *List of sorghum genotypes evaluated at multi-location trials during 2021-2023 main cropping season.*

| Genotype Code | Genotype | Pedigree |
|---|---|---|
| G1 | ETSC14793-1-1 | ICSR56/13sudanint#27 |
| G2 | ETSC15376-4-1 | WSV387/(P9404/2372) |
| G3 | ETSC14828-3-3 | SILA/13sudanint#14 |
| G4 | ETSC14596-4-1 | Meko-1/13sudanint#27 |
| G5 | ETSC14577-9-7 | Dekeba/13sudanint#11-3 |
| G6 | ETSC14576-5-1 | Meko-1/13sudanint#11-3 |
| G7 | ETSC14725-3-2 | 13MIF5#5024/13sudanint#27 |
| G8 | ETSC14719-1-4 | (Meko-1/SRN39)/13sudanint#14 |
| G9 | ETSC14590-1-1 | Gambella1107/13sudanint#13-2 |
| G10 | ETSC14214-7-3 | SILA/SRN39 |
| G11 | ETSC14252-4-1 | ETSL101866/S35 |
| G12 | ETSC14726-1-1 | 13MIF5#5076/13sudanint#27 |
| G13 | ETSC14669-3-1 | Mominay4/13sudanint#14 |
| G14 | ETSC14652-2-2 | Tseadachimure/13sudanint#13-2 |
| - | Fadis 01 | M-36121 X P-9403 |
| - | Melkam | WSV387 |

### 2.2. Experimental Design and Management

Randomized complete block design with three replications was employed. Recommended rates: 12 kg/ha seed, 100 kg/ha NPS, 100 kg/ha Urea (half at planting, half at knee height). Plots: five rows, 3 m length, 0.75 m row spacing, 0.20 m plant spacing. Standard agronomic practices were followed.

### 2.3. Data Collection and Analysis

Data collected: days to flowering (DTF), days to maturity (DTM), plant height (PLH), panicle length (PL), grain yield (GYLD). R software was used for ANOVA. AMMI model [4]:

$$Yij = \mu + Gi + Ej + \Sigma\lambda k\ \alpha ik\ \gamma jk + eij$$

AMMI stability value (ASV) and genotype selection index (GSI) were calculated Purchase et al. [10] and Farshadfar [6]. GGE biplot analysis followed Yan [15].

## 3. Results and Discussion

### 3.1. Combined ANOVA

Pooled ANOVA showed highly significant differences ($p \leq 0.001$) for genotype (G), year (Y), G×Y, and L×Y, and significant differences ($p \leq 0.05$) for location, G×L, and G×L×Y (Table 1). Significant GEI indicated genotypes responded differently to environmental conditions, necessitating multi-location testing.

*Table 2. Combined ANOVA for grain yield and related traits across six environments.*

| Source | Df | SS | MS |
|---|---|---|---|
| Genotype (G) | 15 | 55,266,900 | 3,684,460*** |
| Location (L) | 1 | 2,670,893 | 2,670,893* |
| Year (Y) | 2 | 37,461,217 | 18,730,608*** |
| G × L | 15 | 14,758,997 | 983,933* |
| G × Y | 30 | 41,839,508 | 1,394,650*** |
| L × Y | 2 | 31,585,562 | 15,792,781*** |
| G × L × Y | 30 | 23,530,589 | 784,353* |
| Residual | 190 | 73,204,131 | 385,285 |

***, **, * significant at 0.001, 0.01, 0.05; ns, non-significant

### 3.2. Mean Performance

Combined mean grain yield ranged from 2579.53 to 4625.5 kg $ha^{-1}$ (Table 2). Highest yield from G6 (4625.5 kg $ha^{-1}$) followed by G11 (3963.24 kg $ha^{-1}$). Lowest yield from G12 (2579.53 kg $ha^{-1}$). Early flowering: Melkam (78.8 days), G3 (79 days), G4 (79.6 days). Late flowering: G12 (90.5 days).

