International Journal of Genetics and Genomics
2024, Vol. 12, No. 2, pp. 19-30
https://doi.org/10.11648/j.ijgg.20241202.11

SciencePG
Science Publishing Group

Research Article

Performance Evaluation of Different Sorghum Genotypes (Sorghum bicolour (L.) Moench) Using GGE Bi-plot Stability Analysis

Nesrya Bedru[1, *], Temesgen Matiwos[2], Techale Birhan[2], Tegegn Belete[1]

[1]Jimma Agricultural Research Center, Ethiopian Institutes of Agricultural Research, Addis Ababa, Ethiopia
[2]College of Agriculture and Veterinary Medicine, Jimma University, Jimma, Ethiopia

Abstract

Sorghum (Sorghum bicolor (L.) Moench) is an important essential cereal crop in Ethiopia. Conversely, its productivity is low due to numerous biotic and abiotic factors. There are diverse and dynamic environmental conditions which needs detail and continue study on genotypes by environment interaction (GEI) to develop stable genotypes. The objective of this study was to determine the magnitude of GEI for grain yield of forty two sorghum genotypes and to identify stable and high yielding genotypes across locations. The experiments were laid out at three locations for two growing seasons using alpha lattice design with three replications. The plot size 5 m x 0.75 m x 2 rows (7.5 m^2) and distance between block, replication, and plot was 1m, 1.5m, and 0.75m, respectively. Phonologic, agronomic, diseases and grain yield data were collected but only grain yield was used for stability analysis. The ANOVA revealed highly significant variation ($p < 0.01$) among sorghum genotypes across locations and seasons. Mean grain yield of genotypes ranged from 1.29 to 3.69 with mean grain yield of 2.36, while environment range from 1.18 to 3.63 t/ha. The genotype G1 showed good performance across all test sites which range 5th at E1,3rd at E3 and E4, 15th and 7th at E5 and E6 and maximum grain yield was harvested from E3. Yield data were also analyzed using the GGE (that is, G, genotype +GEI, genotypes-by- environment interaction) bi-plot method. The first two principal components (PC1 and PC2) were used to create a 2- dimensional GGE bi-plot and explained 59.67 and 13.48 % of GGE sum of squares, respectively. GGE bi- plot identified G16, G4, and G1 high yielders and stable and G34 and G25 was the lowest yielding and least stable across locations. On the other hand, the environment E6, E4 and E1 were the most suitable to select desirable genotypes.

Keywords

GEI, AMMI, Multi-environmental Trial, Stability

1. Introduction

Sorghum (Sorghum bicolor (L.) Moech) is important cereal crop belonging to the grass family of poaceae (Gramineae). It is a c4 monocotyledon crop plant [1]. The chromosomes number is 2n =2x=20 and an estimated gnome size of 700Mb [2]. Sorghum was originated in the northeast part of Africa, mostly Ethiopian-Sudan border [3]. Ethiopia is considered as a center of origin and diversity for the four of the five major races in Africa [4]. Sorghum is the most important cereal

*Corresponding author: nesrbintb@gmail.com (Nesrya Bedru)

Received: 11 March 2024; **Accepted:** 24 April 2024; **Published:** 17 May 2024

crop next to maize, rice, wheat, and barley. The grain is used as a staple food for millions of people, while the stalk used as livestock feed and construction purpose [5]. Also used as fiber and biofuels [6]. The grain and fresh or dry biomass has diverse use and good source for sugar, syrup, and molasses industry [7].

Sorghum flour to prepare fermented and unfermented breads, porridges, couscous, and snacks and beverages [8]. It is second preferred crop next to teff or preparing 'injera' [9]. Globally sorghum production is around 60.06 MMT. In Africa, sorghum is the second most widely cultivated cereal crop following maize, with a total production of 32.8 MMT. Ethiopia is the world's fourth largest sorghum producer with production of 4.5 MMT from 1.7 million hectares of land and with the average productivity of the crop are 2.7 t/ha following the United States 11.47 MMT, Nigeria 6.7 MMT and Mexico 4.8 MMT [10]. In Ethiopia, similarly sorghum production was decline starting 2020 from 5.2 MMT to 4.5 MMT at 2022 [11].

The main constraints of sorghum production are drought, low levels use of inputs, parasitic striga, disease, insect pests, low soil fertility and poor storage facilities [12, 13]. Desert locust infestation in different part of country [14]. Lack of high yield and stable varieties across diverse environments is a challenge of sorghum production yield loss in Ethiopia [15]. Also, the yield potential of variety on the farmer field and on research station varies which impact on yield reduction. Shortage of widely adapted and high yielding variety is one of major holdups on sorghum breeding. National sorghum program developed verities through different breeding methods to solve the problem. It is continuous identification of adaptable, diseases resistance/tolerance, stable and high yielding genotypes a country having diverse environmental condition. Identifying and releasing of improved variety is the main goal of sorghum breeding for better yield production across different environmental condition.

Multi-environmental trials (METs) are conducted, in which a series of genotypes are evaluated over environmental conditions and over time [16]. Researches have been conducted to identify superior sorghum varieties for better yield and wide adaptability for intermediate agro ecologies. The nature of GEI effects on sorghum genotypes performance across different sorghum growing area and they reported the existence of high GEI and limited on release of widely adapted sorghum varieties [17].

The study was showed using eighty-four hybrid lines across six locations to identify the most stable and high yielding genotypes. The results specified that yield performance of sorghum genotypes were influenced by genotype, the environments and GEI effect [15]. Similarly, the study as showed using eighty-four hybrid lines across six locations to identify the most stable and high yielding genotypes. The [18] evaluated twenty-five genotypes on three location and three years. This showed the variation due to location and time.

METs are valuable in optimizing time and resource in sorghum breeding programs by evaluating genotypes across various environmental conditions and over time. To achieve wide adaptation in breeding, are commended strategy involves identifying multiple diverse environments within a region and establishing test location in each to assess adaptability and select superior sorghum varieties for improved yield production [19]. This approach helps breeders identify genotypes that perform consistently well across different conditions, leading to the development of high-yielding and adaptable sorghum varieties.

