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Research Article

Genotype x Environment Interaction and Grain Yield Stability of Sorghum (*Sorghum bicolor L.* (Moench) Genotypes in West Hararghe Zone

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Abstract

Sorghum (Sorghum bicolor L. Moench) is a vital staple crop in Ethiopia, particularly in drought-prone and marginal agro-ecologies, where it sustains both food security and rural livelihoods. Despite its resilience, national productivity remains below potential, primarily due to limited adoption of improved cultivars and strong genotype × environment (G×E) interactions that constrain stability and adaptability. Therefore, this study was done to estimate the magnitude of GEI and to select the best genotypes that are adaptable and stable for the districts of the West Hararghe Zone. In the current study, eleven sorghum genotypes including standard check were evaluated in six environments under rain-fed conditions using the RCB Design with three replications in the West Hararghe Zone during the 2023–2024 main cropping seasons. Using combined ANOVA, AMMI, and GGE biplot analyses, yield performance, stability, and adaptability were assessed. Results revealed highly significant ($p < 0.01$) effects of genotype, environment, and G×E interaction for grain yield and related traits, indicating the influence of both genetic variability and environmental heterogeneity. Grain yield ranged from 2.78 to 4.63 t ha^{-1}, with genotype G6 consistently achieving the highest mean yield (4.63 t ha^{-1}) as well as highly stabile across environments. Further AMMI and GGE analyses confirmed G6 as the ideal genotype. Further, among tested sites Mechara were identified as representative and discriminating environments, making them suitable for future varietal evaluations. Overall, G6 selected as a strong candidate because of high yielder and consistent thus promoted to next breeding stage for further evaluation at farmers filed to confirm its ideality before release as a variety.

Keywords: *ANOVA, AMMI, GGE, & GEI.*

1. Introduction

Sorghum (Sorghum bicolor L. Moench) is a diploid crop species (2n = 2x = 20) belonging to the family Poaceae Dogget (1988). It is highly valued for its exceptional drought tolerance Reddy *et al.* (2011) and low fertilizer requirement Kimber *et al.* (2013), making it one of the most important cereals for cultivation in arid, semi-arid, and marginal lands. Beyond its resilience, sorghum is nutritionally important, providing carbohydrates, protein, vitamins, and minerals Mayer *et al.* (2008). Consequently, it serves as a staple food for millions of people in semi-arid tropical regions of Asia, Africa, and Central America Derese *et al.* (2018), and plays a critical role, particularly in sub-Saharan Africa Mace *et al.* (2013).

Ethiopia is the third largest producer of sorghum in Africa, after Nigeria and Sudan FAO (2021). It is the third most widely cultivated cereal in terms of both area and production, following teff and maize CSA (2022). Due to tolerate drought and grow in low-fertility soils makes it a preferred crop in the semi-arid and arid agro-ecologies of eastern Ethiopia Adugna (2007). It is the main staple food crop for millions in lowland areas of the country Kebede (1991). Specifically, in the west Hararghe zone ranked first in both area and production CSA (2021). Besides grain, the stalks are extensively used for livestock feed, construction, and fencing Mengistu *et al.* (2020), underscoring their multifunctional role in rural livelihoods.

Despite its importance, average sorghum productivity in Ethiopia remains low, 2.69 t ha^{-1} nationally and 2.3 t ha^{-1} in West Hararghe Zone CSA (2021), compared to its potential yield of about 6 t ha^{-1} FAO (2017). This wide yield gap is attributed to differences in rainfall, soil fertility, temperature, and other environmental stresses, which result in unstable yields across locations and seasons Tadesse *et al.* (2022). Consequently, genotypes respond differently under varying environmental conditions, leading to what is termed genotype by environment (G×E) interaction Yan & Kang (2003). As a result, G×E interaction complicates breeding efforts because a genotype that performs well in one environment may underperform in another, making the identification of stable, high-yielding varieties challenging Anley *et al.* (2013).

Therefore, the knowledge of G×E interaction is essential to identify high yielder and stabile genotypes Yan *et al.* (2000). In this context, statistical models such as the Additive Main Effects and Multiplicative Interaction (AMMI) and Genotype and Genotype × Environment (GGE) biplot analyses are widely employed Gauch & Zobel (1997) and Yan & Tinker (2006). Specifically, the AMMI model combines analysis of variance with principal component analysis to separate additive (genotype and environment) and multiplicative (interaction) effects, thereby identifying both high-performing and stable genotypes Gauch (2013). Meanwhile, the GGE biplot provides a visual representation of genotypic performance and stability across multiple environments, which facilitates the identification of mega-environments and the “which-won-where” pattern Yan & Tinker (2006).

