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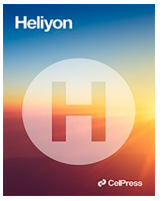

Research article

Genotype by environment interaction, AMMI, GGE biplot, and mega environment analysis of elite *Sorghum bicolor* (L.) Moench genotypes in humid lowland areas of Ethiopia

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ABSTRACT

This study aimed to evaluate high-yielding, stable sorghum genotypes and determine the ideal (representative and discriminating) testing environments for genotypes in the humid lowlands of Ethiopia. A total of forty-two sorghum genotypes were used for a field trial conducted in six different environments using a randomized complete block design. Yield stability, Additive main effect, multiplicative interaction (AMMI), and genotype and genotype by environment interaction (GGE) were computed. The AMMI analysis explained 62.85% of the G×E variance. The AMMI1 biplot revealed that (G4; Mok079 and (G16; Ba066) genotypes had higher grain yields. AMMI2 biplot suggested that genotypes (G18; Y0470),(G23;100620), (G29; PML981475), and (G11; ETSC300373-4) show higher sensitivity to environmental changes because of their strong genotype-by-environment interactions. The GGE captured 79.46% of the GGE variance, and the GGE biplot identified genotypes (G4; Mok079), (G10; Sl081) and (G16; Ba066) were the most stable genotypes whereas(G39; ETSC120051-3) was the least stable genotypes. The GGE biplot identified Assosa (AS20) as a suitable environment, whereas PW20 and JM20 were the most discriminating and non-representative environments. The GGE biplot was found to identify three main mega-environments for sorghum growing in the humid lowlands of Ethiopia., both the AMMI and GGE biplots revealed (G4; Mok079) had the highest level of adaptability to all tested environments and was approved by the National Variety Release Committee for release in 2022.

1. Introduction

Sorghum (*Sorghum bicolor* (L.) Moench) belongs to the grass family *Poaceae* (*Gramineae*). It is a predominantly self-pollinated [1] diploid (2n = 2x = 20) species with a genome size of ca 700Mbp [2]. It is the fifth-largest cereal crop in the world, behind maize, rice, wheat, and barley, were produced 59.3 million metric tonnes (MMT) in 2020–2021 [3]. Sorghum is the second most extensively grown cereal crop in Africa, behind maize, and it produces 29.8 MMT on 29.7 million ha of arable land [3]. In Ethiopia, Five million smallholder farmers cultivate sorghum, which is the third-largest producer of sorghum grain in the world behind the United States (8.6 MMT) and Nigeria (6.7 MMT) [4]. The national sorghum productivity is low, estimated at 2.5 tons ha^{-1} as compared to the global average yield, which is 3.7 tons ha-1, in terms of both output and harvested area [5].

Sorghum is a versatile grain used worldwide for food, feed, fencing, and the sugar and molasses industries [6]. For more than 500 million people in Africa, Asia, and Latin America, especially those living in semi-arid tropical regions, it is a significant crop for food

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and nutritional security [7]. It is preferred for the making of a variety of traditional foods, including Injera (a leavened bread), porridge, and beverages like Tella and Borde since it is ingrained in Ethiopian traditional culture [8]. However, Ethiopia's productivity of sorghum is low due to several issues, including the scarcity of stable, well-adapted cultivars that are resistant to biotic and abiotic pressures [5].

In the field of plant breeding, understanding genotype-environment interaction (GEI) is of paramount importance. The success of selection in a breeding program depends on how genotypes interact with different conditions [9]. As stated in Ref. [9], genotype-environment interaction (GEI) is a phenomenon that occurs when different genotypes react differently to various environmental factors. Plant breeders recognize the importance of considering the entire genetic diversity spectrum, rather than solely focusing on GEI. To effectively distinguish the GEI component from overall genetic variation, modified models are advantageous [10]. The AMMI model and the GGE biplot are examples of such models used for describing, analyzing, understanding, and predicting GEI [10]. GEI presents a significant challenge in crop breeding and plays a pivotal role in comprehending the genetic mechanisms involved in environmental adaptation [11].

Many Ethiopian federal and regional sorghum program breeding initiatives have done studies on sorghum for several agroecological zones (AEZ) with different elevations, temperatures, and rainfall in Ethiopia, and 48 sorghum cultivars have been accredited and registered [12]. However, because of the effects of genotype-environment interaction, selecting superior genotypes based solely on yield at a single location in a year may be ineffective because yield is a complex quantitative feature that is severely influenced by environmental changes [13]. In addition, the released varieties mainly focus on specific AEZs, thus no variety is suitable for all of Ethiopia's agroecologies. Since different genotypes perform better in a diversified environment over a long period, the importance of genotype performance stability in many environment interactions and mega-environment differentiation is evident [14,15].

The success of a crop depends on its ability to thrive in a given environment. However, environmental factors such as fungi, viruses, nematodes, bacteria, rainfall, temperatures, soil chemistry, soil humidity, and disparities in soil type can cause genotype × environment interactions (GEIs) that affect the genetic potential of the crop [16,17]. Therefore, it is important to study the genotype-by-environment interaction to improve crop growth and development. Crop improvement scientists are interested in using agronomic traits such as yield and yield components to detect lasting results to problems governing plant growth and development [18]. Thus, many statistical tools and models have been put in place to analyze GEI effects under mega-environment experiments [19].

GGE and additive main effects and multiplicative interaction (AMMI) model biplots associated with their components are the main models in GEI analysis. AMMI analysis can also help decipher how different genotypes (crop varieties) perform across different environmental conditions (such as varying soil types or climate conditions). This information is crucial for breeding programs to develop robust and adaptable varieties [20]. The biplots generated by principal component analysis (PCA) allow us to understand the relationship between genotypes, environments, and GEI, which helps in identifying stable and high-yielding genotypes for specific environments or across environments [17]. Many researchers [18,20,21] showed the value of the AMMI and GGE methods in their study to detect potential yielding genotypes associated with stable performance across various environmental conditions. The GGE biplot combines a "which-won-where" pattern, environment ranking, mean vs. stability, discriminativeness and representativeness of the environments, genotype rankings, and the use of singular value decomposition (SVD).

However, the two methods work in concert to help us understand GEI impacts, the best genotypes, and conditions that will produce the best genotypes. As a result, it is crucial to comprehend how GE interactions affect genotype adaptability and stability [22]. So far, AMMI and GGE models have aided in the organization of the complicated GEI, the identification of potential and stable genotypes in multidimensional environments, and the availability of numerous breeding lines through genotype-by-environment interaction investigations [22]. Thus, the objectives of this study were (1) to Assess the genotype by environment interaction using AMMI and GGE biplot analyses in sorghum genotypes grown in humid lowland areas of Ethiopia. (2), to Identify sorghum genotypes that are stable and high-yielding across multiple environments, (3) to perform a mega environment analysis to identify sorghum genotypes that perform well across multiple environments in humid lowland areas of Ethiopia.

