

## Annual Research & Review in Biology

23(3): 1-16, 2018; Article no.ARRB.39491  
ISSN: 2347-565X, NLM ID: 101632869

# Yield Adaptability and Stability of Grain Sorghum Genotypes across Different Environments in Egypt using AMMI and GGE-biplot Models

A. M. M. Al-Naggar<sup>1\*</sup>, R. M. Abd El-Salam<sup>1</sup>, M. R. Asran<sup>2</sup>  
and Walaa Y. S. Yaseen<sup>2</sup>

<sup>1</sup>Department of Agronomy, Faculty of Agriculture, Cairo University, Egypt.

<sup>2</sup>Agricultural Research Centre (ARC), Department of Grain Sorghum Research, Field Crops Research Institute, Giza, Egypt.

### Authors' contributions

This work was carried out in collaboration between all authors. Author AMMAN designed the study, performed the statistical analysis, wrote the protocol and wrote the first draft of the manuscript. Authors AMMAN, RMAES and MRA supervised the study and managed the literature searches. Author WYSY managed the experimental process and performed data analyses. All authors read and approved the final manuscript.

### Article Information

DOI: 10.9734/ARRB/2018/39491

#### Editor(s):

(1) George Perry, Dean and Professor of Biology, University of Texas at San Antonio, USA.

#### Reviewers:

(1) Enver Kendal, Mardin Artuklu University, Turkey.

(2) Nebi Bilir, Suleyman Demirel University, Turkey.

Complete Peer review History: <http://www.sciencedomain.org/review-history/22970>

Original Research Article

Received 9<sup>th</sup> November 2017  
Accepted 28<sup>th</sup> January 2018  
Published 2<sup>nd</sup> February 2018

## ABSTRACT

Presence of G×E interaction reduces the correlation between genotypic and phenotypic parameters and complicates progress of selection. Among several methods proposed for evaluation of the GE interaction, the AMMI and GGE-biplot are the most informative models. The objective of this study was to estimate the G×E interaction in sorghum parental lines and to identify sorghum B-lines of stability and adaptability across different environments using the AMMI and GGE-biplot models. Six environments with 25 sorghum B-lines were conducted at two locations in Egypt (Giza and Shandaweel) in two years and two planting dates in one location (Giza). A randomized complete block design was used in each environment (yield trial) with three replications. The AMMI analysis of variance indicated that the genotype (G), environment (E) and GE interaction had significant

\*Corresponding author: E-mail: medhatalnaggar@gmail.com, ahmedmedhatalnaggar@gmail.com;

influence ( $p \leq 0.01$ ) on sorghum grain yield. Based on AMMI model, BTX TSC-20 followed by ICSB-1808 showed both high yielding and stability across the test environments. However, ICSB-8001 (G11) and BTX-407 (G21), showed maximum stability, but with moderate grain yield. Based on GGE-biplot method, BTX TSC-20 (G25) was the winning genotype for the mega-environment which consists of E1 and E3, ICSB-14 (G3) for the mega-environment (E2 and E4), while BTX 2-1 (G20) for E5 mega-environment, ICSB-88003 (G12) and ICSB-70 (G6) for the mega-environment E6. These genotypes are the most adapted to the respective environments.

**Keywords:** *Sorghum bicolor* L.;  $G \times E$  interaction; mega environment; grain yield.

## 1. INTRODUCTION

Grain sorghum [*Sorghum bicolor* L. (Moench)] is the fourth major cereal crop in Egypt in terms of area and production next to wheat (*Triticum aestivum* L.) rice (*Oriza sativa* L.) and maize (*Zea mays* L.). In 2014 season, the cultivated area of grain sorghum in Egypt was about 353,346 feddan (148,456 ha), producing about 804,000 tons with an average productivity of 16.25 ardab/fed (5.42 ton/ha) according to FAOSTAT [1]. Most of grain sorghum cultivated area in Egypt is concentrated in Assiut and Sohag governorates (Upper Egypt), where the atmospheric temperature during the growing season is high, since grain sorghum is more tolerant to high temperature than maize [2-5]. A major challenge of sorghum production in these parts of the country is lack of stable varieties. For the last decades, a number of hybrid sorghum varieties were developed and released for growing in these areas. The parental lines of these single cross hybrid varieties should be tested for stability and adaptability. Adaptability is the response of the genotypes to the differences between the locations, while stability represents the response of genotypes to variations between years [6].