In addition, diverse agro-ecologies, erratic rainfall patterns, and variable soil types create complex conditions for sorghum cultivation in the Hararghe zone Worku *et al.* (2020). Hence, evaluating multiple genotypes across these environments is crucial to identify stable and high-yielding varieties suitable for the region Asfaw *et al.* 2020 and Tadesse *et al.* (2022). Previous research in Eastern Ethiopia has demonstrated that genotypic performance for grain yield and stress tolerance varies significantly across locations, which emphasizes the importance of systematic multi-environment trials Abate *et al.* (2015). Therefore, in the current multi-location trials were conducted with the objectives to estimate the magnitude of GEI and to select the adaptable best genotypes that are high yielder and stable for the study environments.

2. Materials and Methods

2.1. Description of the Study Area

The field experiment was conducted at three locations, namely, Mechara, Tulo (HU sub-site), and Doba (Lencho Wedesaa FTC) at 2023-2024 main cropping seasons. These districts are found in the west Hararghe Zone of Oromia National Regional State, the Eastern part of Ethiopia. A detailed description of the study area is presented in the following Table 1.

Table 1: Description of Experimental Sites

Variables	**Study Areas**		
	Machara	**Hirna**	**Doba**
Dominant Soil type	Sandy loam with a reddish color	Black, Red& vertisoil	Black sandy and loam soil
Altitude (m.a.s.l.)	1796	1758	1739
Annual Temperature (°C)	21	22	20
Minimum	15	13	13
Maximum	28	28	27
Annual rainfall (mm)	1069	943	729
Minimum	963	875	650
Maximum	1175	1010	808

2.2. Experimental Materials and Design

Ten (10) sorghum genotypes with one standard check were evaluated as experimental materials. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications at each site. Each plot measured 15 m^2 (3 m × 5 m) and consisted of four rows with 75 cm spacing between rows. Blocks and plots were separated by 1.5 m and 0.5 m, respectively, to minimize border effects. Sowing was done by drilling seeds at a rate of 12 kg ha^{-1}. Fertilizer application followed national sorghum recommendations: 100 kg ha^{-1}NPS was applied at planting, while 50-kgha^{-1} urea was top-dressed at the vegetative stage before flowering. Standard agronomic practices, including weeding and pest management were uniformly applied across sites to minimize management-related variability.

Table 2: Lists of evaluated sorghum genotypes in 2023-2024 main cropping season

No	Code	Genotypes	Source
1	G3	Hr/14	Collection
2	G2	DL/03	Collection
3	G8	Ch/04	Collection
4	G5	DB/11	Collection
5	G11	Elemo	Variety
6	G4	DL/20	Collection
7	G9	Hr/16	Collection
8	G1	Ch/08	Collection
9	G10	Ch/00	Collection
10	G6	DL/16	Collection
11	G7	DB/21	Collection

2.3. Data Collected

Data were collected using standard sorghum descriptors (IBPGR/ICRISAT, 1993). The details of the data collections are as follows:

- **Days to 50% flowering (days):** Days from seedling emergence until 50% of plants flowered.
- **Days to maturity (days):** Days from seedling emergence until 50% of plants reached physiological maturity.
- **Plant height (cm):** Plant height was measured from five randomly sampled main plants from the two rows at physiological maturity.
- **Head weight (g):** Average panicle weight of five sampled plants.
- **1000-seed weight (g):** Weight of 1000 cleaned grains after threshing.
- **Grain yield (t ha^{-1}):** Yield from the central rows of each plot, threshed, cleaned, adjusted to 12.5% moisture content, and converted to tons per hectare.

2.4. Data Analysis

Combined ANOVA across environments was conducted to partition the total variation into genotype (G), environment (E), and genotype × environment interaction (G×E) effects after confirming homogeneity of variances Steel& Torrie (1980). Since combined ANOVA only quantifies the existence of G×E interaction without explaining its nature, stability, and adaptability, analyses were performed using advanced models. AMMI model (Additive Main Effects and Multiplicative Interaction) used to decompose the G×E interaction into interpretable interaction principal component Zobel *et al*. (1988). However, GGE biplot analysis applied to visualize genotype performance, stability and environmental representativeness Gauch & Zobel (1996) and Yan & Kang (2003). Mean separations were carried out using the Least Significant Difference (LSD) test at 5% probability level, and statistical analyses were performed using R and Genstat 18 edition statistical software packages.