Various factors such as temperature, moisture, growing season length, sub-soil pH, and socio-economic conditions have been identified as sources of GEI in sorghum varieties grown in sub-Saharan Africa [20]. GEI have great significant to solve these problems. Because environments have effect on growth, the yield and yield-related traits of sorghum can vary across different locations due to environmental factors. GEI occurs, when two or more genotypes perform differently in different environments, and are thus described as differential genotypic sensitivities to environments [21].

The knowledge of the pattern and magnitude of GEI and stability analysis is important for understanding the response of different genotypes to varying environments for identification of stable, widely adapted and unstable but specifically adapted genotypes. Therefore, to improve growers' yields, despite GEI that cause no one genotype is wins everywhere and always. So, the growing region should be subdivided into relatively homogeneous environments (to select more stable genotypes across the location) or specialized genotypes bred for each of these environments (this is the expensive ways of breeding) [22].

Several stability statistics used to partition GEI include regression analysis, multivariate analysis, cluster analysis, genotype main effect plus genotype × environment (GGE) bi-plot [23] and additive main effect and multiplicative interaction (AMMI). However, both GGE and AMMI analysis are the most frequently used in analyzing GEI pattern of multi-environment data set. GGE bi-plot analysis is effective for identifying the best performing cultivar in a given environment and the most suitable environment for each cultivar, comparing any pair of cultivars in individual environments, identifying the best cultivars for each environment and mega-environment differentiation, the yield and stability of the genotypes, and the discriminating ability and representativeness of the environments [24].

Melkassa Agricultural Research Center crossed several lines and identifying promising lines at F6 generation then selected and advanced to preliminary variety trial and tested for one year across three locations (Assosa, Jimma and Bako). Then best and superior forty-two genotypes were selected (including two check) advanced to intermediate altitude Sorghum National Variety Trail at three locations and two years. To determine the magnitude and pattern of genotype by environment interaction and yield stability of sorghum genotypes evaluated at different locations in interme-

diate agro ecology of Ethiopia.

2. Material and Methods

2.1. Description of Study Area

The experiment was conducted during main cropping seasons under rainfed conditions of 2020 and 2021 at Jimma, Bako and Assosa Agricultural Research center with total of six environments. The experimental area was selected for representation of intermediate agro ecology. Geographical descriptions of experimental sites are described at (Table 1).

Table 1. Description of experimental site.

Environment code	Description	Altitude (m.a.s.l)	Rainfall (mm)	Soil type	Ave. Temp. (°C)	
					Max.	Min.
E1	Assosa2020	1553	1291.2	Nitisols	28.6	14.6
E2	Assosa2021	1553	1130	Nitisols	30	-
E3	Bako2020	1650	1425.3	Nitisols	29	12.48
E4	Bako2021	1650	1245	Nitisols	34	-
E5	Jimma2020	1753	1639	Nitisols	27.6	9.8
E6	Jimma2021	1753	1561	Nitisols	27.4	11.0

Source: Jimma, Bako and Assosa Research center

2.2. Experimental Materials

In this study, a total of 42 breeding lines, including two reference checks, were used. The breeding lines were initially crossed at the Melkassa Agricultural Research Center and then evaluated and advanced using pedigree method of plant breeding at Bako, Jimma, and Assosa by the Ethiopian National Sorghum Breeding Program. Promising lines at the F6 generation were further tested in preliminary variety trials across three locations for one year, and the best performing genotypes were selected for an intermediate altitude Sorghum national variety trial conducted at three locations over a period of two years. The parental lines used in the study were developed from landrace collection and characterizations were crossed for grain yield and resistance to various biotic and a biotic stresses. The parental lines used in the experiment were created by selecting specific traits related to grain yield and resistance to various diseases.

Table 2. List of experimental materials used in the experiment.

#G. code	Genotype	Pedigree	#G. code	Genotype	Pedigree
1.	NJ003	NJ003	22.	ETSL 100346	ETSL 100346
2.	ETSC 300376-1	(ETS639/SRN-39)/Adukara	23.	ETSL 100620	ETSL 100620
3.	Mok087	Mok087	24.	ETSL 100644	ETSL 100644
4.	Mok079	Mok079	25.	ETSL 100861	ETSL 100861
5.	Bmb097	Bmb097	26.	ETSL 101515	ETSL 101515
6.	ETSC 300373-4	(ETS639/SRN-39)/Jorgocolle#1	27.	PML981442	PML981442
7.	Bmb102	Bmb102	28.	PML981446	PML981446
8.	Ba119	Ba119	29.	PML981475	PML981475
9.	Man069	Man069	30.	PML981488	PML981488

#G. code	Genotype	Pedigree	#G. code	Genotype	Pedigree
10.	Sl081	Sl081	31.	BTx378	BTx378
11.	ETSC 300382-1	(ETS639/SRN-39)/Jorgocolle#1	32.	ETSL101699	ETSL101699
12.	Bam075	Bam075	33.	13MW6029	13MW6029
13.	Mok085	Mok085	34.	13MW6042	13MW6042
14.	Bmb095	Bmb095	35.	ETSC10022-44-2	ETSC10022-44-2
15.	Boj007	Boj007	36.	07MW6002	07MW6002
16.	Ba066	Ba066	37.	ETSC10022-40	ETSC10022-40
17.	Bs082	Bs082	38.	ETSC10020-22-1	ETSC10020-22-1
18.	Y047	Y047	39.	ETSC120051-3	ETSC120051-3
19.	Qon070	Qon070	40.	ETSC12004-11	ETSC12004-11
20.	Qon072	Qon072	41.	Assosa-1	Bambasi-9
21.	ETSL 100124	ETSL 100124	42.	Bonsa	97BK6129/85MW4138

2.3. Experimental Design and Field Management

The experiments were laid out by alpha lattice design (3*14) with three replications. The total area of an experiments was 1246.5m^2 (22.5m x 55.5m) with the plot size 5 m x 0.75 m x 2 rows (7.5m^2). The distance between block, replication, and plot was 1m, 1.5m, and 0.75m, respectively. Later the plants were thinned with spacing of 15cm. All management practices were uniformly applied at all locations.