2. Materials and methods

The experiment was conducted at four experimental sites: Assosa Agricultural Research Center (AsARC), Pawe Agricultural Research Center (PARC), and Jimma Agricultural Research Center (JARC). These locations represent the humid lowland sorghum-growing areas of the southwest part of Ethiopia. AsARC (10° 03′ N and 34° 59′ E) is situated at 1450 m above sea level (asl), has Eutric Dystric Nitosols soil type, 1275 mm annual rainfall, and has minimum and maximum air temperatures of 14 °C and 39 °C, respectively. PARC (11°19′N and 36°24′E) has an altitude of 1120 m. a.s.l., minimum and maximum air temperatures of 16.3 °C and 32.6 °C, and soil is characterized by Vertisol. JARC (10°57 N/39°47E) is located at 1753 m a.s.l., has Vertisol, receives 1572 mm of annual rainfall, and has minimum and maximum air temperatures of 9 °C and 28 °C, respectively. The trial was executed during the main rainy seasons (July to December) of 2019 and 2020.

The current study comprised 42 genotypes in total, containing the widely used and released variety Assosa-1 (a standard Check) that was adapted to Ethiopia's humid lowland area. The genotypes used in this study were obtained from both the core collection and advanced breeding lines maintained by the Ethiopian Institute of Agricultural Research, based at the Assosa agricultural research center. The treatments were laid out in a randomized complete block design (RCBD) with three replications. The genotypes of the seeds were planted in 5 m by 7.5 m^2 plots using 0.75 m and 0.15 m spacing between rows and plants, respectively. Fertilizer was applied at a rate of 50 and 100 kg ha^{-1} as Urea and Diammonium Phosphate (DAP), respectively. Data were collected on days to flowering, days to maturity, plant height (m), and grain yield (t ha^{-1}).

2.1. Data analysis

The combined analysis of variance across locations was done using PROC GLM with the MIXED model of the SAS computer program (SAS Institute, 2002), where genotypes and locations were fixed while years, all the interactions, including, replications, blocks, and errors, were random. For the combined ANOVA, the following model was utilized:

$$Y_{ijkm(1)} = \mu + r_1 + (pt)_{jk} + b_m(Ptr)_{jkl} + g_i + p_j + t_k + (gp)_{ij} + (gt)_{ik} + (pt)_{jk} + (gpt)_{ijk} + e_{ijkm(1)}$$

where Y_{ijkm} is the yield of the ith genotype in the Jth location and the kth year in the Ith block within the lth replication, μ is the grand mean, $r_{1(pt)_{jk}}$ r_1 $(pt)_{jk}$ is the effect of the lth replication within locations and years, $b_{m(ptr)_{jkl}}$ is the effect of the mth block within the lth replication that is also within locations and years, g_i, p_j, and t_k are the main effects of the genotype, locations, and years, $(gp)_{ij}$, $(gt)_{ik}$, $(pt)_{jk}$ are the first order interactions and $(gpt)_{ijk}$ is the second-order interaction, and finally $e_{ijkm(l)}$ is the pooled error term. The terms i = 1, 2, 3 … 20; j = 1, 2, 3, 4, 5; k = 1, 2; l = 1, 2, 3 and m = 1, 2, 3, 4, 5.

As stated by Ref. [23]and more recently by Ref. [24], the necessary F-test was conducted for a mixed model with fixed genotypes, fixed locations, and random years. The combined experiments operate under the supposition that the sum of the effects of random interactions at each level of a fixed factor is zero. [25], Briefly stated, the mean squares for genotypes, genotypes × locations, genotypes × years, and genotypes × locations × years were compared to the pooled error mean square, while the mean square of replications within the locations and years was compared to the mean square of genotypes [23]. Bartlett's test [26] was used for homogeneous variance assumption to detect for assessing the significance of genotype by environment interactions, as it helps to identify whether the genetic effects on the phenotype vary across different environmental conditions.

The AMMI model [27] was employed to analyze the components of variance influencing genotype by environment interactions and the consistency of sorghum grain yield across trials. AMMI syndicates multivariate principal component analysis (PCA) with univariate analysis of variance (ANOVA). PCA was then used to integrate the trait data using the standardized residuals from the ANOVA model, which was utilized to examine the trait data with the main effects of genotype and environment but without the interaction. These residuals consist of the experimental error and GEI effect. The following formulas can be used to represent the analytical model for the ith genotype in the jth environment [][28–30].

$$Y_{ijr} = \mu + \mathrm{g}i + ej + br(ej) + \sum_{n=1}^{k} \lambda k \alpha i \kappa \gamma jk + \rho ij + \varepsilon ij$$

where Y_{ijr} is the mucilage or yield of genotype i in environment j for replicate r, μ is the grand mean, gi is the deviation of genotype i from the grand mean, ej is the environment main effect as deviation from μ, λk is the singular value for the interaction principal component (IPC) axis k, αik and γjk are the genotype and environment IPC scores (i.e. the left and right singular vectors) for axis k, $br(ej)$ is the effect of the block r within the environment j, r is the number of blocks, ρij is the residual containing all multiplicative terms not included in the model, n is the number of axes or IPC that were retained in the model, and εij is error under independent and identically distribution assumptions,

$$\varepsilon ij \sim \left(N, \frac{\delta^2}{r}\right)$$

AMMI Stability Value (ASV) was calculated using the formula developed by Ref. [31] where SSIPCA1 is sum of squares of interaction principal component analysis 1 (IPCA1) and SSIPCA2 is sum of squares of IPCA2. Sum of the absolute value of the IPC (SIPC) was calculated by a formula developed by Ref. [32],

$$ASV = \left[\frac{SSIPCA - 1}{SSIPCA - 2}(IPCA - 1score)^2\right] + (IPCA2score)^2\ \Bigg]$$

where SSIPCA1 is the sum of squares of interaction principal component analysis 1 (IPCA1) and SSIPCA2 is the sum of squares of IPCA2. Sum of the absolute value of the IPC (SIPC) was calculated by a formula developed by Ref. [32]. The biplot graph of the AMMI1 (IPCA1 scores vs. additive main effects from genotypes and environments) and AMMI2 (IPCA1 vs. IPCA2) were constructed.

Pi is the sum of squares of differences of mean genotype i in each environment from the mean of the best genotype in the corresponding environment [32,33].

$$SIPC = \sum_{1}^{n} |IPCA_{n|}$$

$$\frac{[n\left(\overline{X} + \overline{M} + \sum_{j+1}^{n}\left(X_{ij} - \overline{X}_i - m_j + \overline{M}\right)\right.^2}{2n}$$

$\overline{X}$ i: is the yield mean of the i th cultivar in the n environments and $\overline{M}$ i is the mean of the maximum response in the n environments. According to Ref. [34], the first part of the Pi expression quantifies the genetic deviation and the second quantifies GEI. The mean rank of each genotype in all environments was calculated as the genotype mean rank

The combined data from 3 locations and 2 years were subjected to biplot analysis by genotype and genotype x environment [35]. The GGE bi-plots were generated with Genstat Version 18 [36]. The GGE biplot reveals the stability of genotypes close to the biplot origin, which are thought to be broadly adapted, while genotypes far from the origin are considered specifically adapted. The bi-plots visually represent genotypic performance in multiple environments based on principal components and compare environments to a hypothetical ideal environment, as well as the genotypes to an ideal environment.