3. Results and Discussion

3.1. Analysis of Variance

The combined analysis of variance revealed highly significant differences among genotypes, environments, and their interaction for grain yield and most yield-related traits (Table 3). This result confirms that genetic variability, environmental effects, and their combined influence simultaneously governed sorghum performance. The presence of significant genetic variability indicates sufficient diversity among the tested genotypes, providing opportunities for selection and improvement, as breeding success depends on the availability of heritable variation Falconer & Mackay (1996). The strong environmental effect highlights the role of site-specific factors such as rainfall distribution, soil fertility, and temperature, which have been reported as major determinants of sorghum productivity in Ethiopia and sub-Saharan Africa Abubakar & Bubuche (2013) and Desalegn *et al*. (2024). In addition, the significant genotype by environment interaction (GEI) demonstrated that genotypes responded inconsistently across locations, resulting in crossover effects where varieties superior in one environment performed poorly in another. This complicates the identification of universally adaptable varieties but also offers opportunities to target genotypes to specific environments. Similar findings have been reported in cereals by Basford & Cooper (1998) and Kang & Pham (1991), and Oladosu *et al.* (2017), emphasizing that yield stability is largely determined by the combined action of genetic and environmental factors. Since ANOVA only indicated the difference and quantifies the magnitude of GEI without describing its pattern thus analysis through mean comparison are necessary to identify superior genotypes Gomez & Gomez (1984) and multivariate models is required for stability.

Table 3: Combined mean values of yield and yield-related for sorghum genotypes across locations in the 2023 to 2024 cropping season at Mechara, Doba, and Tulo.

Genotype	**DF**	**DM**	**PH**	**HW**	**1000w**	**GY**
G1	124.0ab	191.4bc	390.0a	112.9ab	33.86ab	3.106def
G2	120.8bc	191.4bc	358.2 c	108.6bc	31.48 cd	3.367de
G3	119.9c	187.3bcd	366.6bc	105.3bcd	30.77d	3.441cd
G4	110.6f	174.8cde	326.4ef	97.3cde	35.34a	3.457cd
G5	113.5df	175.1cde	314.9fg	91.2e	32.65bc	2.979ef
G6	112.7ef	170.4de	329.9 de	91.2e	35.12 a	4.636 a
G7	116.4d	178.3bcde	246.7 h	110.1bc	34.35ab	3.324de
G8	125.4a	224.6a	373.0 b	124.0a	30.53d	4.272ab
G9	114.8de	186.8bcd	340.0 d	91.5e	35.01a	2.784f
G10	112.4ef	171.5de	309.6g	105.8bcd	34.81a	3.127def
G11	107.4g	166.5e	340.2d	90.6 e	35.32a	3.879bc
GM	116.19	183.9	336.0	102.8	33.57	3.49
G	**	**	**	**	**	**
E	**	**	**	**	**	**
G*E	**	**	**	NS	*	**
CV (%)	4.2	14.4	5.8	19.4	8.4	19.5
LSD (0.05)	3.185	17.41	12.84	13.17	1.86	0.44

Note = *, ** significant and highly significant, respectively, DF: Days to Flowers, DM: Days to Maturity, PH: Plant Height (cm), HW: Head Weight (gm), 1000w: Thousand Seed Weight (gm), GY: Grain Yield (tha^{-1}), G: Genotypes, E: Environments, G*E: Genotype by Environment interaction.

3.2. Mean Comparisons for Grain Yield

Following the significant differences revealed by ANOVA, mean comparisons were conducted to identify superior genotypes across environments (Table 4). The results showed a wide range of yield performance, with G6 (4.63 t ha^{-1}) and G8 (4.27 t ha^{-1}) achieving the highest grain yields, surpassing the grand mean of 3.49 t ha^{-1}. In contrast, G9 (2.78 t ha^{-1}) and G5 (2.97 t ha^{-1}) were among the lowest yielding genotypes. The variation across locations further justify the presence of strong GEI, as genotypes like G6 and G8 demonstrated consistent superiority across multiple sites, while others showed location-specific advantages. These results imply that some genotypes are broadly adaptable, whereas others are better suited to specific environments. However, while mean comparison provides useful insights into yield performance, it does not fully capture the stability or interaction patterns of genotypes across test locations. Therefore, to complement these results and identify varieties that combine high yield with stability, advanced models such as AMMI Zobel *et al.* (1988) and GGE biplot Gauch & Zobel (1996) andYan & Kang (2003) were applied in this study.