2.4. Data Collection

Grain yield (Ton ha^{-1}): It was adjusted to standard moisture level at 12.5% to get the grain yield per plot in grams and converted to ton per hectare for analysis.

2.5. Statistical Analysis

2.5.1. Analysis of Variance

Analysis of variance (ANOVA) from combined data was conducted for grain yield according to Gomez and Gomez [25]. Bartlett's (1974) test was used to assess the homogeneity of variances between environments to determine the validity of the combined analysis of variance of the data over environments were homogeneous. Analysis of variance for grain yield and related traits for each location and the combined analysis of variance over environments were performed with the PROC GLM procedure using SAS (2014) versions 9.3 software and R software. Comparison of treatment means were done by Fischer's least significant difference (LSD) at 5% probability levels. The combined analysis of variance was carried out to estimate years, genotype and G x Y x L of GEI. Significance levels of these components were determined using F- test. The combined analysis for, Genotype x location x year analysis of variance (ANOVA)was performed on grain yield and related traits using a mixed model (where genotypes and locations were fixed while years, all the interactions involving year, replications, blocks and error were random with the following statistical model All statistical analyses were performed in R statistical software version 4.2.1.

2.5.2. GGE Bi-plot Analysis

The GGE bi-plot was constructed by using Genotype by environment interaction with R-Software (GEA-R). GGE bi-plot methodology, which is composed of two concepts, the bi-plot concept [26] and the GGE concept [27], was used to graphically analyze the performance of the wheat genotypes at different environments. This methodology uses a bi-plot to show the factors (G and GE) that are important in genotype evaluation and that are also the sources of variation in GEI analysis of MET data [23].

The general model for GGE Bi-plot is as follow: Y_{ij}-μ-β_j = $\lambda 1 \varepsilon_i 1 \eta j 1 + \lambda 2 \varepsilon_i 2 \eta_j 2 + \varepsilon_{ij}$ where: Y_{ij} = The performance of the i th genotype in the j th environment; μ =The grand mean; β_j = The main effect of the environment j: λl and λ2 = Singular value for IPCA1 and IPCA2, respectively: Ɛi1 and Ɛi2 = Eigen vectors of genotype i IPCA1andIPCA2, respectively: ηj1 and ηj2 = Eigen vectors of environment j for IPCA1 andIPCA2, respectively; Ɛij = Residual associated with genotype i and environment j.

3. Result and Discussion

3.1. Mean Performance of Sorghum Genotypes Across Tested Locations

The individual location ANOVA result revealed highly significant differences ($p<0.001$) among genotypes for grain yield and yield related traits at all environments. The significant difference among genotype explained that genotype differed in their yield potential and indicated the presence of variation among the tested genotypes for grain yield so it is possible to identify high yielder genotype for possible use in these locations (Table 3).

Mean yields of genotypes across environments ranged from 5.4-1.3 t/ha at E1, 2 - 0.13 t/ha at E2, 5 -1.8 t/ha E3, 4.3-0.4 t/ha at E4, 2.9-0.4 t/ha at E5 and 5.8-0.3 t/ha at E6. The genotype G1 was good performance across all test site which ranked 5th at E1, 3rd at E2, 1st at E3 and E4, 15th and 7th at E5 and E6 respectively (Table 1). Also G4 was good yield at all location except E2 which has low yield due to below average number of head. In other hand G41 and G42 were check genotypes there performance were low grain yield for most of environment except G41 at E1 and E3, G42 at E3. Among the test locations the maximum mean grain yield for sorghum genotype were recorded at E3, which was 3.63 t/ha, while the minimum yield was obtained at E2 and E5 which was 1.18 t/ha and E5 1.48 t/ha respectively.

Table 3. *Mean grain yield in (t/ ha) performance of 42 sorghum genotype evaluated at each of the six locations.*

Genotype	Assosa2020 (E1)	Assosa2021 (E2)	Bako2020 (E3)	Bako2021 (E4)	Jima2020 (E5)	Jima2021 (E6)	Mean	Rank
G1	4.59^{d}	2.38^{a}	4.99 ^{b}	4.33 ^{a}	1.89^{d-f}	3.88^{f}	3.69	1
G2	3.35^{q}	0.89^{k-m}	4.98 ^{b}	2.05^{kl}	1.23^{h-k}	1.40^{tu}	2.15	19
G3	3.91^{h-j}	2.13^{ab}	3.97 $^{d-i}$	3.07^{ef}	2.18^{b-e}	3.72^{g}	3.17	6
G4	5.05^{b}	0.70^{l-n}	4.90^{b}	3.03^{fg}	2.89^{a}	4.75^{d}	3.55	2
G5	3.53^{n-p}	1.3 $^{f-j}$	4.35^{cd}	2.77^{h}	2.52^{ab}	3.46^{h}	3.01	8
G6	3.39^{pq}	1.96^{bc}	3.54 $^{h-n}$	2.42^{j}	1.40^{gh}	1.73^{p}	2.41	14
G7	3.79^{j-l}	1.65^{c-g}	3.59^{h-n}	1.38^{qr}	2.45^{b-e}	2.78^{kl}	2.57	11
G8	3.92^{h-j}	2.40^{a}	3.89^{e-j}	2.12 ^{kl}	1.91^{d-f}	2.06^{n}	2.72	10
G9	2.97^{r}	1.50 $^{d-i}$	4.29^{c-e}	2.93 $^{f-h}$	1.91^{d-f}	1.37^{uv}	2.47	12
G10	5.45^{a}	0.65^{l-o}	4.08^{d-g}	4.21^{a}	1.47^{gh}	3.19^{i}	3.17	6
G11	3.72^{k-m}	1.58^{c-h}	1.77^{v}	1.46^{pq}	2.46^{bc}	3.00^{j}	2.34	15
G12	3.58^{m-o}	1.78^{b-e}	3.85^{f-k}	3.24^{de}	2.43^{bc}	5.18^{b}	3.34	5
G13	4.14^{ef}	1.70^{c-f}	2.96^{p-s}	3.94^{b}	2.32^{b-d}	5.80^{a}	3.48	3
G14	3.62^{mn}	2.39^{a}	3.46 $^{j-o}$	4.32^{a}	2.09^{c-f}	5.00^{c}	3.48	3
G15	4.15^{ef}	1.17^{i-k}	3.59^{h-n}	2.51^{j}	2.89^{a}	2.54^{m}	2.80	8
G16	5.05^{b}	1.45^{e-i}	4.61^{bc}	2.89^{gh}	2.09^{c-f}	4.39^{e}	3.41	4
G17	4.16^{e}	1.23^{g-k}	4.80 ^{b}	3.34 ^{cd}	1.47^{gh}	3.38^{h}	3.07	7
G18	3.56^{no}	1.75 $^{b-e}$	3.85^{f-k}	2.01 ^{lm}	2.38^{bc}	2.81^{k}	2.73	9
G19	2.56^{u}	1.89^{bc}	2.48^{tu}	2.21 ^{k}	1.69^{fg}	2.67^{lm}	2.25	16
G20	3.86^{i-k}	1.92^{bc}	4.67^{bc}	1.31^{qr}	2.45^{bc}	4.28^{e}	3.07	7
G21	2.62^{tu}	1.11^{i-j}	2.76^{r-u}	0.77^{s}	0.84^{k-n}	1.86^{o}	1.66	29
G22	2.72st	0.45^{n-s}	3.52^{i-o}	1.77^{no}	0.98^{i-m}	1.48^{s-u}	1.83	25
G23	3.45^{o-q}	0.13^{s}	3.86^{f-k}	1.86^{mn}	0.46^{no}	1.53^{r-t}	1.87	23
G24	2.87^{rs}	0.15^{rs}	3.38^{l-p}	1.25 ^{r}	0.76^{o}	1.21^{w}	1.61	32