Genotype-by-environment interaction (GEI) is reflected in inconsistent crop yield across environments. Variations in climate change and soil properties and the inherent potential of genotypes are among the major factors for variable crop yield. Fortunately, the possibility exists to find or develop stable and high-yielding genotypes (fit genotypes) for the mega-environments [7]. Among several methods proposed for evaluation of the GE interaction, the additive main effect and multiplicative interaction (AMMI) model [8,9], and genotype plus genotype-by-environment (GGE) biplot [10-12] are frequently applied procedures for genotype, environment and genotype-by-environment analysis based on crop attributes. AMMI separates the genotype and environment main

effects and the GEI effects [13] and provides much insight into GEI [8]. The GGE biplot emphasis on genotype and genotype-by-environment interaction becomes efficient in the mega-environment analysis and genotype evaluation which includes attribute-based genotypes ranking [12].

It is important to show the relationship between genotypes and environments for selected traits graphically by use of a genotype by genotype by environment (GGE) biplot that allows visual assessment of genotype by environment interaction (GEI) pattern of multi-locational or multi-environment data [14,15]. GGE is the most recent approach for analysis of GEI and increasingly being used in GEI studies in plant breeding research [16]. The model was proposed by Yan et al. [14], and has shown extensive usefulness and a more comprehensive tool in quantitative genetics and plant breeding [17,18]. The model covers very critical areas in the study of stability of multi-locational trials, like the which-won-where pattern, mean performance and stability of genotypes, discriminating ability, mega-environment investigation, and representativeness of environments. The GGE method emphasizes on two concepts, whereby in the first concept, it clearly points out that even though the measured yield is a result of combination effect by Genotype (G), Environment (E) and genotype x environment interaction (GEI), only G and GEI are relevant and must be considered simultaneously when evaluating genotypes, thus the name GGE. The second concept is based on the biplot technique which was developed by Gabriel [19] which is used to estimate and show the GGE of MEYT, hence the name GGE biplot. The GGE biplot is made by the first two principal components (PC), PC1 and PC2 also known as the primary and secondary effects, respectively. This is derived from subjecting the environment centered yield data (due to GGE) to singular value decomposition. This now makes it very easy for one to see which genotype won in which

environments, thus facilitating mega-environment (ME) identification [14,17]. This is facilitated in the form of a polygon to visualize the interaction patterns between genotypes and environments [20], whereby furthest genotypes are connected from the biplot origin such that all genotypes are contained in the polygon [21]. Some genotypes will be located on the vertices of the polygon and they are either the best or the poorest in one or more environments [14,20,22]. The rays are drawn perpendicular to the sides of the polygon dividing it into sectors, such that the vertex genotypes in each sector is also the best genotype for sites whose markers fall into respective sector so that sites within the same sector share the same winning genotype [14,23]. GGE biplot is a visual display of the G + GE of multi-environmental data where groups of locations with similar cultivar responses are presented and it identifies the highest yielding varieties for each group. PC1 tend to correlate highly with the genotype means, the ideal cultivar is the one which possess large scores for PC1, thus indicating high average yield and small PC2 scores indicating less GEI and greater stability. The present study was done to analyze the multi-environmental yield data on 25 grain sorghum B-lines from across six environments conducted at two locations in Egypt (Giza and Shandaweel) in two years and two planting dates in one location (Giza). The objectives were (i) to identify sorghum B-lines with stable and high yield performance across different environments by using AMMI analysis, (ii) to measure the correlation among the six test environments, (iii) to determine whether the test-environments

belong to a single mega environment or not and (iv) to rank environments based on discriminating ability and representativeness by using the GGE biplot analysis.