Table 4: Mean Performance of 11 Sorghum Genotypes in 6 Environments

Genotypes	**Mecharaa**			**Hirna**			**Doba**			**TM (tha-^{1})**
	2023	**2024**	**mean**	**2023**	**2024**	**mean**	**2023**	**2024**	**mean**	
G1	2.26	2.79	2.5	3.52	3.07	3.29	3.32	3.67	3.49	3.10
G2	3.22	2.52	2.87	3.19	3.17	3.18	3.92	4.18	4.05	3.36
G3	3.31	2.64	2.97	2.96	3.31	2.96	3.96	4.47	4.21	3.44
G4	2.62	2.36	2.49	4.88	2.90	3.89	3.21	4.76	3.98	3.45
G5	3.34	2.07	2.70	3.61	2.71	3.16	2.42	3.72	3.07	2.97
G6	**4.55**	**4.41**	**4.48**	**4.56**	**4.60**	**4.58**	**4.54**	**5.15**	**4.84**	**4.63**
G7	3.68	1.80	2.74	3.90	2.90	3.4	4.10	3.57	3.83	3.32
G8	3.82	3.63	**3.72**	3.66	5.42	**4.54**	4.41	4.70	4.4	4.27
G9	2.78	2.37	2.57	3.64	2.60	3.12	3.20	2.12	2.66	**2.78**
G10	3.53	2.34	2.93	3.62	3.07	3.34	2.79	3.42	3,10	3.12
G11	4.34	2.37	3.35	5.08	3.23	4.15	2.95	5.31	4.13	3.87
GM	3.40	2.66	3.03	3.88	3.36	3.62	3.53	4.10	3.81	3.49

Note: CM: Combine Means, Mechara 2023, Mechara2024, Hirna2023, Hirna2024, Doba2023, Doba2024.

3.3. AMMI analysis of variance for grain yield

To further dissect the GEI structure beyond ANOVA, the AMMI model was employed (Table 5). The analysis revealed highly significant differences for genotypes, environments, and their interaction, with genotypes, environments, and GEI accounting for 27%, 19%, and 24% of the total variation, respectively. The substantial contribution of genotypic effects confirms the presence of exploitable heritable variation, whereas the sizeable GEI component reflects differential responses of genotypes across sites Gauch (1992), Crossa (1990) and Oladosu *et al.* (2017). Partitioning GEI into interaction principal component axes (IPCAs) revealed that IPCA1 and IPCA2 explained 47% and 20% of the variation, respectively, with a cumulative contribution of 67%. According to Gauch & Zobel (1996), such a proportion indicates that the AMMI model reliably captured the underlying interaction structure. These results demonstrate that AMMI is an effective analytical tool for unraveling the complexity of sorghum genotype responses in heterogeneous environments, thereby enabling precise selection of promising genotype.

Table 5: AMMI analysis of variance for grain yield

Source	DF	SS	M.S	SS%	V.r	Fpr
Total	197	207.56	1.054			
Treatments	65	147.50	2.269	71	4.89	<0.001
Genotypes	10	56.91	5.691	27	12.25	<0.001
Environments	5	40.39	8.078	19	22.37	<0.001
Interactions	50	50.20	1.004	24	2.16	<0.001
IPCA 1	14	23.64	1.688	47	3.64	<0.001
IPCA 2	12	10.50	0.875	20	1.88	0.0428
Residuals	24	16.06	0.669		1.44	0.1026
Error	120	55.73	0.464			

Note: DF=Degree of freedom, SS: Sum of squares, MS: Mean of squares, SS %: percentage of sum of squares, IPCA: Interaction principal Interaction principal component analysis, AMMI: Additive mean and Multiplicative Interactions.