Genotype	Assosa2020 (E1)	Assosa2021 (E2)	Bako2020 (E3)	Bako2021 (E4)	Jima2020 (E5)	Jima2021 (E6)	Mean	Rank
G25	2.12^{vw}	0.48^{n-s}	3.67^{g-n}	0.85^{s}	0.38^{o}	1.14^{w}	1.44	34
G26	4.09^{e-g}	0.6^{l-q}	3.64^{g-n}	2.19^{k}	0.99^{i-m}	1.66^{pq}	2.19	17
G27	1.96^{w-y}	1.96^{bc}	3.87^{e-k}	0.85^{s}	0.90^{k-m}	1.58^{q-s}	1.86	24
G28	3.66^{l-n}	0.27^{o-s}	3.56^{h-n}	1.76^{no}	0.92^{k-m}	0.66^{xy}	1.81	27
G29	1.99^{v-y}	1.93^{bc}	4.27^{c-f}	1.84^{n}	1.34^{g-j}	0.79^{x}	2.04	21
G30	1.80^{z}	0.98 $^{j-l}$	3.80^{g-l}	3.07ef	0.69 $^{n-o}$	0.35^{B}	1.78	28
G31	3.94^{g-j}	0.53 $^{m-r}$	3.97^{d-h}	3.48c	0.99^{i-m}	1.68^{pq}	2.42	13
G32	1.87^{yz}	1.87 $^{b-d}$	3.61^{h-n}	0.84s	0.38^{o}	1.26^{vw}	1.64	30
G33	2.07^{v-x}	0.22 $^{p-s}$	3.25^{n-q}	1.36^{qr}	0.91^{k-m}	0.33^{B}	1.37	35
G34	1.93^{x-z}	0.49 $^{n-s}$	3.43^{k-o}	0.48^{t}	0.99^{i-m}	0.46^{AB}	1.29	36
G35	4.06^{e-h}	0.61 $^{l-p}$	2.37^{u}	3.49^{c}	0.77^{l-o}	1.74^{op}	2.17	18
G36	2.74st	0.37 $^{n-s}$	2.52^{s-u}	2.59^{ij}	0.90^{k-m}	0.61^{yz}	1.62	31
G37	3.99 $^{f-i}$	0.67 $^{l-n}$	3.70^{g-m}	1.63^{op}	1.23^{h-k}	1.39^{uv}	2.09	20
G38	3.02^{r}	0.24^{p-s}	3.34^{m-q}	2.76 ^{hi}	1.36^{g-i}	1.46^{s-u}	2.03	22
G39	1.31 ^{A}	1.61^{c-h}	2.79^{r-u}	2.55 ^{j}	0.93^{j-m}	1.64^{p-r}	1.82	26
G40	2.49 ^{u}	1.23^{h-j}	2.91^{q-t}	2.84^{h}	1.11^{h-l}	1.52^{r-t}	2.03	22
G41	4.82 ^{c}	0.68^{l-n}	3.08 $^{o-r}$	1.46^{pq}	1.34^{g-j}	1.65^{p-r}	2.17	18
G42	2.14^{v}	0.21^{q-s}	3.69 $^{g-n}$	1.40^{qr}	1.06^{h-m}	0.49^{zA}	1.51	33
Mean	3.33	1.18	3.63	2.30	1.48	2.24	2.36	
CV (%)	3.2	9.9	7.7	4.8	7.9	3.9		
LSD at 5%	0.17	0.19	0.46	0.18	0.19	0.14		

3.2. Combined Analysis of Variance Over Locations

The combined analysis of variance results for the data from Assosa, Bako, and Jimma over two years showed that genotype, location, and year had a highly significant difference ($p<0.01$), indicating that the performances of genotypes varied across different locations and years. Genotype explained 24.9% of the total variation, while locations and years explained 11.4% and 11.46% respectively, suggesting that the environmental conditions were relatively consistent within these three locations and two years. Additionally, the interactions between genotypes and location, genotypes and year, and location and year also had a highly significant difference ($p<0.01$), impacting grain yield and related traits. The result indicated that mean grain yield (t/ha) was significantly influenced by the interaction effect. This accounted 8.89%, 5.31% and 20.53% of the total variation, GxL, GxY and YxL respectively. Environments explain large variation due to interaction between years and location importantly this shows that evaluation of genotype with in different location and years was paramount. The mean performance genotype affected by both year and location which lead to see the effect of environment on genotypes (Tables 3 and 4). The significant variation due to GxLxY explained that the response of genotypes was different change in location and years. The result designated the reliability of the multi-environment year trials. This is used to identifying seasonal variation due to different environmental factors with in the location and between locations.