The GGE biplot allows for a visual exploration of relationships between test environments, genotypes, and genotype-environment interactions. Therefore, the first two main components (PC1 and PC2) were used to graph the G×E and identify the rank of test genotypes and environments [37]. The GGE biplot analysis was based on the simplified model with two principal components generated by the model [38].

$$Y_{ij=}\mu + \beta j + \lambda_1 \varepsilon_{j1\eta j1} + \lambda_2 \varepsilon_{i2}\eta_{j2} + \varepsilon_{ij}$$

where, $Y_{ij=}$ is the trait mean for genotype i in environment j, μ is the grand mean, βj is the main effect of environment j, $\mu + \beta j$ being the mean yield across all genotypes in environment j, λ1, and λ2 are the singular values (SV) for the first and second principal components (PC1 and PC2), respectively, ε_{j1} and ε_{i2} are eigenvectors of genotype i for PC1 and PC2, respectively, $\eta j1$ and η_{j2} are eigenvectors of environment j for PC1 and PC2, respectively, ε_{ij} is the residual associated with genotype i in environment j. In GGE biplot analysis, scores of PC1 were plotted against PC2 [35].

Stability analyses were calculated utilizing the [34] formula for computing the cultivar superiority of genotypes. Using a genotype's variance across environments, static stability was assessed (S2xi). The environmental variance will be lower for a desired genotype since it won't respond to shifting environmental variables [39]. When the G×E effects for each genotype are squared and added across the test environments, the result is an indicator of stability known as ecovalence (Wi) [40]. The mean and variance of the ranks of each genotype across the environments, as well as the absolute differences of pairs of ranks, were based on [41].

3. Results and discussion

3.1. Analysis of variance

Table 1 shows the results of the variance analysis for the pooled data from various locations and years. The combined ANOVA in the present study showed highly significant ($P < 0.001$) differences among sorghum genotypes, test environments, and G×E effects. Furthermore, environmental variation had a significantly larger contribution to the overall variability than genotype and G×E effects, which were determined by the highest sum of squares for grain yield. Consistent with the present finding [42,43], observed significant differences in the effects of G, L, and G×L on grain yield. In addition, significant differences for L ($P < 0.001$), Y ($P < 0.001$), L×Y ($P < 0.01$), G ($P < 0.01$), and G×L ($P < 0.001$) were also reported by Ref. [25].

3.2. Genotype means performance

The combined analysis of variance (Table 2) of three locations with two years of data shows that the year, locations and G×E indicated highly significant ($p \leq 0.001$) G, E, and G×E effects on grain yield. The presence of significant G×E in this experiment requires further analysis to determine the size of G×E and to separate it into multiplicative component terms, a mega-environmental classification, and an estimate of the yield stability of the genotypes. Genotypes 4 (Mok079) and G 16 (Ba066) were the first and second highest-yielding genotypes 4.793 and 4.646 t ha^{-1} respectively, whereas ETSC120051-3 (G39; 1.077 t ha^{-1}) was the lowest.

In terms of days to maturity, genotypes ETSC 300373-4 (191.611) and G16 (191.056) were the highest, while ETSL101699 (G32; 161.389) and G25 (161.611) were the genotypes that were fewest days to maturity. The two high-yielding genotypes, G4 and G16, had long maturity dates, 188.667, 191.056, and taller plant heights 301.19, and 315.11 respectively. According to Ref. [44], the growth of a plant is directly related to its height, influencing the formation of nodes and the subsequent development of leaves. When a plant receives sufficient light, it tends to produce more leaves, thereby enhancing its photosynthetic potential and ultimately boosting

Table 1
Combine analysis of variance of 42 sorghum genotypes tested at three locations for two years.

Source of Variation	Degree of freedom	Mean square			
		DTF	DTM	PTH	YLD
Genotype(G)	41	7114.6**	1946.06**	82766.36**	11.70**
Replication(R)	2	24.9	290.2	2868.07	0.24
Location(L)	2	30822.22**	130855.98**	2868.07**	145.13**
Year(Y)	1	12385.71**	120259.55**	1419755.98**	10.20**
G×L	8	798.51**	398.3**	72083.86**	2.67**
GxY	41	390.67**	349.3**	7664.32**	1.2**
GxYxL	82	187.61**	238.14**	3725.91*	1.00**
Residual	492	63.79	71.06	2543.42	0.24

Note: ** Significant at 0.01, and * 0.05 probability level.
DTF = Days to flower; DTM = Days to maturity PTH=Plant height, YLD=Yield.

Table 2
Mean grain yield and other agronomic traits of sorghum genotypes tested at three Locations for two years.

Identification	Code	DTF	DTM	PHT	YLD
NJ003	G1	129.444 ^{hi}	189.333 ^{abcd}	279.06 ^{klm}	4.051 ^{b}
ETSC 300376-1	G2	136.611 ^{bcdef}	186.778 ^{abcde}	321.94 ^{efghi}	1.981 ^{b}
Mok087	G3	129.056 ^{hi}	190.611 ^{ab}	301.19 ^{hij}	3.331 ^{cd}
Mok079	G4	132.611 ^{fgh}	188.667 ^{abcd}	348.92 ^{abcd}	4.648^{a}
Bmb097	G5	130.5 ^{ghi}	178.722 ^{fg}	313.39 ^{ghij}	3.195 ^{de}
ETSC 300373-4	G6	138.056 ^{bcde}	191.611^{a}	310.94 ^{ghij}	2.220 ^{opqr}
Bmb102	G7	132.833 ^{efgh}	189.5 ^{abcd}	361.72 ^{ab}	2.901^{efgh}
Ba119	G8	132.556 ^{fgh}	187.833 ^{abcde}	365.11^{a}	3.567^{c}
Man069	G9	132.889 ^{efgh}	186.111 ^{abcde}	355.17 ^{abc}	2.471 ^{jklmo}
Sl081	G10	132.944 ^{defgh}	188.889 ^{abcd}	320.42 ^{efghi}	4.557^{a}
ETSC 300382-1	G11	145.444^{a}	184.444 ^{de}	307.5 ^{hij}	2.704 ^{hijkl}
Bam075	G12	135.444 ^{cdefg}	187.222 ^{abcde}	336.42 ^{cdef}	2.767 ^{ghijk}
Mok085	G13	138.333 ^{bc}	187.778 ^{abcde}	297.81^{jk}	3.049 ^{defg}
Bmb095	G14	130.389^{ghi}	185.056 ^{cde}	332.17 ^{defg}	2.785 ^{ghij}
Boj007	G15	141.5 ^{ab}	187.833 ^{abcde}	341.14 ^{bcde}	3.577^{c}
Ba066	G16	131.556 ^{fghi}	191.056^{a}	315.11 ^{fghij}	4.6461^{a}
Bs082	G17	138.167 ^{bcd}	184.778 ^{de}	294.75 ^{jkl}	2.4828 ^{jklmno}
Y047	G18	129.944 ^{hi}	185.333 ^{bcde}	349.56 ^{abcd}	2.46 ^{jklmo}
Qon070	G19	131.556 ^{fghi}	190.5 ^{abc}	314.19 ^{ghij}	2.8106 ^{fghi}
Qon072	G20	139 ^{bc}	175.111 ^{gh}	340.53 ^{bcde}	2.8517 ^{fghi}
ETSL 100124	G21	93.944 ^{m}	169.722 ^{hijk}	244.17°	2.125 ^{pqrs}
ETSL 100346	G22	85.167^{n}	166.111 ^{iklmn}	219.17^{p}	2.2806 ^{mopqr}
ETSL 100620	G23	93.278 ^{m}	171.833 ^{hi}	246.67 ^{no}	2.9206 ^{efgh}
ETSL 100644	G24	91.611 ^{m}	166.556^{klmn}	200.06 ^{pqr}	2.687 ^{efgh}
ETSL 100861	G25	91.722 ^{m}	161.611 ^{mn}	177.22 st	1.7833 ^{tu}
ETSL 101515	G26	103.333 ^{l}	168.611^{kl}	261.17 ^{mno}	3.1278 ^{def}
PML981442	G27	92.667 ^{m}	169.944 ^{hijk}	187.28 ^{rst}	2.0372 ^{rst}
PML981446	G28	83.333^{n}	166.556 ^{iklmn}	154.17^{u}	2.9778 ^{efgh}
PML981475	G29	92.667 ^{m}	168.333 ^{ijkl}	180.43 ^{rst}	2.0728 ^{qrst}
PML981488	G30	90.5 ^{m}	162.833^{mn}	187.27 ^{rst}	1.6094 ^{uv}
BTx378	G31	95 ^{m}	167.556 ^{ijkl}	273.72 ^{lm}	2.55 ^{ijklm}
ETSL101699	G32	85.111^{n}	161.389^{n}	122.22^{v}	1.3744 ^{vw}
13MW6029	G33	123.556 ^{jk}	170.667 ^{hij}	189.83 ^{qrs}	2.0333 ^{rst}
13MW6042	G34	106 ^{l}	169.722 ^{hijk}	185.16 ^{rst}	2.0517 ^{qrst}
ETSC10022-44-2	G35	136.611 ^{bcdef}	182.833 ^{ef}	299.44 ^{jkl}	2.4189 ^{lmop}
07MW6002	G36	105.889^{l}	166.944 ^{ijklm}	178.39 ^{rst}	2.0306 ^{rst}
ETSC10022-40	G37	118.611^{k}	184.556 ^{ed}	279.03 ^{klm}	2.3572 ^{lmop}
ETSC10020-22-1	G38	102.778^{l}	168.667 ^{jkl}	210.39 ^{pq}	2.541 ^{ijklm}
ETSC120051-3	G39	126.778^{ij}	188.667 ^{abcd}	271.22 ^{m}	1.0767^{w}
ETSC12004-11	G40	107.833^{l}	169.056 ^{jkl}	266.67 ^{nm}	2.23 ^{opqr}
Assosa-1(Check)	G41	139.444^{bc}	190.389 ^{abc}	198.78 ^{pqrs}	2.87 ^{fgh}
Bonsa	G42	105.333^{l}	164.778^{lmnk}	166.17^{tu}	1.8778^{stu}
Mean		118.095	178.440	266.800	2.668
CV (%)		6.763	4.724	12.587	18.265