3.4 AMMI Stability Value (ASV) and Genotype Selection Index (GSI)

Complementing the AMMI analysis, stability was assessed using AMMI Stability Value (ASV) and Genotype Selection Index (GSI) (Table 6). Genotypes G10, G1, G2, and G6 displayed the lowest ASV values, indicating greater stability across environments, while G11 and G8 recorded higher ASVs, reflecting greater sensitivity to environmental fluctuations. Nevertheless, stability alone is insufficient for varietal recommendation Yan (2003). The Genotype Selection Index (GSI), which integrates mean yield and ASV ranks Kang & Pham (1991), was employed to identify superior genotypes. Accordingly, G6 was the most desirable genotype, combining the highest grain yield (4.636 t ha^{-1}) with good stability, followed by G2, which exhibited moderate yield with high stability. Although G10 and G1 were not top yielding, their superior stability makes them suitable for stress-prone environments, whereas G11, despite its relatively high yield, was unstable and thus more suited to favorable conditions. Overall, the combined ASV and GSI analyses confirmed G6 as the ideal genotype a finding consistent with the GGE biplot results Yan & Kang (2002), making it a strong candidate for promoting to next breeding stage for further evaluation and release in the study area. While ASV and GSI provide only numerical stability rankings without illustrating GEI patterns Yan *et al.* (2000), GGE biplot analysis, in contrast, visually integrates both genotype performance and GEI in a single, interpretable graph Yan *et al.* (2001).

Table 6: Mean grain yield and stability parameters for 11 sorghum genotypes

Geno	GY	r GY	IPCAg1	IPCAg2	ASV	r ASV	GSI	r GSI
G10	3.12	8	-0.09	-0.24	0.28	1	10	3
G8	4.27	2	0.83	0.41	1.32	10	12	5
G1	3.10	9	0.23	0.08	0.36	2	11	4
G5	2.97	10	-0.36	0.00	0.55	6	16	8
G7	3.32	7	-0.07	-0.51	0.52	5	12	5
G2	3.36	6	0.27	0.19	0.46	3	9	2
G6	4.63	1	0.30	0.09	0.47	4	5	1
G4	3.45	4	-0.69	0.25	1.07	9	13	6
G11	3.87	3	-1.03	0.25	1.57	11	14	7
G3	3.44	5	0.36	0.42	0.70	7	12	5
G9	2.78	11	0.22	-1.00	1.06	8	19	9

Note: ASV: AMMI stability value; rASV: Rank of AMMI stability value; rGY: Rank of Mean grain yield; GSI: Genotypic selection index; rGSI: Rank of Genotypic selection index.

3.5. GGE biplot Analysis

One of the attractive features of a GGE biplot is its ability to show the which-won-where pattern of a genotype by environment that graphically addresses important concepts such as crossover GE, mega-environment differentiation, and specific adaptation Yan *et al. (*2000). The polygon is formed by connecting the genotypes located farthest from the origin so that all other genotypes are contained within the polygon then perpendicular lines to each side of the polygon are drawn, starting from the biplot origin, which divide the testing environments and genotypes into different sectors Yan *et al*. (2002). Therefore, the six testing environments were divided into three mega environments, while the 11 genotypes were divided into five genotype groups (Figure 1). The first mega environments consisted of three environments Mech 2023, Mech2024, Hirna 2024 and Doba 2024, while the second and third are Doba 2023 and Hirna 2023. The genotype at each vertex is a winner of a sector Yan and Kang (2002). Accordingly, G6, G8 and G11 are the winners of respective sectors. However, vertex genotypes where no environment fell in the sector were less stable across the environments Oladosu *et al*. (2017). Thus, (G9, and G5) were the least stable across environments.