The GEI was significant showing variable performance of the genotypes in the various environments. The variation in grain yield was attributed to factors such as genotypic variation, soil fertility, rainfall patterns, temperature, and moisture availability across different locations and years. This highlights the importance of evaluating genotypes in various environments and considering the impact of these environmental factors on crop performance. The presence of significant genotype-by-environment interaction (GEI) means that the performance of one genotype can be better in one environ-

ment (location and year) but, worse in another. This complicates the breeding program for developing stable crop varieties across different locations and years. While year variation cannot be controlled, breeders need to focus on developing varieties that are adapted to specific locations or have wider adaptability to overcome the challenges posed by GEI.

The presence of variations among different genotypes for specific traits suggests that there is a greater opportunity for improving the crop through selective breeding. This also indicates that the performance of genotypes can vary across different environments, highlighting the need to consider environmental factors when selecting and developing crop varieties. The effect of environment is concern on the variation of genotype with different agro ecology for yield and yield related traits. In line with the current study [18, 28] were discussed on the effect of location and year (environment) on grain yield. So, there is different response of genotype for varying location this lead to identification of genotypes for specific location but it needs to identifying genotypes which is wider adaptation and yielding. Than analysis of stability is very important and significant for identification of stable genotypes.

Table 4. *Combined ANOVA for grain yield (t/ha) and percentage of sum of squares of the variance.*

Source of variation	Df	SS	%SS	MS
Genotypes	41	342.99	24.84	8.36***
Location (Loc)	2	158.75	11.49	79.37***
Years (Yr)	1	156.51	11.34	156.51***
Gen x Loc	82	122.73	8.89	1.49***
Gen x Yr	41	72.87	5.28	1.78***
Gen x Loc x Yr	82	148.56	10.76	1.81***
Residuals	496	93.04	6.74	
Total	755	1382.08		
Mean= 2.36		CV =18.35	R^2=93	

3.3. Genotype Main Effect and Genotype-by-Environment Interaction (GGE) Bi-plot Analysis

The GGE (genotype main effect (G) and genotype-by-environment interaction (GE)) concept is based on the understanding that genotype main effect (G) and genotype-by-environment interaction (GEI) are the two sources of variation that are relevant to genotype evaluation and that they must be considered simultaneously for appropriate genotype evaluation [23]. The graphical method was employed to investigate environmental variation and interpret GXE interaction. The partitioning of GXE interaction through GGE bi-plot analysis showed that IPCA 1 and IPCA 2 accounted for 59.67% and 13.48% of sum of squares, respectively, with a total of 73.15 % variation for grain yield.

3.3.1. Ranking of Varieties Based on Mean Grain Yield and Stability Performance

Figure 1 shows ranking of genotypes based on their mean yield and stability performance by AEC line which passes through the bi-plot origin. Genotypes on the right of vertical line had low performance (below average mean yield). Hence, G2, G6, G9, G21, G23, G22, G24, G25, G26, G27, G27, G28, G29, G32, G31, G35, G37, G36, G38, G39, G40, G41, G42. The genotypes on the left side of the ordinate line were G1, G8, G9, G10, G12, G11, G13, G14, G15, G16, G17, G18, G20 gave above average mean yield across locations. A longer projection to the AEC ordinate, regardless of the direction, represents a greater tendency of the GEI of a genotype, which means it is more variable and less stable across environments or vice versa. The stability of the genotypes is determined by their projection on to the middle horizontal line.

The greater the absolute length of the projection of a genotype, the less stable it is. According the bi-plot (Figure 1) genotype G16, G4, and G1 have the shortest vector from the ATC abscissa were high yield and most stable genotype indicating wide range of environmental adaptation. Thus genotype G13, G10 G14 and G12 was longer projection from average line and indicating highest yielding but less stable genotype while, genotypes G34 and G25 was the lowest yielding and least stable across locations in the present study having large environmental variation across location. G41 and G42 were check genotype due to estimate by the projections ranked along the average-tester axis (ATC abscissa),

with the horizontal line based on their average performance were below mean yield as well as low stable across the six locations but had a large contribution to the GEI.

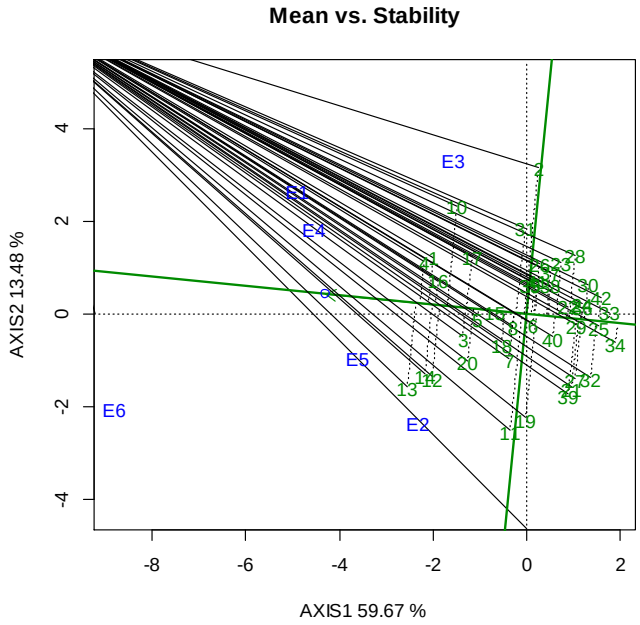

Figure 1. *Average environment coordination (AEC) views of the based on environment-focused scaling for the mean grain yield performance and stability of 25 bread wheat genotypes tested across six environments. Details of environment are given in Table 1. Numbers 1 to 42 represent genotypes as indicated in Table 2.*

3.3.2. Evaluation of Varieties Based on the Ideal Genotype

The GGE bi-plots can place genotypes based on relative to the ideal genotypes (Figure 2) from this G16 was the "ideal" variety with the highest mean grain yield followed by G4 and G1 which fall closer to the center of concentric circles, and they are desirable genotypes in terms of high yield and stability as compared to other genotypes. On the other hand, genotypes which are located distant from the first concentric circle and the right side AEC abscissa, there were performing below mean yield and undesirable genotypes. Similar result was reported [27, 29, 30, 31].