Note: DTF = Days to Flowering; DTM = Days to Maturity; PTH = Plant Height; YLD = Yield.
Means with the same letter in the column are not significantly different at 0.05 probability level.
CV (%) = coefficient of variation.

productivity. The sorghum genotype ETSL101699 (G32) exhibited the earliest maturity date (161.389) and also demonstrated the lowest grain yield.

When the grand mean values of the six environments were compared, AS20 had the highest sorghum grain yield (3.382 t ha^{-1}), JM20 came in second (3.355 t ha^{-1}), and PW20 had the lowest (1.618 t ha^{-1}). As a result, AS20 and PW20 were considered the environments with the highest and lowest yields, respectively. The highest grain yields were obtained by the two genotypes G10 (SI081) (5.61 t ha^{-1}) and G15 (Boj007) (4.053 t ha^{-1}) (Table 3).

3.3. Stability analyses

Six environments (location and year combinations) were used to calculate the estimates of six stability coefficients for the 42 sorghum genotypes in Table 4. Based on cultivar superiority stability statistics, G4 (0.082) and G16 (0.086), which had comparably lesser values, were the most stable genotypes, while G39 (7.473) and 32 (6.43) were the least stable.

Based on static stability, G24 (0.041) and G40 (0.07) were assigned smaller static stability coefficient estimates, indicating they are more stable types. G11 and G29, which showed significantly larger values (3.199 and 2.938), were the least stable nonetheless. Although static stability is typically linked with a relatively low yield level [39], G41 maintained a greater grain yield.

The genotypes G4 and G10 sorghum genotypes with low ecovalence ratings had also better grain production. The result coincided with identifying two sorghum genotypes with low ecovalence values and higher grain yield [5,45].

Table 3
Mean grain yield (t ha^{-1}) of 42 sorghum genotypes across six environments (location and year combinations).

Genotype		Environments						Mean
Identification	Code	PW19	JM19	AS19	PW20	JM20	AS20	
NJ003	G1	3.650	4.720	3.900	3.433	3.907	4.697	4.051
ETSC 300376-1	G2	1.480	2.070	2.020	0.497	2.397	3.417	1.980
Mok087	G3	2.820	3.330	2.630	2.223	5.023	3.963	3.332
Mok079	G4	4.440	4.840	4.690	3.197	5.517	5.207	4.648
Bmb097	G5	3.120	3.870	2.570	2.26	3.817	3.537	3.196
ETSC 300373-4	G6	1.513	2.650	2.560	1.047	2.153	3.4	2.221
Bmb102	G7	1.970	3.140	2.710	1.417	4.303	3.86	2.900
Ba119	G8	4.460	2.160	4.660	2.4	3.767	3.96	3.568
Man069	G9	1.400	2.340	2.490	0.907	4.707	2.983	2.471
Sl081	G10	3.630	4.120	4.740	3.76	5.487	5.61	4.558
ETSC 300382-1	G11	0.970	2.200	3.190	0.68	5.39	3.793	2.704
Bam075	G12	2.510	2.070	3.210	0.853	4.303	3.657	2.767
Mok085	G13	2.160	2.200	2.680	2.013	4.98	4.263	3.049
Bmb095	G14	2.130	2.830	2.920	1.357	3.857	3.62	2.786
Boj007	G15	1.900	2.510	3.680	4.053	5.12	4.2	3.577
Ba066	G16	4.720	4.910	4.470	3.173	5.403	5.2	4.646
Bs082	G17	2.297	2.110	2.550	1.257	2.41	4.273	2.483
Y047	G18	1.810	1.540	2.510	0.36	4.943	3.597	2.460
Qon070	G19	2.200	3.670	3.290	0.623	4.483	2.597	2.811
Qon072	G20	1.720	3.000	2.610	0.997	4.837	3.947	2.852
ETSL 100124	G21	1.517	2.210	2.720	1.56	2.113	2.63	2.125
ETSL 100346	G22	1.967	2.183	2.730	1.973	2.113	2.717	2.281
ETSL 100620	G23	3.617	1.563	3.453	3.9	1.457	3.533	2.921
ETSL 100644	G24	2.373	2.860	2.760	2.517	2.727	2.883	2.687
ETSL 100861	G25	1.960	1.003	2.157	2.483	0.967	2.13	1.783
ETSL 101515	G26	1.843	2.977	4.200	2.597	2.943	4.207	3.128
PML981442	G27	1.643	3.073	1.883	0.673	3.023	1.927	2.037
PML981446	G28	1.730	3.580	3.580	1.713	3.57	3.693	2.978
PML981475	G29	0.213	4.070	2.010	0.203	4.003	1.937	2.073
PML981488	G30	0.533	2.523	1.837	0.533	2.457	1.773	1.609
BTx378	G31	1.650	2.017	3.983	1.683	1.923	4.043	2.550
ETSL101699	G32	0.367	1.930	1.883	0.383	1.833	1.85	1.374
13MW6029	G33	1.663	2.987	2.120	0.4	2.947	2.083	2.033
13MW6042	G34	0.700	3.587	1.813	0.707	3.587	1.917	2.052
ETSC10022-44-2	G35	1.073	2.107	4.050	1.083	2.04	4.16	2.419
07MW6002	G36	1.083	2.407	2.703	0.877	2.347	2.767	2.031
ETSC10022-40	G37	1.503	1.963	4.030	0.573	2.01	4.063	2.357
ETSC10020-22-1	G38	2.077	2.530	3.067	2.117	2.397	3.057	2.541
ETSC120051-3	G39	0.570	1.390	1.383	0.453	1.383	1.28	1.077
ETSC12004-11	G40	1.887	2.313	2.423	1.913	2.343	2.5	2.230
Assosa-1	G41	1.360	2.070	3.390	1.67	3.753	4.977	2.870
Bonsa	G42	1.200	2.257	2.070	1.437	2.173	2.13	1.878
Mean		**1.986**	**2.711**	**2.960**	**1.618**	**3.355**	**3.382**	**2.669**