## 2. MATERIALS AND METHODS

The field work of this study was carried out at two locations, namely Giza (Middle Egypt) and Shandaweel (Upper Egypt) Research Stations of the Agricultural Research Center, Egypt in 2012 and 2013 growing seasons of grain sorghum.

### 2.1 Breeding Materials

Twenty five grain sorghum parental B-lines kindly provided by Grain Sorghum Res. Dept., Field Crops Research Institute, Agric. Res. Center (ARC), Egypt were used as breeding material of this study. Designation, name and origin of these lines are presented in Table 1.

### 2.2 Field Experiments

Six field experiments represent different environments (E1, E2, E3, E4, E5 and E6) were carried out; four of them (E1 through E4) at Giza (two planting dates x two seasons) and two (E5 and E6) at Shandaweel (one planting date x two seasons). The two planting dates at Giza were on 1<sup>st</sup> of June and 1<sup>st</sup> of July in both growing seasons (2012 and 2013). The planting date at Shandaweel was on 1<sup>st</sup> July in both seasons (2012 and 2013). Characterization of the six environments used in this study is presented in Table 2.

**Table 1. Designation, name and origin of grain sorghum B-lines used in this study**

Genotype no.	Name	Origin	Genotype no.	Name	Origin
G1	ICSB-1	ICRISAT- India	G14	ICSB-88005	ICRISAT- India
G2	ICSB-11	ICRISAT- India	G15	ICSB-30	ICRISAT- India
G3	ICSB-14	ICRISAT- India	G16	ICSB-88010	ICRISAT- India
G4	ICSB-20	ICRISAT- India	G17	ICS B-88015	ICRISAT- India
G5	ICSB-37	ICRISAT- India	G18	ICSB-90001	ICRISAT- India
G6	ICSB-70	ICRISAT- India	G19	ICSB-91003	ICRISAT- India
G7	ICSB-102	ICRISAT- India	G20	BTX 2-1	Texas- USA
G8	ICSB-122	ICRISAT- India	G21	BTX-407	Texas- USA
G9	ICSB-155	ICRISAT- India	G22	BTX-409	Texas- USA
G10	ICSB-1808	ICRISAT- India	G23	BTX-630	Texas- USA
G11	ICSB-88001	ICRISAT- India	G24	BTX-631	Texas- USA
G12	ICSB-88003	ICRISAT- India	G25	BTX TSC-20	Texas- USA
G13	ICSB-88004	ICRISAT- India			

Source: Grain sorghum Res. Department, Field Crops Res. Institute, Agric. Res. Center, Egypt

**Table 2. Location, latitude, longitude, altitude, planting date, air temperature and relative humidity (RH) of the six tested environments (E1 to E6)**

Environment	Location	Latitude	Longitude	Altitude	Planting	Temperature (°C)			RH%
					Date	Max.	Aver.	Min.	
<b>E1</b>	Giza	30° 02' N	31° 13' E	22.5 masl	1/6/2012	37.6	29.6	24.8	64.0
<b>E2</b>	Giza	30° 02' N	31° 13' E	22.5 masl	1/7/2012	37.7	29.4	24.8	58.7
<b>E3</b>	Giza	30° 02' N	31° 13' E	22.5 masl	1/6/2013	35.2	28.8	22.4	60.4
<b>E4</b>	Giza	30° 02' N	31° 13' E	22.5 masl	1/7/2013	37.2	30.3	23.7	60.7
<b>E5</b>	Shandaweel	26° 33' N	31° 41' E	67.0 masl	1/7/2012	41.1	30.5	26.2	33.7
<b>E6</b>	Shandaweel	26° 33' N	31° 41' E	67.0 masl	1/7/2013	40.8	33.6	25.5	32.2

*masl = meter above sea level*

## 2.3 Experimental Design

A randomized complete block design in three replications was used in each of the six experiments. Each experimental plot consisted of one ridge of five meters length and 0.7 width. Therefore, the experimental plot area for each B-line was 3.5 m<sup>2</sup>. Seeds were sown in hills at 20 cm apart, thereafter (before the first irrigation) were thinned to two plants/hill to achieve a plant density of 60,000 plants/fed (142,800 plants/ha).