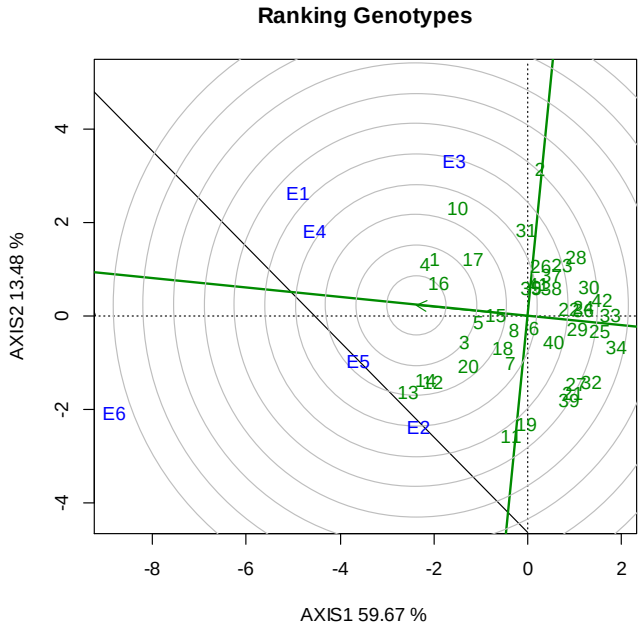

Figure 2. *GGE biplot with scaling focused on genotypes, for the evaluation based on the ideal genotype of 25 bread wheat genotypes across*

six environments. Details of environment are given in Table 1. Numbers 1 to 42 represent genotypes as indicated in Table 2.

3.3.3. Evaluation of Environments Relative to Ideal Environments

As shown in figure 3, E6 followed by E4 and E1 had the longest vector with small IPCA, which fell into near to center of concentric circles was considered as an ideal environment in terms of being the most representative of the overall environments and the most powerful to discriminate genotypes. Similar to ideal genotype, the ideal environment is located in the first concentric circle in the environment focused bi-plot, and desirable environments are close to the ideal environment. In addition E1 were closed to the ideal environment; therefore, it should be regarded as the most suitable to select widely adapted genotypes. This result in combined with [27, 30, 31, 32].

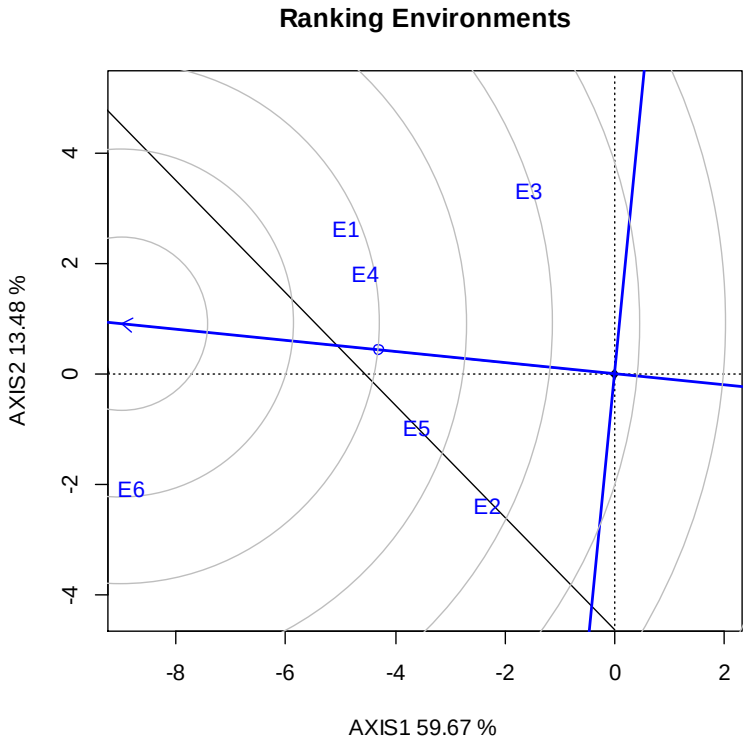

Figure 3. *GGE biplot with scaling focused on environment, for the comparison of environments with ideal environment. Details of environment. Details of environment are given in Table 1. Numbers 1 to 42 represent genotypes as indicated in Table 2.*

3.3.4. The Polygon View of the GGE Bi-plot (The "Which-Won-Where" Patterns)

The polygon view of a GGE bi-plot explicitly displays the which-won-where pattern, and hence is a brief summary of the GEI pattern of a MET data set [33]. One of the most attractive features of a GGE bi-plot is its ability to show the which-won-where pattern of a genotype by environment dataset. Use of a bi-plot intriguing, as it graphically addresses important concepts such as crossover GE, mega-environment differentiation, specific adaptation [21]. A polygon is first drawn on genotypes that are furthest from the bi-plot origin so that all other genotypes are contained within the polygon. (Figure 4) showed that, The vertex genotypes in this investigation were G2, G10, G11, G13 and G34 that means genotypes located on the vertices of the polygon performed either the best or the poorest in one or more environments [21].

The vertex genotype in each sector represents the highest yielding genotypes (the winning genotype) in the location that falls within that particular sector [34, 35]. Polygon views the GGE bi-plot showing the mega-environments and their respective highest yielding cultivars [36]. The genotype (G10) was high yielding variety at E1, E3 and E4, the genotype (G13) high yielder at E6 and genotype (G11) was high yielder at E5. The vertex genotype G34 was the poorest (low performing) almost all of the test environments since it had the longest distance from the origin of the bi-plot on the opposite side of the environments and It had also been observed that no environments fell into sectors of those genotype. Genotype G12, G4 and G1 were located near to the origin implying the genotypes were broadly adapted similar result was

obtained by [21, 32, 37, 17] the genotypes were broadly adapted similar result was obtained by [21, 32, 36, 37].