Note: AS19 = Assosa 2019, AS20 = Assosa 2020, JM19 = Jimma 2019, JM20 = Jimma 2020, PW19 = Pawe2019 = PW2020 = Pawe 2020.

By mean rank stability coefficients, Mok079 (2.50) and Sl081 (2.67) were rated as the least stable genotypes, respectively; they were also more stable. However, the least stable with the highest mean rank stability score was scored by the genotypes G32 (39.5) and G39 (40.5). The genotypes ETSL 100620 (1.267) and G4 (1.533) were found to be the most stable using mean absolute differences of pairs of ranks (MADPR), while ETSL 100620 (20) and G29 (17.933) were found to be the least stable. According to variances of ranks, G4 (1.1) and G10 (1.9) were the two most stable genotypes, while G23 (270.67) and G29 (253.1) were the two least stable. G4 was ranked first by cultivar superiority and mean rank stability coefficients; G14 was ranked first by Wricke's ecovalence of ranks and ranked sixth by two MADPRs and Variances of ranks of the stability coefficients. In contrast, the most unstable genotypes among the used stability coefficients were recorded on PML981475 (G29), ETSL 100620 (G23), and ETSC 300382-1 (G11).

3.4. AMMI model

The results of the AMMI analysis of variance were significantly affected by the genotypes (G), and environments (E), and their interactions (G×E) of variance were significant ($P < 0.01$) Table 5. Several authors have also reported significant G×E interactions and conducted stability analyses of wheat [46], Plantago species [47], and groundnut [48].

The result from the AMMI model showed that 80.25% of the total sum of squares was attributable to the environment component, indicating the significant effect of environmental variables on changes in grain yield. Also, environmental components gave the largest contribution to the total variation of grain yields. Similar results from other studies indicate the large proportion of environmental conditions in the total variation of GEI with root, concerning sugar and white sugar yield [49]. Partition of GEI mean squares revealed

Table 4
Stability coefficients for grain yield of 42 lowland sorghum genotypes tested on six environments (three locations and two years).

Genotype		Cultivar superiority		Static stability		Wricke's ecovalence		Mean ranks		MADPR		Variances of ranks	
Code	Mean	Value	Rank	Value	Rank	Value	Rank	Value	Rank	Value	Rank	Value	Rank
1	4.051 ^{b}	0.475	4	0.29	8	1.549	18	6.67	4	5.067	7	21.07	7
2	1.981 ^{b}	4.43	35	0.94	22	0.882	10	31.75	39	6.033	11	24.38	10
3	3.331 ^{cd}	1.405	6	1.049	25	2.038	22	12.33	6	7.467	15	45.07	16
4	4.648^{a}	0.082	1	0.651	13	0.527	3	2.5	1	1.533	2	1.9	2
5	3.195 ^{de}	1.563	8	0.446	10	1.764	20	15	9	10.4	26	71.6	24
6	2.220 ^{opqr}	3.782	29	0.715	15	0.953	11	26.5	29	5.933	10	25.1	11
7	2.901^{efgh}	2.192	12	1.21	27	1.094	13	16.58	12	5.567	8	21.44	8
8	3.567^{c}	1.346	5	1.106	26	5.579	38	12.83	7	12.6	31	108.97	31
9	2.471 ^{jklmo}	3.346	24	1.774	34	2.96	27	25.17	26	9	18	65.37	23
10	4.557^{a}	0.158	3	0.738	16	0.541	5	2.67	2	2	4	2.67	3
11	2.704 ^{hijkl}	3.209	22	3.199	42	6.53	39	22.25	22	14.9	34	147.97	34
12	2.767 ^{ghijk}	2.568	16	1.512	31	2.249	26	19.92	18	12.1	28	99.84	28
13	3.049 ^{defg}	2.034	10	1.585	32	3.075	29	15.42	10	10.3	25	73.84	25
14	2.785 ^{ghij}	2.361	13	0.867	20	0.331	1	18	14	3.867	6	10	6
15	3.577^{c}	1.415	7	1.391	30	5.33	36	10.83	5	9.533	20	60.97	19
16	4.6461^{a}	0.086	2	0.631	12	1.048	12	3	3	2.267	5	3.6	5
17	2.4828 ^{jklmno}	3.147	21	0.979	24	2.237	25	21.33	21	12.133	29	106.67	30
18	2.46 ^{jklmo}	3.568	25	2.628	40	5.496	37	27	31	15.333	36.5	159.2	36
19	2.8106 ^{fghi}	2.659	18	1.794	35	3.832	31	18.33	15	13.333	32	134.67	33
20	2.8517 ^{fghi}	2.48	14	1.988	39	2.976	28	19	16	9.2	19	58	18
21	2.125 ^{pqrs}	4.026	31	0.261	7	0.866	9	26.75	30	6.967	14	31.77	13
22	2.2806 ^{mopqr}	3.611	26	0.125	3	1.538	17	24.25	25	9.7	22	63.38	21
23	2.9206 ^{efgh}	2.908	19	1.218	28	12.673	42	20.33	19.5	20	42	270.67	42
24	2.687 ^{efgh}	2.601	17	0.041	1	1.661	19	17.67	13	9.867	23	63.47	22
25	1.7833 ^{tu}	5.403	39	0.411	9	6.88	40	29.75	37	15.9	40	180.38	39
26	3.1278 ^{def}	1.918	9	0.86	19	2.172	24	13.33	8	9.6	21	62.67	20
27	2.0372 ^{rst}	4.351	33	0.819	18	2.135	23	28.33	33	12.267	30	103.47	29
28	2.9778 ^{efgh}	2.083	11	0.949	23	0.784	7	16.5	11	6.733	13	30.3	12
29	2.0728 ^{qrst}	4.923	38	2.938	41	8.271	41	29.5	35.5	17.933	41	253.1	41
30	1.6094 ^{uv}	5.677	40	0.789	17	1.246	16	33.83	40	10.067	24	76.97	26
31	2.55 ^{ijklm}	3.279	23	1.305	29	4.05	32	23	23	15.333	36.5	154.8	35
32	1.3744 ^{vw}	6.43	41	0.6	11	0.528	4	39.5	41	1.267	1	1.1	1
33	2.0333 ^{rst}	4.358	34	0.912	21	1.799	21	28.5	34	11.533	27	89.9	27
34	2.0517 ^{qrst}	4.587	36	1.685	33	4.482	33	29.5	35.5	15.267	35	169.9	37
35	2.4189 ^{lmop}	3.72	28	1.905	36	4.633	34	24.17	24	15.667	39	174.57	38
36	2.0306 ^{rst}	4.322	32	0.693	14	0.475	2	28	32	5.733	9	23.2	9
37	2.3572 ^{lmop}	3.861	30	1.979	38	4.72	35	26.17	28	15.533	38	184.97	40
38	2.541 ^{ijklm}	2.955	20	0.192	4	1.227	15	19.75	17	7.5	16	38.38	15
39	1.0767^{w}	7.473	42	0.195	5	0.691	6	40.5	42	1.933	3	2.7	4
40	2.23 ^{opqr}	3.705	27	0.07	2	1.19	14	26	27	8.533	17	50	17
41	2.87 ^{fgh}	2.531	15	1.97	37	3.451	30	20.33	19.5	14	33	134.27	32
42	1.8778^{stu}	4.725	37	0.197	6	0.86	8	30.25	38	6.7	12	34.17	14

Note: MADPR = Means absolute differences of pairs of ranks. Rank shows the position of each genotype according to the stability coefficient in the previous column.