## 2.4 Cultural Practices

Flood irrigation was given at planting, the first irrigation after 21 days and the next irrigations at 10-15 day intervals depending on the requirement of plants. Nitrogen fertilizer was added at the rate of 100 kg N/fed (238 kg/ha) as Urea (46.5% N) in two equal doses; the first dose before the first irrigation and the second before the second irrigation. Calcium Superphosphate fertilizer (15% P<sub>2</sub>O<sub>5</sub>) was added at the rate of 30 kg P<sub>2</sub>O<sub>5</sub>/fed as soil application before sowing during preparation of the soil for planting. Potassium fertilizer at the rate of 24 kg K<sub>2</sub>O/fed was added as soil application before the second irrigation as Potassium Sulfate (48% K<sub>2</sub>O). Other cultural practices were carried out following the recommendations of ARC, Egypt. Weed control was performed chemically with Stomp herbicide (active constituent: 455 g/l Pendimethalin; manufactured by BASF, Australia) before the planting irrigation and just after sowing and manually by hoeing twice, the first before the first irrigation and the second before the second irrigation. Pest control was performed when required by spraying plants with Lannate (Methomyl) 90% (manufactured by DuPont, USA) against borers.

Grain yield/plant (GYPP) in g was estimated on 20 guarded plants/plot as the average weight of grain yield/plant adjusted at 14% grain moisture.

## 2.5 Biometrical Analyses

Analysis of variance of the randomized complete block design (RCBD) was performed for each of the six environments on the basis of individual plot observation using the DSAASTAT Version 1.1 (Update: 18/03/2011). Combined analysis of variance across the six environments was also performed if the homogeneity test was non-significant. Least significant difference (LSD) values were calculated to test the significance of

differences between means according to Steel et al. [24].

## 2.6 Stability Analyses

Stability analysis of the 25 grain sorghum lines was carried out for characters under study. Three different approaches were adopted for estimating the stability using AMMI and GGE biplot methods of stability analysis. AMMI and GGE biplot models were computed using the GeneStat-17.1.13780 software program.

### 2.6.1 Additive mean effect and multiplicative interaction (AMMI) model

The AMMI model is as follows:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum n \lambda_n \gamma_{gn} \delta_{en} + \epsilon_{ger} + \rho_{ge};$$

where  $Y_{ger}$  was the observed yield of genotype (g) in environment (e) for replication (r); Additive parameters:  $\mu$  was the grand mean;  $\alpha_g$  is the deviation of genotype g from the grand mean,  $\beta_e$  is the deviation of the environment e; Multiplicative parameters:  $\lambda_n$  was the singular value for interaction principal component axis (IPCA) n,  $\gamma_{gn}$  was the genotype eigenvector for axis n, and  $\delta_{en}$  is the environment eigenvector;  $\epsilon_{ger}$  is the error term and  $\rho_{ge}$  are PCA residuals. Accordingly, genotypes with low (regardless of the sign) IPCA scores showed general or wider adaptability, while those with high IPCA scores showed specific adaptability [25].

#### 2.6.1.1 AMMI Stability Value (ASV)

The ASV is the distance from the coordinate point to the origin in a two-dimensional plot of IPCA1 scores against IPCA2 scores in the AMMI model [26]. Because the IPCA1 score contributes more to the G x E interaction sum of squares, a weighted value is needed. This was calculated for each genotype and each environment according to the relative contribution of IPCA1 to IPCA2 as follows:

$$ASV = \{[(SS_{IPCA1} \div SS_{IPCA2}) (IPCA1 \text{ score})]^2 + (IPCA2 \text{ score})^2\}^{1/2}$$

Where  $SS_{IPCA1}/SS_{IPCA2}$  was the weight given to the IPCA1-value by dividing the IPCA1 sum of squares by the IPCA2 sum of squares. The larger the ASV value, either negative or positive, the more specifically adapted a genotype was to certain environments. A smaller ASV value

indicated a more stable genotype across environments [26].