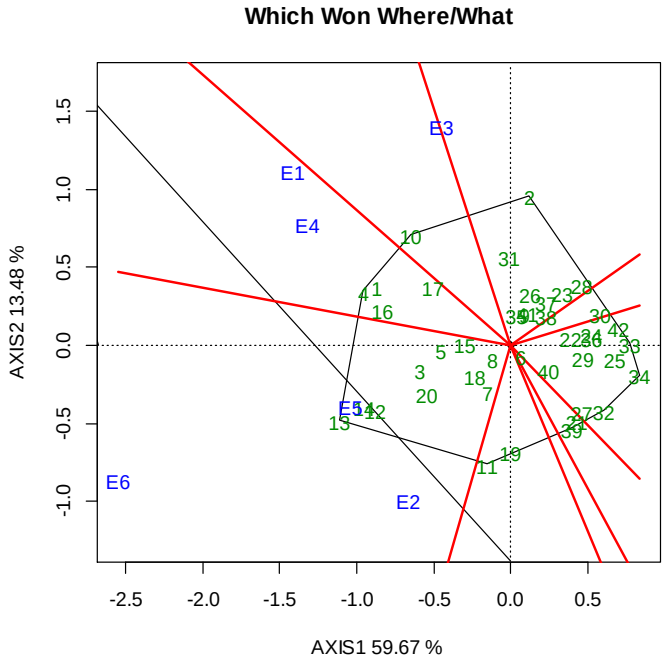

Figure 4. *Polygon view of the GGE biplot using symmetrical scaling for the which-won-where pattern of the genotypes environments. Details of environment. Details of environment are given in Table 1. Numbers 1 to 42 represent genotypes as indicated in Table 2.*

4. Summary and Conclusion

Selecting stable genotypes is challenging due to genotype-environment interaction causing performance fluctuations across locations and years. The results of this study indicated that sorghum grain yield performances were highly influenced by environmental, genotype and interactions effects. Sorghum genotypes showed cross over GEI across environment and among genotypes tested, there were desirable genotypes in terms of mean yield and stability. GGE bi-plot methods were used to evaluation genotype graphical by consider environmental variation and help to understand partitioning of GEI over bi-plot analyses, were showed IPCA1 and IPCA2 which accounted 59.69% and 13.48% of sum of squares. The bi-plot can evaluate genotypes based on mean grain yield and stability, According to bi-plot G16, G4 and G1 were high yielding and most stable. On the other hand G13, G10 and G14 were high yielding but less stable genotypes as a result of length of ATC abscissa. Center of concentric circles can identifying ideal genotypes and environment. Genotypes and environment near to ATC line were high, stable and most representative over all environments and most powerful to discriminate genotype G16 and E6 respectively.

Abbreviations

GEI: Genotype by Environment Interaction
ATC: Average Test Coordination
MET: Meta-Environmental Trial
MMT: Million Metric Ton

Acknowledgments

The authors would like to acknowledge the financial support provided by the national Sorghum breeding program for conducting the field experiments.

Author Contributions

Nesrya Bedru: Conceptualization, Resources, Data curation, Software, Formal Analysis, Writing - original draft, Methodology
Temesgen Matiwos: Software, Supervision, Visualization
Techale Birhan: Supervision, Visualization
Tegegn Belete: Writing - review & editing

Conflicts of Interest

The authors declare no conflicts of interest.

References

[1] Poehlman, J. M. and D. A. Sleper, 1995. Breeding Field Crops. 4th ed, Iowa State University Press, Ames, Iowa. pp. 494.

[2] Paterson, A. H., Bowers, J. E., Bruggmann, R., Dubchak, I., Grimwood, J., Gundlach, H., Haberer, G., Hellsten, U., Mitros, T., Poliakov, A. and Schmutz, J., 2009. The Sorghum bicolor genome and the diversification of grasses. *Nature*, *457*(7229), pp. 551-556.

[3] Doggett, H. 1988. Sorghum. 2nd edition. Longman Scientific and Technical, London.

[4] Stemler, A. B. L., J. R. Harlan, and J. M. J. de Wet. 1977. The Sorghums of Ethiopia. Springer on behalf of New York Botanical Garden Press. 31(4), pp. 446-460.

[5] Habte, N., Girma, G., Mekonen, M., Tirfessa, A., Seyoum, A., Bejiga, T., Birhanu, C., Dessalegn, K., Senbetay, T., Ayana, G., Tesso, T., Ejeta, G., Mengiste, T. 2021. Genome-wide association analysis reveals seed protein loci as determinants of variations in grain mold resistance in sorghum. TheorAppl Genet. 134(4): pp. 1167-1184.

[6] Mesfin A., 2016. Assessment of Striga infestation and Evaluation of sorghum landraces for Resistance/Tolerance to [Strigahermonthica (Del.) Benth] in North-Western Ethiopia. Haramaya University, Dire Dawa, Ethiopia.

[7] McGuire, S. J. 2007. Vulnerability in farmer seed Systems: Farmer practices for coping with seed insecurity for sorghum in Eastern Ethiopia. Economic Botany 61(3), pp. 211-222.

[8] Adugna, A., 2014. Analysis of in situ diversity and population structure in Ethiopian cultivated Sorghum bicolor (L.) landraces using phenotypic traits and SSR markers. *SpringerPlus*, *3*(1), pp. 1-14.

[9] Ethiopian Institute of Agricultural Research (EIAR). 2019. Sorghum Breeding Manual.

[10] USDA World Agricultural Production U.S. Department of Agriculture, March (2022). Foreign Agricultural Service / Global Market Analysis International Production Assessment Division (IPAD).

[11] USDA World Agricultural Production U.S. Department of Agriculture, (2023). Foreign Agricultural Service / Global Market Analysis International Production Assessment Division (IPAD).

[12] Adugna, A., Tesso, T., Deressa, A., 2005. Sorghum production and research experiences in Ethiopia: a production manual, Ethiopian Agricultural Research Organization, Addis Ababa, Ethiopia. pp 31.

[13] Ethiopian Institute of Agricultural Research (EIAR) 2014. Ethiopian strategy for sorghum 2014-2024, Pp 1-10.