Table 5
The AMMI analysis of variance for grain yield of 42 sorghum genotypes on six. Environments.

Source of variation	DF	SS	MS	SS explained (%)	GE explained (%)
Treatments	251	1163.9	4.637		
Genotypes	41	479.8	11.702	13.07	
Environments	5	332.1	66.424	80.25	
Interactions	205	352	1.717	6.68	
IPCA 1	45	170.1	3.78		48.33
IPCA 2	43	80.2	1.866		22.80
Residuals	117	101.6	0.869		
Error	492	116.9	0.238		

Note: DF = Degree of freedom = Sum of square; MS = Mean square; **Significant at 0.01 probability level.

that the first two IPCAs captured 70.13 % of the total GEI for sorghum reported that the first (42%) and second (17%) interaction vectors accounted for 59% of the total variation of G×E, which is consistent with the present investigation [50] investigated significant IPCAs ($P < 0.1$) in the first (50.7%) and second (18%) to explain the entire interaction [51]divided the G×E effect into two significant ($P < 0.01$) IPCAs, both of which contributed 65.98% to the interaction. However [52], revealed that three significant ($P < 0.05$) IPCAs with contributions of 45.53, 29.87, and 13.21% explained the G×E. Only one significant IPCA was reported [53].

The AMMI1 biplot (Fig. 1) indicated that G4 and G16 had higher grain yields than other genotypes, G39, G32, G30, G25, and Bonsa, which had below-average grain yields. G24 had a grain yield that was on par with the overall average. G×E levels were high in G23, G29, and G39. The G×E of G41, G36, G42, G22, G24, and G6 were lowered, and the G×E of the remaining genotypes was moderate. The larger the IPCA1 score, either negative or positive, the more specifically adapted a genotype is to certain environments [54,55]. The highest sorghum grain production was in AS20. Environments AS19, JM19, and JM20 all had above-average grain yields. The yields for PW19 and PW20 were below average.

Hence, they were low-yielding environments. In addition, JM20 and PW20, in that order, made greater contributions to the interaction. Environments PW19 and AS19 made the least contribution to the interaction, whereas environments AS20 and JM19 made a substantial contribution. The length of the environmental vectors from the origin in the AMMI2 biplot, when G and E are plotted against PCA1 and PCA2, reveals the strength of the interaction exerted by the environments on the genotypes [56]. The distance of the genotypes from the origin also reveals how vulnerable the genotypes are to various environmental factors [57].

The AMMI2 biplot is divided into four quadrants, and the nearer the genotypes are to the ordinate axis, the more they show their general adaptation [48]. The AMMI2 biplot, JM20, and PW20 exhibited stronger interactions, which means that these environments have a higher capacity for genotype discrimination than the others do. AS20 and JM20 interacted moderately. PW19 and AS19, on the other hand, exerted the least G×E on the system, suggesting that while they are more representative, they are also the least

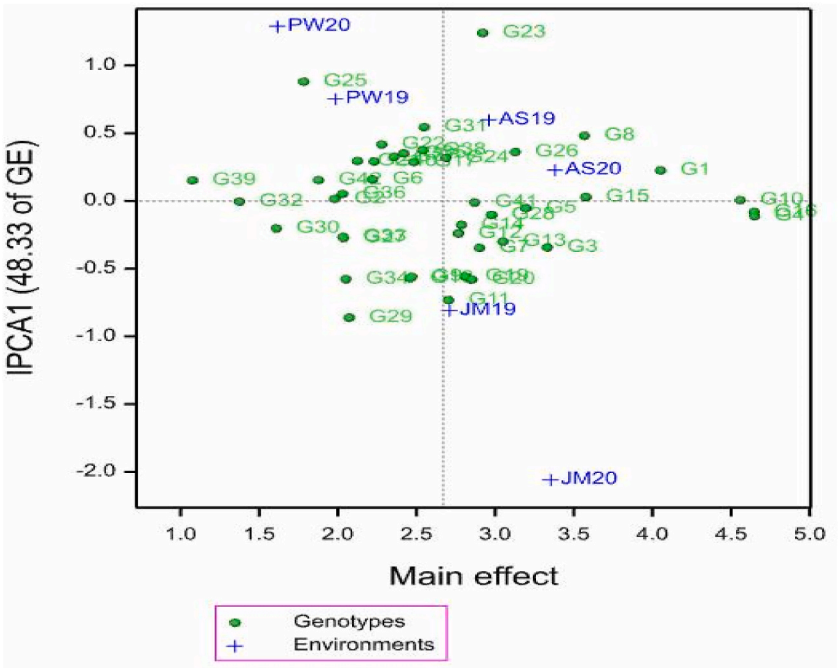

Fig. 1. AMMI biplot of 42 sorghum genotypes and environments, and IPCA1 using symmetrical scaling. Note: AS19 = Assosa 2019, AS20 = Assosa 2020, JM19 = Jimma 2019, JM20 = Jimma 2020, PW19 = Pawe 2020, PW20 = Pawe2020.

discriminating environments.

G18, G23, G29, and G11 all have higher G×E (far from the origin), making them, more sensitive to environmental changes and hence better suited to their environments. These genotypes are considered more stable and have a better response to environmental changes than other genotypes [58,59]. In contrast, the wide-adapted genotypes G36, G6, G2, G14, and G10 exhibited fewer interactions because they were close to the origin and therefore less vulnerable to environmental changes. However, the other genotypes interacted only with insignificantly similar outcomes, as also reported by Ref. [60].

3.5. GGE biplots analysis

In the GGE analysis (Fig. 3), the first two PCAs (PCA1 = 59.03, PCA2 = 20.44) effectively captured 79.47% of the total GGE variance. This result is consistent with [4] that the first two PCAs accounted for 79.78% (PCA1 = 46.46, PCA2 = 33.32%) of the variance. Additionally [61], reported that 65.05% of GGE variance was explained by the first 18.33% and second 46.72% PCAs, respectively. The concentric circles on the biplot, as shown in (Fig. 3), help to visualize the length of the environment vectors, which is proportional to the standard deviation within the respective environments and is a measure of the discriminatory ability of the environments. The genotype that is found in the middle of the concentric circle is considered an ideal genotype for grain production, which has to have a high suggestive overall mean performance, which should have a high mean performance (Large PC1) and great stability (small absolute PC2) across environments [35].