### 2.6.2 GGE Biplot analysis

To evaluate the phenotypic stability and adaptability, the GGE biplot analysis was performed, considering the simplified model for two main components. In this approach, the effects of genotype (G) and genotype by environment (GE) were considered as random in the model. In this case, the best linear unbiased prediction (BLUP) of G and GE effects are calculated.

The components of genotypic variance, of the variance of GE interaction and residual were estimated by the method of restricted maximum likelihood (REML). For analysis of variance the software package SAS 9.2 version was used. GGE biplot software was used to explain relationship between genotype and locations graphical [20].

The model for a GGE biplot [23] based on singular value decomposition (SVD) of the first two principal components is:

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij} \quad (1)$$

where  $Y_{ij}$  is the measured mean (DBH) of genotype  $i$  in environment  $j$ ,  $\mu$  is the grand mean,  $\beta_j$  is the main effect of environment  $j$ ,  $\mu + \beta_j$  being the mean yield across all genotypes in environment  $j$ ,  $\lambda_1$  and  $\lambda_2$  are the singular values (SV) for the first and second principal component (PC1 and PC2), respectively,  $\xi_{i1}$  and  $\xi_{i2}$  are eigenvectors of genotype  $i$  for PC1 and PC2, respectively,  $\eta_{j1}$  and  $\eta_{j2}$  are eigenvectors of environment  $j$  for PC1 and PC2, respectively,  $\varepsilon_{ij}$  is the residual associated with genotype  $i$  in environment  $j$ .

PC1 and PC2 eigenvectors cannot be plotted directly to construct a meaningful biplot before the singular values are partitioned into the genotype and environment eigenvectors. Singular-value partitioning is implemented by,

$$g_{i1} = \lambda_1^{f1} \xi_{i1} \text{ and } e_{j1} = \lambda_1^{1-f1} \eta_{j1} \quad (2)$$

Where  $f1$  is the partition factor for PC1, Theoretically  $f1$  can be a value between 0 and 1, but 0.5 is most commonly used.

To generate the GGE biplot, the formulae (1) was presented as:

$$Y_{ij} - \mu - \beta_j = g_{i1} e_{1j} + g_{i2} e_{2j} + \varepsilon_{ij} \quad (3)$$

If the data was environment-standardized, the common formula for GGE biplot was reorganized as follows:

$$Y_{ij} - \mu - \beta_j / s_j = \sum g_{i1} e_{1j} + \varepsilon_{ij} \quad (4)$$

Where,  $s_j$  is the standard deviation in environment  $j$ ,  $l = 1, 2, \dots, k$ ,  $g_{i1}$  and  $e_{1j}$  are PC1 scores for genotype  $i$  and environment  $j$ , respectively.

We used environment standardized model (4) to generate biplot of "which-won where". For the analysis of relationship between the trials, genotype and environment evaluation, we used unstandardized model (3).

## 3. RESULTS AND DISCUSSION

Development of a stable variety is one of the major objectives of all breeding programs. Phenotypically stable varieties are usefully sought for commercial production of crop plants. In any breeding program, it is necessary to screen and identify phenotypically stable genotypes, which could perform more or less uniformly under different environmental conditions. Several models have been proposed for stability analysis; the most important are AMMI and GGE Biplot models.

### 3.1 Mean Performance of B-lines in Each and Across Environments

Means of grain yield/plant of each B-line under each environment and average across all the six environments are presented in Table 3. Ten genotypes were above grand mean yield. The highest genotype yield was produced by genotype 25 (BTX TSC-20) followed by genotypes 12, 10 3 and 1, in descending order. The highest yielding genotypes were G25 followed by G6 in environment E1, G3 followed by G12 in environment E2, G25 followed by G10 in E3, G12 followed by G3 in E4, G2 followed by G20, G22 and G13 in E5 and G12 followed by G6 in E6.