*Table 3. Combined mean grain yield and yield components.*

| Genotype Codes | GYLD (kg ha-1) | DTF | DTM | PLH (cm) | PL (cm) |
|---|---|---|---|---|---|
| G1 | 2944.23 fg | 85.3 b | 138.3 a | 216 ab | 27.1 a |
| G2 | 2835.08 g | 81.4 e-g | 137.1 ab | 175.2 h | 24.3 ef |
| G3 | 3743.77 b-d | 79 h | 137.1 ab | 180 f-h | 25.3 c-e |
| G4 | 3470.22 c-e | 79.6 gh | 136.7 a-c | 187.8 e-g | 25.4 b-e |
| G5 | 2915.52 fg | 82.5 c-f | 135.7 b-d | 224.7 a | 25.8 a-e |
| G6 | 4265.5 a | 82 c-f | 135.5 b-d | 179.5 f-h | 23.8 fg |
| G7 | 3805.48 bc | 80.4 f-h | 135.2 c-e | 191 ef | 25.7 a-e |
| G8 | 3321.96 ef | 83.7 b-d | 135.1 c-f | 178.1 gh | 26 a-d |
| G9 | 3374.28 de | 81.4 e-g | 134.8 d-f | 187.9 e-g | 22.6 g |

| Genotype Codes | GYLD (kg ha-1) | DTF | DTM | PLH (cm) | PL (cm) |
|---|---|---|---|---|---|
| G10 | 2915.71 fg | 81.5 d-g | 134.6 d-f | 186.4 e-h | 24.4 ef |
| G11 | 3963.24 ab | 78.5 h | 134.4 d-f | 195.5 de | 26 a-d |
| G12 | 2579.53 g | 90.5 a | 134.4 d-f | 202.9 cd | 26.8 ab |
| G13 | 3395.1 c-e | 82.3 c-f | 133.9 d-f | 211 bc | 26.2 a-d |
| G14 | 3496.5 c-e | 83.1 b-e | 133.6 ef | 209.7 bc | 24.7 d-f |
| Fadis 01 | 3579.35 b-e | 83.8 bc | 133.3 f | 182.2 f-h | 26.4 a-c |
| Melkam | 3267.86 ef | 78.8 h | 130.4 g | 155.6 i | 27.1 a |
| Mean | 3365.69 | 82.11 | 135.00 | 191.46 | 25.47 |
| CV | 18.63 | 4.24 | 2.02 | 9.30 | 8.91 |
| LSD | 413.01 | 2.29 | 1.80 | 11.73 | 1.49 |

GYLD= Grain yield in kg/ha; DTF= Days to 50% flowering; DTM= Days to physiological maturity, PLH= Plant height; PL= Panicle length

## 3.3. AMMI Analysis

AMMI ANOVA showed highly significant differences ($P \leq 0.001$) for genotype, environment, and GEI (Table 3). Grain yield variation: genotype (18.54%), environment (25.15%), interaction (28.86%). IPCA1 accounted for 52.6% and IPCA2 for 22.96% of GEI variation, together explaining 75.56%. This is in agreement with the findings of Gauch and Zobel [7] who stated that the most accurate model for AMMI can be predicted using the first two IPCAs. Similar to the present study, Untung et al. [14] also reported that the first two PCAs explained 88.8% of the total variation of genotype × environment interaction on yield in rice genotypes in Indonesia under irrigated environment.

***Table 4.** AMMI analysis of variance for grain yield.*

| Source | d.f. | SS | MS | G × E explained (%) | Cumulative (%) |
|---|---|---|---|---|---|
| Genotypes | 15 | 55286032 | 3685735** | 18.54 | |
| Environments | 5 | 75016883 | 15003377** | 25.15 | |
| Block | 12 | 5441200 | 453433 ns | 1.82 | |
| Interactions | 75 | 86163689 | 1148849** | 28.89 | |
| IPCA 1 | 19 | 45323212 | 2385432** | 52.6 | 52.6 |
| IPCA 2 | 17 | 19783021 | 1163707** | 22.96 | 75.56 |
| IPCA 3 | 15 | 12576836 | 838456* | 14.6 | 90.16 |
| Residuals | 11 | 242021 | 22002 | | |

Note: d.f. = Degree of freedom; SS= Sum of square; MS = Mean square; ** and * =Significant at 0.01 and 0.05 probability level respectively.