Therefore, genotypes located closer to the ideal genotype are more desirable than others [62]. Hence, G4, G10, and G16 are very close to the ideal genotype as compared to others. These three genotypes could be considered suitable genotypes for the six environments. Similarly, Ref. [5] identified suitable genotypes, WSV-387 × E−36-2 is the most ideal genotype for sorghum grain production in a yield stability trial. The relative contribution of stability and grain yield for identifying desirable genotypes found in this study by the ideal genotype procedure of GGE biplot was also similar to Ref. [63] Teff variety stability studies (Fig. 3).

The GGE biplot also identified the least suitable G39 genotype, which is very far from the concentric circle. Generally, different authors investigated crop yield stability to find suitable genotypes (high-yielding and stable) [60,61,64]. The length of the environment vectors is a measure of the environment's discrimination capacity, and a test environment with a smaller angle with the average-environment axis (AEA) is more representative than the other environments [35,65]. Hence, PW20 and JM20 were more discriminating (informative) and non-representative environments useful for selecting specifically adapted genotypes (Fig. 4). On the other hand, JM19 was the least discriminating or non-informative environment, which is less useful because it provides little

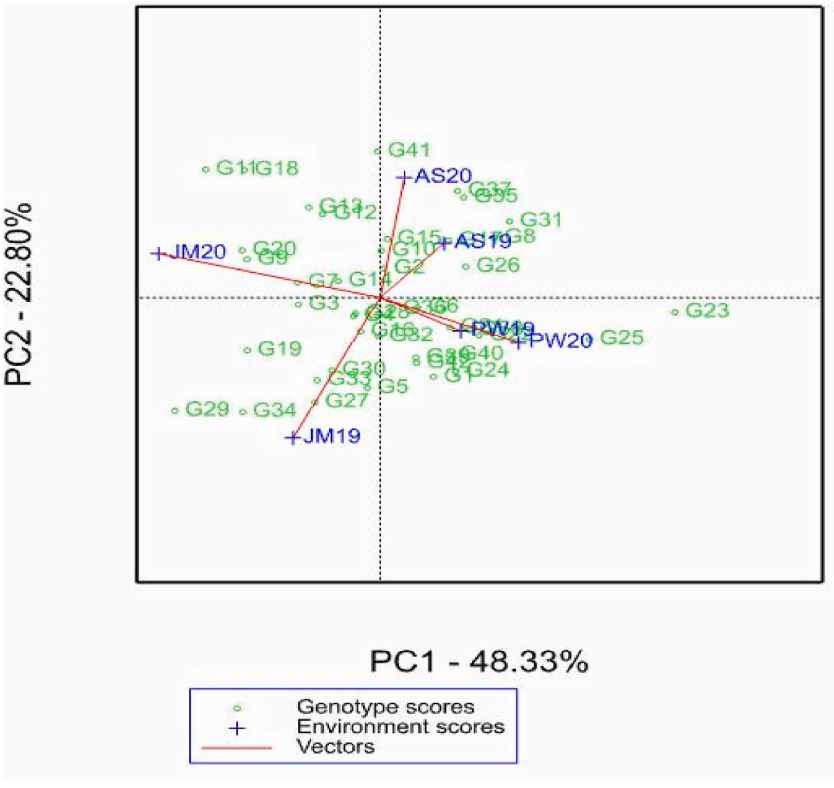

Fig. 2. AMMI2 biplot of 42 sorghum genotypes and environments plotted against PCA1 and PCA2 using symmetrical scaling. Note: AS19 = Assosa 2019, AS20 = Assosa 2020, JM19 = Jimma 2019, JM20 = Jimma 2020, PW19 = Pawe 2020, PW20 = Pawe2020. Genotype abbreviations are given in Table 2.

discriminating information about the genotypes. Environment AS20 was a more discriminating and generally representative environment [35,43] claim that environments that are both discriminating and representative are appropriate to test conditions for choosing genotypes that are widely adapted. Therefore, Assosa (AS20) is the ideal environment for selecting lowland sorghum varieties that are often adapted for Ethiopia's humid lowlands. The environment for JM20, however, was the least suitable one.

3.6. Mega environment identification

The analysis of variance showed the presence of highly significant G×E mean squares for grain yield across the test environments. For the mega-environment, Which-Won-Where identified the greatest winning genotypes. This also implies that genotype evaluation is possible in those few mega-environments with good yield data outcomes. Fig. 5 shows how the biplot of lines that originated from the origin can be used to split the six environments into three mega-environments: (1) JM19 and JM20; (2) PW19, AS19, and AS20; and (3) PW20, which created the mega-environments [66] showed that the GGE biplot analysis of the twenty-two sorghum genotypes tested in fourteen environments identified three mega environments. However, results revealed [42] using 20 hybrids of grain sorghum with the same methodology, in Brazil, identified two mega environments.

The mega-environments obtained are shown in Fig. 5, with this model defined in "which one-where. The vertex genotypes were G29, G11, G23, G25, and G39 (Fig. 5). These genotypes had the largest vectors in each direction. The vector of length and direction is an extension of the genotype responsible for the tested environments. All other genotypes were contained within the polygon and had smaller vectors; that is, they were less sensitive compared to the interaction with the environments of each sector. The G4 genotype was the vertex of the mega-environment 1 sector, and it performed best in this group. G10 was the vertex of the mega environment 2 sectors, and it was the most adapted genotype in this group. Lastly, the G23 genotype was the most adapted in mega-environment 3 (Fig. 5). Closer relationships between the test environments indicate that the same information can be obtained from fewer environments. As a result, a similar environment may be specified for later sorghum grain testing in a new environment [62,67–69].

The genotypes and environments found within the polygon were less responsive to environmental cues (Fig. 2). Genotypes from polygon vertices that did not cluster in any environment were not suitable for the environments tested. The vertex genotypes (G39) and (G25) had the lowest average grain yields in all environments because they had no corresponding environment. Similar results were reported for an environmentally inappropriate genotype tested in the Teff GGE biplot analysis [63].