Means and the estimates of environmental index (Table 3) exhibited that differences among the environments were significant, indicating that they were diverse. Results showed that E5 (Shandaweel, 2012) was the best performing environment for grain yield/plant followed by E6

(Shandaweel, 2013), while E1 and E3 were the poorest gain yielding environments. This variation in the environmental index showed that the performance of the genotypes varied from location to location and from planting date to another and from season to season. Shandaweel location, 1<sup>st</sup> year (E5) was therefore the most favorable environment for realizing the yield potential of grain sorghum parental lines with the location possessing favorable environmental resources, particularly better soil variables. Although most genotypes were adapted to E5 environment, some genotypes demonstrated specific adaptation to poorer environments, suggesting other climatic conditions were the determining factors for the performance of grain sorghum genotype and confer either broad or specific adaptation to such environments. It is worthy to mention that 2<sup>nd</sup> planting date (1<sup>st</sup> of July) expressed in average of E1 and E3 environments, produced higher average grain

yield/plant (45.40 g) than that produced by the 1<sup>st</sup> planting date (1<sup>st</sup> of June) as average across E2 and E4 (36.47 g).

### 3.2 Additive Main Effects and Multiple Interaction (AMMI) Model

#### 3.2.1 AMMI analysis of variance

Combined analysis of variance revealed highly significant ( $P \leq 0.01$ ) variances due to environments, genotype  $\times$  environment interaction and IPCAs (Table 4). This result revealed that there was a differential yield performance among the grain sorghum genotypes across testing environments and the presence of strong genotype by environment (G  $\times$  E) interaction. As G  $\times$  E interaction was significant, further calculation of genotype stability is possible.

**Table 3. Mean grain yield/plant (g) of 25 grain sorghum B-lines under each of the six environments (E1 through E6)**

Genotype no.	B-line name	Environments						Average
		E1	E2	E3	E4	E5	E6	
G1	ICSB-1	43.03	54.83	41.53	54.07	58.00	56.33	51.28
G2	ICSB-11	38.30	39.60	36.87	38.97	79.00	50.87	47.28
G3	ICSB-14	43.33	63.00	43.10	64.17	59.33	36.33	51.53
G4	ICSB-20	44.83	39.10	37.37	35.00	61.00	49.33	44.43
G5	ICSB-37	36.63	44.23	32.53	44.10	50.00	49.00	42.73
G6	ICSB-70	45.67	43.97	38.93	42.87	52.67	62.73	47.82
G7	ICSB-102	29.50	37.47	26.80	36.70	60.00	52.53	40.50
G8	ICSB-122	36.80	39.17	36.40	37.90	68.00	59.00	46.22
G9	ICSB-155	23.37	38.10	18.77	36.77	67.67	43.07	37.98
G10	ICSB-1808	48.03	55.73	48.70	57.87	70.00	46.07	54.40
G11	ICSB-88001	39.33	46.93	38.57	45.37	67.00	53.00	48.37
G12	ICSB-88003	40.67	63.37	39.73	64.67	57.67	66.47	55.45
G13	ICSB-88004	41.13	39.33	39.27	38.90	71.67	46.07	46.07
G14	ICSB-88005	42.20	46.33	41.67	49.67	62.00	45.33	47.87
G15	ICSB-30	36.57	41.00	36.70	39.90	67.33	36.47	43.00
G16	ICSB-88010	42.33	38.03	41.67	44.57	68.33	46.27	46.87
G17	ICS B-88015	38.43	40.83	35.90	38.97	65.33	53.87	45.55
G18	ICSB-90001	37.50	43.00	37.33	42.03	65.00	46.20	45.17
G19	ICSB-91003	33.23	44.77	28.67	46.63	62.67	55.00	45.17
G20	BTX 2-1	31.47	49.33	29.90	48.67	75.67	36.07	45.20
G21	BTX-407	39.20	47.33	37.67	47.50	66.67	49.13	47.92
G22	BTX-409	37.33	38.07	37.13	37.17	72.00	44.20	44.32
G23	BTX-630	40.70	39.00	38.57	38.37	65.00	51.53	45.53
G24	BTX-631	40.27	46.67	37.57	46.50	62.67	59.60	48.90
G25	BTX TSC-20	56.07	56.77	56.13	57.07	67.67	54.80	58.10
	<b>Average</b>	<b>39.44</b>	<b>45.44</b>	<b>37.50</b>	<b>45.37</b>	<b>64.89</b>	<b>49.97</b>	<b>47.10</b>
	Environ. index	-7.66	-1.66	-9.6	-1.73	17.79	2.87	
	LSD 0.05	8.84	7.24	10.63	9.99	5.7	13.41	9.78
	LSD 0.01	11.79	9.66	14.18	13.33	10.6	17.89	12.89