## 3.4. AMMI1 Biplot

The AMMI1 biplot (Figure 1) showed G6, G11, G7, and G3 as higher-yielding above average, while G12, G2, G5, G1, and G10 had below-average yield. Genotypes G6, G14, G2, and G13 showed weak environmental influence (lower interaction effect) while genotypes' (G4, G12, G5 and Fadis 01) grain yield was strongly influenced by environmental factors (higher interaction effect). G6, closest to IPCA 0, was most adaptable, high-yielding, and stable across environments.

The average genotype grain yield ranged from 2579.5 kg ha$^{-1}$ (G12) to 4265.5 kg ha$^{-1}$ (G6), while the average environment grain yield was ranged from 3918.79 kg ha$^{-1}$ at Fadis-22 to 2417.0 Kg ha$^{-1}$ at Erer-23 (Table 5). Higher mean grain yield was recorded for genotype G6 (4265.5 Kg ha$^{-1}$) followed by G11 (3963.2 Kg ha$^{-1}$) and G7 (3805.5 Kg ha$^{-1}$) while the lowest grain yield was recorded from genotype G12 (2579.5 Kg ha$^{-1}$) and G2 (2835.1 Kg ha$^{-1}$) across all tested environments (Table 5).

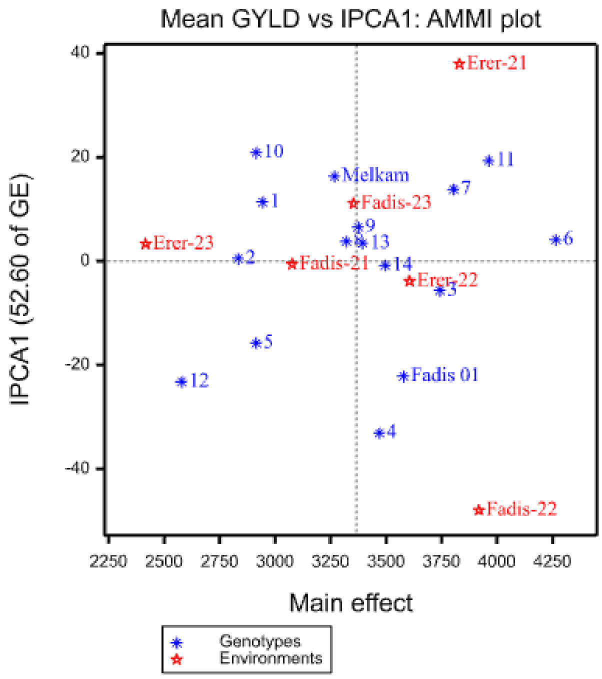


***Figure 1.*** *AMMI biplot of grain yield (symmetrical scaling).*

***Table 5.*** *Combined mean grain yield (Kg ha−1) of 16 sorghum genotypes across six environments .*

| Genotype Code | Environments | | | | | | Mean | Yield adv. (%) |
|---|---|---|---|---|---|---|---|---|
| | Erer-22 | Erer-23 | Erer-24 | Fadis-22 | Fadis-23 | Fadis-24 | | |
| 1 | 4011.9 | 3208.8 | 1988.9 | 2586.7 | 3027.7 | 2841.5 | 2944.3 | |
| 2 | 3403.3 | 3064.1 | 2333.3 | 2423.7 | 3365.3 | 2420.7 | 2835.1 | |
| 3 | 4029.6 | 3978.4 | 2788.9 | 3285.9 | 4619.8 | 3760 | 3743.8 | |
| 4 | 3035.3 | 4100.5 | 1800 | 3555.6 | 5710.7 | 2619.3 | 3470.2 | |