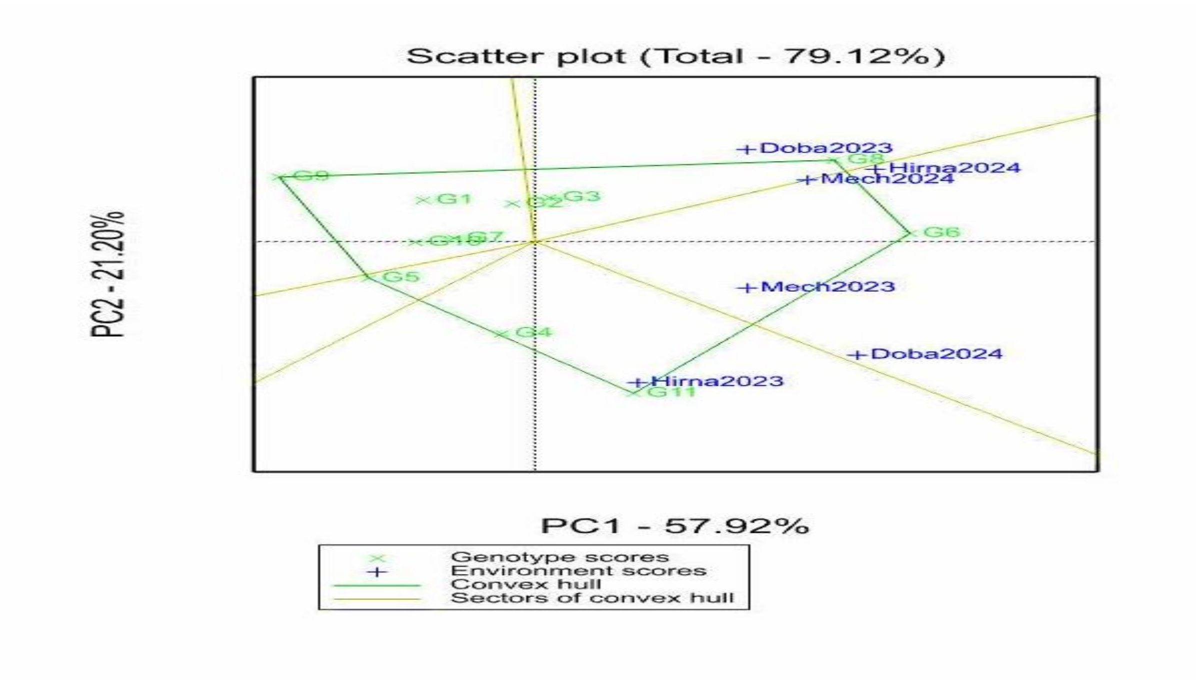

Figure 1: Polygon view of GGE biplot (which–won–where) for 11 sorghum genotypes evaluated at six environments.

3.6. Ranking of genotypes relative to the ideal genotype

Genotype evaluation based on both mean performance and stability across environments provides critical insight for effective selection in plant breeding. According to Yan and Kang (2002), an ideal genotype is characterized not only by high mean performance but also by consistency across multiple environments. In the present study, the GGE biplot analysis revealed that genotype G6 occupies the center of the concentric circle (Figure 2), indicating its status as the ideal genotype Farshadfar *et al*. (2012). This central position reflects both superior performance and stability, making G6 a benchmark for comparing other genotypes Yan (2001). Further genotypes located near the ideal genotype are considered desirable because they combine relatively high performance with stability Yan & Tinker (2006). In this context, G8 can be regarded as desirable due to its proximity to G6. Conversely, genotypes positioned farther from the ideal such as G5 exhibit lower stability or performance, rendering them less suitable for production in the tested environments Kaya *et al*. (2006). According to this finding G6 it is ideal as consequence should promote to next breeding stage for further evaluation and release as variety.