**Table 4. Additive main effects and multiplicative interaction analysis of variance for grain yield/plant of 25 grain sorghum genotypes across six environments**

SOV	df	MS	Explained (%)
Blocks (Environments)	12	134.7**	2.27
Treatments	149	400.3**	83.82**
Genotypes (G)	24	362.2**	14.57**
Environment (E)	5	7222.2**	60.55**
Interaction (G×E)	120	123.7**	24.88**
IPCA 1	28	234.7**	44.29**
IPCA 2	26	194.8**	34.12**
Residuals	66	48.5*	21.59**
Error	288	34.4	
Total	449	158.5	

\*, \*\* Significant at  $P \leq 0.05$  and  $P \leq 0.01$ , respectively

The analysis of variance (Table 4) showed that genotype (14.57%), environment (60.55%), and GEI (24.88%) effects were significant ( $P \leq 0.01$ ). Even though the proportion of the environment is the largest, genotype and GEI effects have paramount importance for genotype evaluation [20]. Furthermore, GEI effect was larger (24.88%) than the genotypic effect (14.57%), indicating a high loss of potential genetic gain [27]. Thus, the potential of genotypes was more exploited if the best performed genotypes were identified for the specific environments.

This result revealed that there was a differential yield performance among the grain sorghum genotypes across testing environments and the presence of strong genotype by environment (G X E) interaction. Similarly, Rono et al. [27] evaluated eight sweet sorghum genotypes at five different locations in two growing seasons and reported that significant variances due to genotypes, environments and environment G × E interaction were recorded and thus necessitate stability analysis. Several authors also reported significant G × E interaction and thus stability analysis for bread wheat [28], rice [29], finger millet [30,31], barley [32,33] and soybean [34]. Substantial percentage of G × E interaction was explained by IPCA-1 (44.29%) followed by IPCA-2 (34.12%) (Table 2). The interaction effect was concentrated in the first two IPCA scores (78.41%) explaining the magnitude of interaction effect on yield. The remaining IPCA axes (residual) contributed only 21.59% to G × E interaction. Because of their maximum, the first two principal components (IPCA-1 and IPCA-2) were used to plot a 2-dimensional GGE biplot. Gauch and Zobel [25] suggested that the most accurate model for AMMI can be predicted by using the first two IPCAs. Several authors took the first two IPCAs for GGE biplot analysis

because the greater percentage of genotype by environment interaction (GEI), in most cases, were explained by the first IPCA such as for maize [35], bread wheat [36], common bean [37], finger millet [31] and field pea [38]. This indicated that AMMI biplot model is the best fit for this data set, which is in agreement with several investigators [15,25,30,39].

A large sum of squares shows that environments were diverse, influencing yields differently which was in harmony with the findings of Reddy et al. [40] in sweet sorghum production. Identification of adaptable, stable, and high yielding genotypes under different environmental conditions prior to release has been reported by Lule et al. [31] to be the first and foremost steps for plant breeding. Environment expresses most of the total yield variation while genotype and genotype by environment interactions were less effective [41]. The soil's constituents such as moisture content, mineral availability and pH that is an integral part of environment cause large annual variation in yield performance of a crop. GEI can be reduced by identifying genotypes that are most stable [42].