| 5 | 2714.1 | 3124.8 | 1800 | 2381.6 | 4278.6 | 3194.1 | 2915.5 | |
| 6 | 4508.1 | 4068.9 | 3977.8 | 4045.9 | 4452.7 | 4539.3 | 4265.5 | 16.1 |
| 7 | 5125.9 | 4097.3 | 2988.9 | 3324.4 | 3841.5 | 3454.8 | 3805.5 | |
| 8 | 4131.5 | 3693.3 | 1155.6 | 3043 | 3905.5 | 4003 | 3322.0 | |
| 9 | 4382.8 | 3489.3 | 3138.9 | 2240 | 3845.1 | 3149.6 | 3374.3 | |
| 10 | 3919.4 | 2940.6 | 1933.3 | 2478.8 | 2423.6 | 3798.5 | 2915.7 | |
| 11 | 5462.2 | 4373.4 | 2777.8 | 4029.6 | 3628.3 | 3508.1 | 3963.2 | |
| 12 | 1523.5 | 2461.7 | 2700 | 1863.7 | 3997.9 | 2930.4 | 2579.5 | |
| 13 | 4100.7 | 3617.5 | 1888.9 | 2782.2 | 3969.4 | 4011.9 | 3395.1 | |
| 14 | 3778.9 | 3979.9 | 2333.3 | 3585.2 | 3909 | 3392.6 | 3496.5 | |

| Genotype Code | Environments | | | | | | Mean | Yield adv. (%) |
|---|---|---|---|---|---|---|---|---|
| | Erer-22 | Erer-23 | Erer-24 | Fadis-22 | Fadis-23 | Fadis-24 | | |
| Fadis 01 | 3362.3 | 4105 | 2333.3 | 3810.4 | 5142.1 | 2723 | 3579.4 | ---- |
| Melkam | 3792.60 | 3389.60 | 2733.30 | 3792.60 | 2583.50 | 3315.60 | 3267.87 | |
| Env. Mean | 3830.13 | 3605.82 | 2417.01 | 3076.83 | 3918.79 | 3353.90 | 3367.08 | |

The mean performance of tested genotypes across testing locations ranged from 2417.01 kg/ha to 3918.79 kg/ha. Environments Fadis-23, Erer-22, Erer-23 and Fadis-24 recorded above-average grain yield; however, Erer-24 and Fadis-22 recorded below-the average grain yield (Table 5).

## 3.5. Stability Analysis

Based on ASV (Purchase *et al.,* 2000), genotype G2 was most stable (ASV=5.16), followed by G14 (6.13), G13 (9.47), G3 (12.96), and G6 (18.91). Unstable genotypes: G4 (77.86), G12 (61.33), Fadis 01 (52.02). GSI (lowest-most stable): G6 (GSI=6), G3 (8), G13 (11), G7 (12), while G12 (31) and G10 (27) were unstable.