[14] FAO (Food and Agriculture Organization of the United Nations) (2020). Available from: http://www.fao.org/faostat/en/#data/QC

[15] Teressa, T., Bejiga, T., Semahegn, Z., Seyoum, A., Kinfe, H., Nega, A., Ayele, L., Nadew, D., Salah, M., Siraw, S. and Bekele, M., 2021. Evaluation of advanced sorghum (Sorghum bicolor L. Moench) hybrid genotypes for grain yield in moisture stressed areas of Ethiopia. *Journal of agricultural science and food technology*, *7*(2), pp. 212-219.

[16] Van Eeuwijk, F. A., Bustos-Kortsa, D. V. and Malosetti, M. 2016. What Should Students in Plant Breeding Know About the Statistical Aspects of Genotype × Environment Interactions? Crop Science 56(5), pp. 2119-2140.

[17] Amare, S., Amare, N., Kedanemaryam, W., Taye, T., Diriba, T., Alemu, T., Habte, N., Adane, G., Sewmehone, S., Tsegaye, G., Chalachew, E., Hailemariam, S., Tamirat, B., Tokuma, L., David, J., Emma, M., Daniel, N., Ligaba, A. and Meron, B. 2020. Multi Environment and Spatial Analysis of Early Maturing Sorghum [*Sorghum bicolor* (L.) *Moench*] Genotypes in Dry Lowland Areas of Ethiopia. African Journal of Agricultural Research, 15(2), pp. 278-290.

[18] Habte, N., Seyoum, A. and Gebreyohannes, A. 2016. Evaluation of Yield Performance of Intermediate Altitude Sorghum (*Sorghum bicolor (L.) Moench*) Genotypes Using Genotype × Environment Interaction Analysis and GGE Biplot in Ethiopia. International Journal of Trend in Research and Development, 3(2), pp. 27-35.

[19] Gauch, H. and Zobel, R. W., 1997. Identifying mega-environments and targeting genotypes. Crop Science, 37(2), pp. 311-326.

[20] Bänziger, M. and Diallo, A. O. 2004. Progress in developing drought and N stress tolerant maize cultivars for eastern and southern Africa. In: Friesen, D. K. and Palmer, A. F. E. (Eds.). Integrated Approaches to Higher Maize Productivity in the New Millennium. Proceedings of the 7th Eastern and Southern Africa Regional Maize Conference. CIMMYT/KARI, Nairobi, Kenya. pp. 189-194.

[21] Yan and Tinker, 2006. Biplot analysis of multi-environment trial data: Principles and applications. Canadian J. Plant Sci, Pp 623-645.

[22] Parfitt. R. C. 2000. Genotype x Environment Interaction among Secondary Variety Trials in the Northern Region of the South African Sugar Industry, Proc S AfrSugTechnol Ass.

[23] Yan W. 2001. GGE biplot-A Windows application for graphical analysis of multi-environment trial data and other types of two-way data. Agronomy Journal 93: 1111-1118.

[24] Yan W, and Kang M. 2003. GGE biplot analysis: a graphical tool for breeders, geneticists and agronomist. CRC Press, Boca Raton, FL.

[25] Gomez, K. A. and Gomez, A. A., 1984. *Statistical procedures for agricultural research*. John wiley&sons. Toronto, Canada. 58(4), Pp. 1029-1034.

[26] Gabriel, R. 1971. The bi-plot graphic display of matrices with application to principal component analysis. Biometrika, 58(3), pp. 453-467.

[27] Yan, W., Hunt, L. A., Sheng, Q. and Szlavnics, Z. 2000. Cultivar evaluation and mega environment investigation based on the GGE bi-plot. Crop Sci. 40(3), pp. 597-605.

[28] Adugna, A., 2007. Assessment of yield stability in sorghum. *African Crop Science Journal*, *15*(2), pp. 83–92.

[29] Yan, W., Kang, M. S., Baoluo, M., Woods, S. and Cornelius, P. L. 2007. GGE Bi-plot vs. AMMI analysis of genotype-by-environment data. Crop Sci. 47(2), pp 643-655.

[30] Gebeyehu, C., Bulti, T., Dagnachew, L. and Kebede, D., 2019. Additive main effect and multiplicative interactions (AMMI) and regression analysis in sorghum [Sorghum bicolor (L). Moench] varieties. *Journal of Applied Biosciences*, *136*, pp. 13877-13886.

[31] Tegegn B, B., 2019 Genotype x Environment Interaction and Grain Yield Stability of Tef (Eragrostistef (Zucc.) Trotter) Varieties in South and South Western Ethiopia MSc Thesis.

[32] Belay, F., Mekbib, F. and Tadesse, T., 2020. Genotype by environment interaction and grain yield stability of Striga resistant sorghum [Sorghum bicolor (L.) Moench] genotypes in Ethiopia. Ethiopian Journal of Crop Science, 8(2).

[33] Yan, W. and Rajcan, I. 2002. Biplot analysis of test sites and trait relations of soybean in Ontario. Crop Science. 42(1), pp. 11–20.

[34] Alidu Haruna, Gloria Boakyewaa Adu, Samuel Saaka Buah, Roger A. L. Kanton, Amegbor Isaac Kudzo, Abdulai Mashark Seidu & Obeng-Antwi Kwadwo | (2017) Analysis of genotype by environment interaction for grain yield of intermediate maturing drought tolerant top-cross maize hybrids under rain-fed conditions, Cogent Food & Agriculture, 3(1).

[35] Yan, W. and Tinker, N. A. (2005) An Integrated Biplot Analysis System for Displaying, Interpreting, and Exploring Genotype × Environment Interaction. Crop Science, 45, pp. 1004-1016.

[36] Hussein, M. A., Bjornstad, A. and Aastveit, A. H. 2000. Sasg x Estab A SAS program for computing genotype x environment stability statistics. Agronomy Journal Madison, 92(3), pp. 454-459.

[37] Badu-Apraku, B., Yallou, C. G., Obeng-Antwi, K., Alidu, H., Talabi, A. O., Annor, B., Oyekunle, M., Akaogu, I. C. and Aderounmu, M., 2017. Yield gains in extra-early maize cultivars of three breeding eras under multiple environments. *Agronomy Journal*, *109*(2), pp. 418-431.