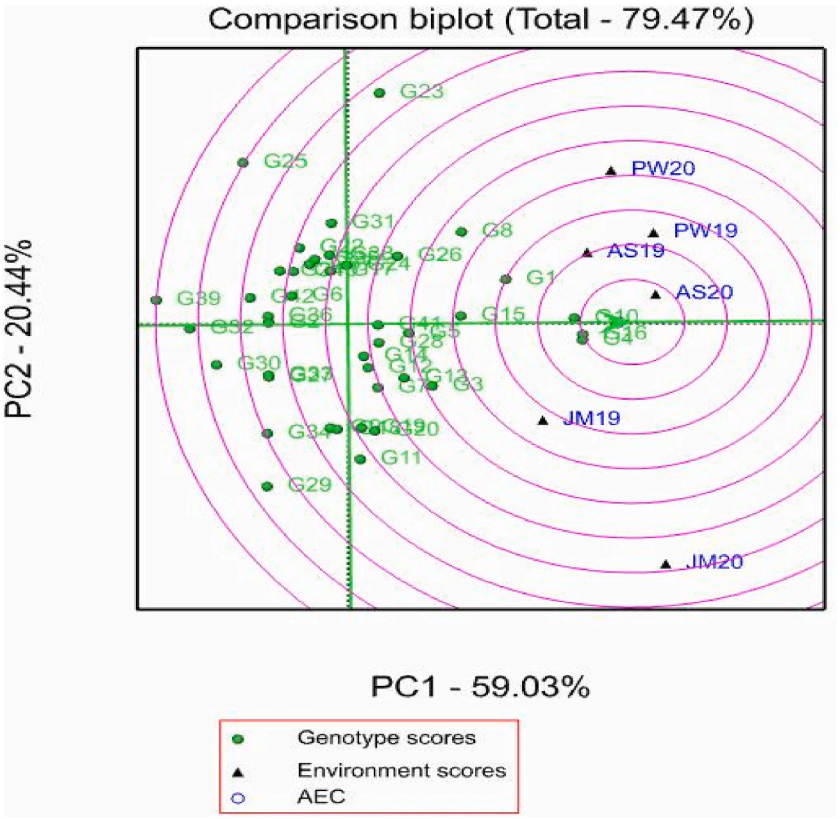

Fig. 3. GGE biplot of sorghum genotypes on 6 environments using genotype-centered scaling. Note: AS19 = Assosa 2019, AS20 = Assosa 2020, JM19 = Jimma 2019, JM20 = Jimma 2020, PW19 = Pawe 2020, PW20 = Pawe2020. Genotype abbreviations are given in Table 2.

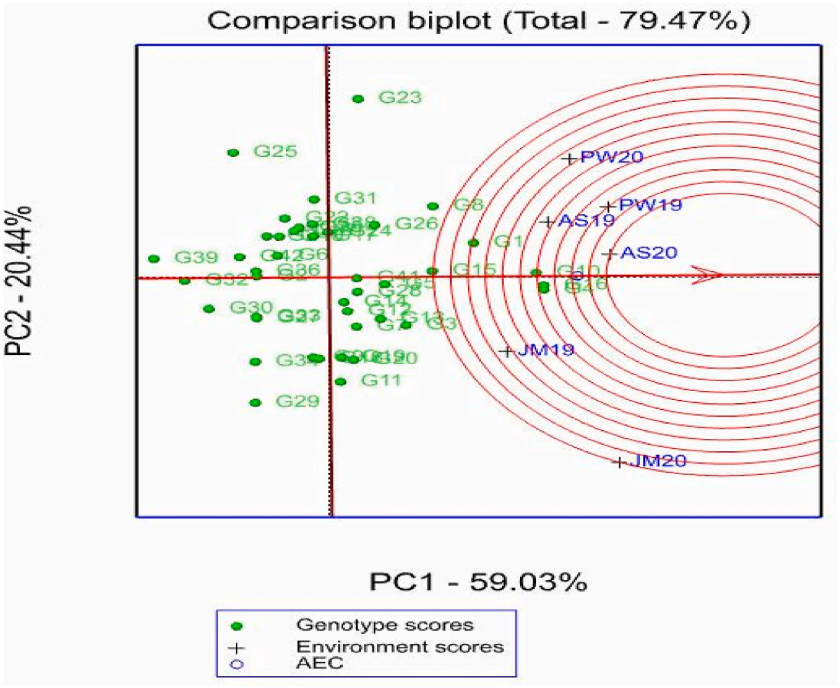

Fig. 4. The ideal testing location for 42 sorghum genotypes used in evaluations using environment-centered scaling. Note: AS19 = Assosa 2019, AS20 = Assosa 2020, JM19 = Jimma 2019, JM20 = Jimma 2020, PW19 = Pawe 2020, PW20 = Pawe2020. Genotype abbreviations are given in Table 2.

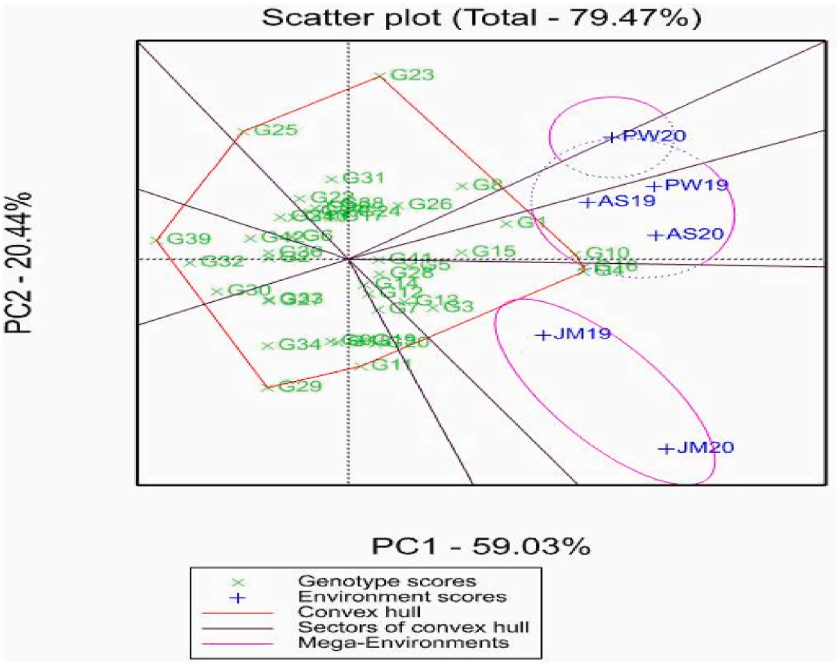

Fig. 5. Mega-environments obtained by the genotype main effects + genotype × environment interaction (GGE) biplot for grain yield of 42 sorghum genotypes evaluated during the crop season of 2019/2020.

4. Conclusions

The results derived from both the AMMI and GGE analyses demonstrated the existence of genotypes exhibiting diverse levels of adaptability in various environments. Notably, the remarkable adaptability of genotypes G4, G10, and G16 stood out prominently across both the AMMI and GGE evaluations. The mean grain yield was significantly influenced by both genotype variation and environmental conditions. From the grand mean of grain yield of six environments, AS20 had the highest sorghum grain yield (3.382 t ha^{-1}), JM20 came in second (3.355 t ha^{-1}), and PW20 had the lowest (1.618 t ha^{-1}). AMMI2 model identified the genotypes G18, G23, G29, and G11 are particularly sensitive to environmental alterations due to their greater G×E (placed away from the origin), which helps them adapt better to their specific environments. Conversely, the more broadly adapted genotypes, G36, G6, G2, G14, and G10, showed fewer interactions because of their closeness to the origin. These genotypes are therefore less vulnerable to alterations in their environments. From the tested 42 different genotypes, G4 (Mok079) and G16 (SI081) stood out as high-yielding and consistently stable genotypes. In addition to their impressive productivity, these genotypes also exhibited beneficial traits like taller plant height. This characteristic can be advantageous for small-scale farmers, as it can function as a natural fence and even provide a source of fuel. G4 was released under the name Assosa-2 after receiving clearance from the National Variety Release Committee of Ethiopia in 2022. G4 is also well-suited to Ethiopia's humid lowland agroecology, where sorghum holds significant importance and its adaptability with the long rain-fall pattern prevalent in this region. Environments AS20 were the most representative, while environments PW20 and JM20 were the most discriminating. Therefore, these environments should be used to select superior genotypes for specific agro-ecologies.

Data availability

No data was used for the research described in the article.

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CRediT authorship contribution statement

Habtamu Demelash: Writing – review & editing, Writing – original draft, Visualization, Software, Methodology, Investigation, Formal analysis, Data curation, Conceptualization.

Declaration of competing interest

The author confirms that the content of this article has no competing interests.

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