***Table 6.*** *Stability coefficients for grain yield of 16 sorghum genotypes tested on six environments.*

| Genotype Code | Y | rY | Wi | rWi | ASI | rASI | ASV | rASV | GSI |
|---|---|---|---|---|---|---|---|---|---|
| G1 | 2944.229 | 12 | 598001 | 4 | 6.042552 | 8 | 26.31795 | 8 | 20 |
| G2 | 2835.076 | 15 | 388191 | 3 | 1.185433 | 1 | 5.163077 | 1 | 16 |
| G3 | 3743.774 | 4 | 165543 | 1 | 2.974903 | 4 | 12.957 | 4 | 8 |
| G4 | 3470.222 | 7 | 5173311 | 16 | 17.87709 | 16 | 77.86253 | 16 | 23 |
| G5 | 2915.524 | 14 | 1272615 | 8 | 8.305478 | 10 | 36.17398 | 10 | 24 |
| G6 | 4265.453 | 1 | 896980 | 6 | 4.342021 | 5 | 18.91139 | 5 | 6 |
| G7 | 3805.481 | 3 | 1171988 | 7 | 7.330157 | 9 | 31.92603 | 9 | 12 |
| G8 | 3321.961 | 10 | 2100160 | 10 | 4.715615 | 7 | 20.53856 | 7 | 17 |
| G9 | 3374.278 | 9 | 1587256 | 9 | 4.448973 | 6 | 19.37722 | 6 | 15 |
| G10 | 2915.711 | 13 | 2252962 | 11 | 11.06646 | 13 | 48.19927 | 13 | 27 |
| G11 | 3963.243 | 2 | 2266609 | 12 | 10.66702 | 12 | 46.45951 | 12 | 14 |
| G12 | 2579.529 | 16 | 4645374 | 15 | 14.12807 | 15 | 61.53389 | 15 | 31 |
| G13 | 3395.1 | 8 | 869839 | 5 | 2.174235 | 3 | 9.469741 | 3 | 11 |
| G14 | 3496.501 | 6 | 309111 | 2 | 1.40731 | 2 | 6.12945 | 2 | 8 |
| Fadis 01 | 3579.349 | 5 | 2637357 | 14 | 11.94346 | 14 | 52.01897 | 14 | 19 |
| Melkam | 3267.86 | 11 | 2385935 | 13 | 8.698498 | 11 | 37.88575 | 11 | 22 |

## 3.6. GGE Biplot Analysis

The GGE biplot (PC1=52.6%, PC2=22.96%) captured 75.56% of GGE variance. Polygon view identified vertex genotypes: G6, G4, G12, G10, G11 (Figure 2). Three mega-environments formed: MGE1 (Erer-21, Fadis-23, Erer-23) with winning genotypes G7, G11, G14, G13; MGE2 (Erer-22, Fadis-21) with G6; MGE3 (Fadis-22) with G4 and Fadis-01.