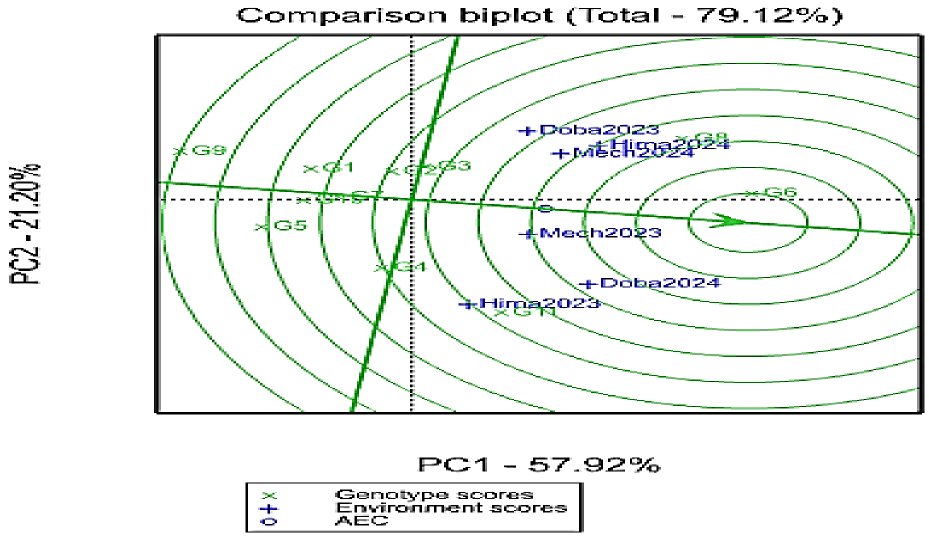

Figure 2: GGE biplot analysis showing the stability of genotypes

3.7. Ranking of test environment

In multi-environment trials, identifying ideal test environments is critical for effective genotype evaluation. The results showed that Hirn2024 was located at the center of the concentric circles in the GGE biplot (Figure 3), indicating that it is highly representative of the target region and possesses strong discriminating ability among genotypes Kaya *et al.* (2000) and Yan & Kang (2003). Similarly, MECH 2023 and MECH 2024 were positioned close to the ideal environment, suggesting that these locations are favorable for evaluating broadly adapted genotypes Kaya *et al.* (2006). Conversely, Doba2023 and Hirna2023 were located farther from the ideal environment, implying reduced discriminating power and lower representativeness, which makes them less effective for general genotype selection. This indicates that Hirn2024, MECH 2023, and MECH 2024 are the most suitable environments for identifying widely adapted sorghum genotypes, whereas Doba2023 and Hirna2023 may primarily help to identify genotypes with specific adaptation. In other words, genotypes evaluated in ideal or favorable environments are more likely to show stable performance across diverse locations, while those evaluated in less favorable environments may not reliably reflect true genotypic potential. Therefore, prioritizing trials in ideal and favorable environments enhances the efficiency and accuracy of genotype selection, increasing the likelihood of releasing cultivars with high yield potential and broad adaptability Yan & Kang (2003) and Kaya *et al.* (2006).

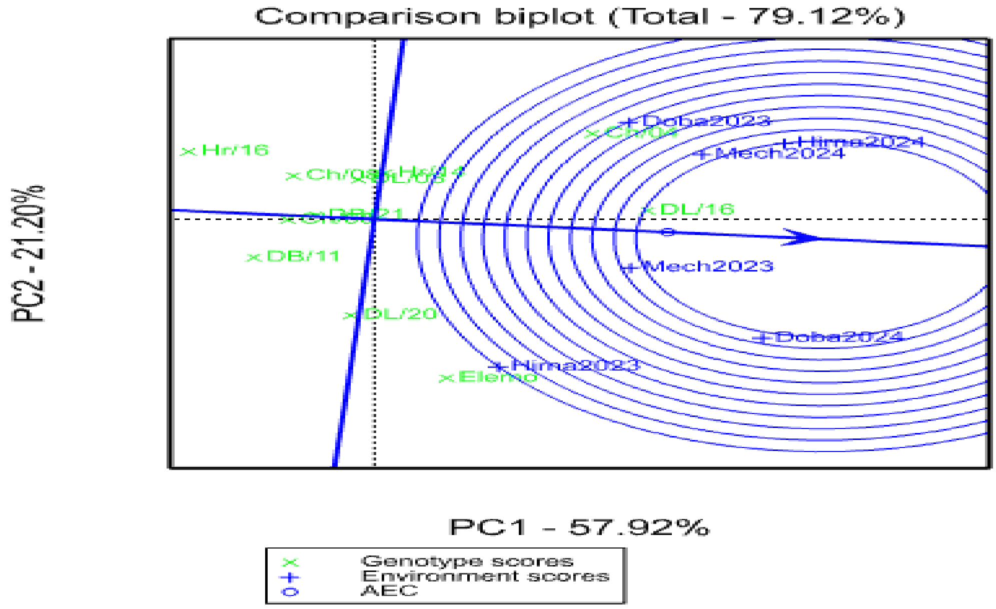

Figure 3: The average genotypes coordination (AGC) views to rank genotypes relative to the center of concentric circles.

4.Conclusions and Recommendations

The study demonstrated that genotype, environment, and their interaction (G × E) significantly influence sorghum performance. Consequently, evaluating stability and adaptability across diverse environments is essential for identifying superior genotypes. In this context, G6 consistently exhibited the highest grain yield (4.63 t ha^{-1}) and 19.6% superior over standard check. Additionally, AMMI and GGE analyses confirmed G6 as the most stable and adaptable genotype, making it a strong candidate for wider cultivation in West Hararghe. Regarding Environments, Mecharaa were found to be representative and discriminative, ensuring reliable evaluation of genotypes in future studies. Therefore, based on its consistent performance and adaptability, G6 should be advance to the Variety Verification Trial (VVT) to confirm its stability and yield across multiple environments.

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