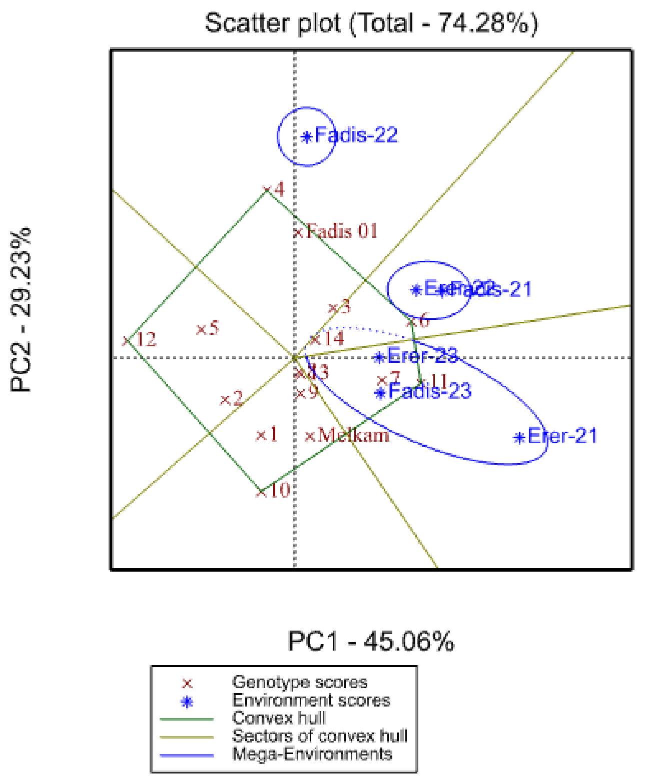


***Figure 2.*** *GGE biplot polygon view for which-won-where pattern.*

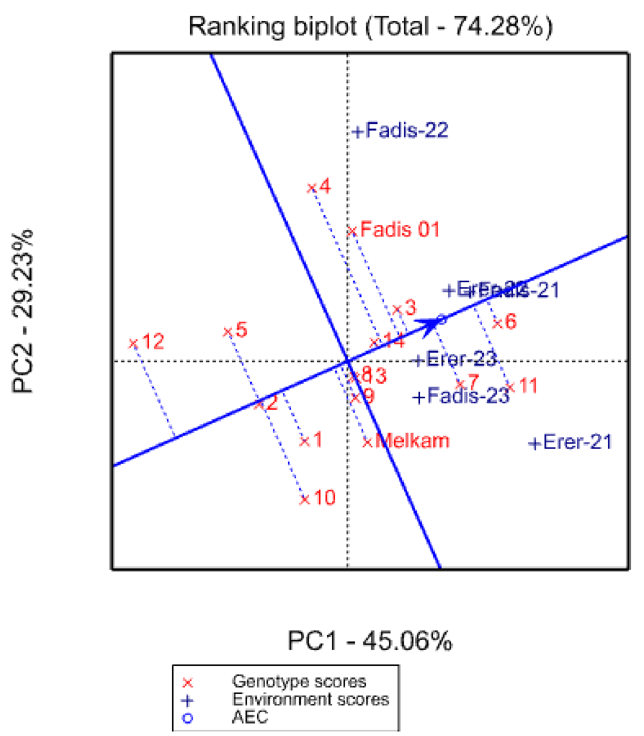


***Figure 3.*** *GGE biplot ranking genotypes for yield and stability.*

Ranking based on mean performance and stability (Figure 3) identified G6 followed by G11 and G7 as closest to the ideal genotype, making them most desirable for testing environments. Genotypes that are close to the ideal genotype are more desirable, while those far from it would not be high yielding and stable [16]. On the other hand, other genotypes like genotype G12, G10, and G5 were far from the ideal genotype and considered as undesirable. The result confirms those by Sharma et al. [12], who found outstanding genotypes near to the ideal genotype in wheat for five consecutive years.

## 4. Conclusion and Recommendation

AMMI and GGE biplot models effectively analyzed multi-environment trait data. Combined ANOVA showed highly significant (P<0.001) effects for genotype, environment, and GEI. Grain yield variation: environment (25.15%), genotype (18.54%), GEI (28.89%). Vertex genotypes (G4, G6, G10, G11, G12) showed greatest responsiveness to environmental change. From combined mean analysis, AMMI, and GGE biplot, genotype G6 (ETSC14576-5-1) was the highest yielder (4265.5 kg $ha^{-1}$) and most stable across six environments. This genotype is recommended for variety verification and possible release in study areas and similar agro-ecologies.

## Abbreviations

| | |
|---|---|
| AMMI | Additive Main Effects and Multiplicative Interaction |
| ANOVA | Analysis of Variance |
| ASV | AMMI Stability Value |
| CV | Coefficient of Variation |
| d.f. | Degree of Freedom |
| DTF | Days to 50% Flowering |
| DTM | Days to Physiological Maturity |
| FAO | Food and Agriculture Organization |
| G | Genotype |
| GEI | Genotype × Environment Interaction |
| GGE | Genotype Main Effects and Genotype × Environment Interaction |
| GSI | Genotype Selection Index |
| GYLD | Grain Yield |
| IPCA | Interaction Principal Component Axis |
| L | Location |
| LSD | Least Significant Difference |
| MGE | Mega-Environment |
| MS | Mean Square |
| PL | Panicle Length |
| PLH | Plant Height |
| SNNPR | Southern Nations, Nationalities, and Peoples' Region |
| SS | Sum of Square |
| Y | Year |

## Author Contributions

**Zeleke Legesse:** Conceptualization, Data curation, Formal Analysis, Investigation, Methodology, Resources, Software, Writing – original draft, Writing – review & editing

**Fikadu Tadesse:** Data curation, Investigation, Methodology, Supervision

**Berhanu Diribsa:** Data curation, Investigation, Methodology, Supervision

**Jifara Gudeta:** Data curation, Methodology, Supervision, Writing – review & editing

## Conflicts of Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper. The research was conducted independently by the Oromia Agricultural Research Institute (IQQO); Fadis Agriculture Research Center, and the authors have no conflicts of interest to disclose.

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