### 3.2.2 AMMI Stability Value (ASV)

The IPCA1, IPCA2 scores and AMMI stability values (ASV) of six environments and 25 genotypes are presented in Tables (5 and 6), respectively. Environments and genotypes with least ASV and IPCA scores (either negative or positive) are considered the most stable. According to ASV, the environment E3 (Giza, 1<sup>st</sup> planting date, 2013) was the most stable and the lowest grain yielding (Table 5), followed by E1 (Giza, 1<sup>st</sup> planting date, 2012). On the contrary, environment E5 (Shandaweel, 2012) was the most unstable, but was the highest yielding.



Environment E3 attained the smallest IPCA-1 and the 2<sup>nd</sup> smallest IPCA-2. Moreover, environment E1 attained the smallest IPCA-2 and the 2<sup>nd</sup> smallest IPCA-1. These two environments are therefore considered the most stable based on IPCA-1, IPCA-2 and ASV scores; hence they were the least interactive environments for grain yield. On the contrary, the most unstable environment was E5 based on IPCA-1 and ASV scores and the environment E6 based on IPCA-2 scores, hence they were the most interactive environments for grain yield.

Furthermore, the IPCA2 scores of genotypes in AMMI analysis indicate stability of genotypes

across environments; high IPCA2 scores (either negative or positive) are unstable while those with low scores are stable [43]. An ideal genotype should have high mean grain yield and small ASV. Accordingly, ICSB-8001 (G11) and BTX-407 (G21), showed the lowest ASV (0.34 and 0.38), respectively and moderate grain yield (48.37 and 47.92 g/plant), respectively (Table 6). Furthermore, BTX TSC-20 (G25) was the highest yielding genotype (58.08 g per plant) with relatively low ASV (1.43). These results revealed that those genotypes are showing relatively better stability than the rest of genotypes. However, stability needs to be considered in combination with yield [44]. The genotypes

**Table 5. Environment means, IPCA scores and AMMI stability value (ASV) of grain yield/plant**

Environment	Mean	IPCA-1	IPCA-2	ASV
E1	39.44	0.20	-0.25	0.20
E2	45.44	-3.25	0.86	-3.30
E3	37.50	0.08	0.65	0.02
E4	45.37	-3.65	1.68	-3.60
E5	64.89	4.80	2.85	4.72
E6	49.97	1.05	-5.55	1.37

**Table 6. Means, scores of IPCA-1 and IPCA-2 and AMMI stability value (ASV) of 25 Genotypes for grain yield/plant**

Genotype no.	B-line name	General mean	IPCA-1	IPCA-2	ASV
G1	ICSB-1	51.30	-1.79	-0.77	2.45
G2	ICSB-11	47.27	2.36	0.49	3.10
G3	ICSB-14	51.54	-3.40	2.54	5.09
G4	ICSB-20	44.44	0.76	-0.71	1.21
G5	ICSB-37	42.75	-1.46	-1.01	2.14
G6	ICSB-70	47.81	-0.67	-2.67	2.81
G7	ICSB-102	40.50	0.63	-1.25	1.49
G8	ICSB-122	46.21	1.49	-1.39	2.38
G9	ICSB-155	37.96	1.12	0.47	1.53
G10	ICSB-1808	54.40	-1.07	1.64	2.15
G11	ICSB-88001	48.37	0.20	-0.21	0.34
G12	ICSB-88003	55.43	-2.91	-1.61	4.10
G13	ICSB-88004	46.06	1.50	0.64	2.05
G14	ICSB-88005	47.87	-0.77	0.63	1.18
G15	ICSB-30	42.99	0.60	1.69	1.86
G16	ICSB-88010	46.87	0.83	0.57	1.21
G17	ICS B-88015	45.56	0.90	-0.83	1.43
G18	ICSB-90001	45.18	0.31	0.35	0.53
G19	ICSB-91003	45.16	-0.20	-0.89	0.93
G20	BTX 2-1	45.18	0.26	2.73	2.75
G21	BTX-407	47.92	-0.11	0.35	0.38
G22	BTX-409	44.32	1.67	0.82	2.32
G23	BTX-630	45.53	0.98	-0.58	1.40
G24	BTX-631	48.88	-0.16	-1.37	1.39
G25	BTX TSC-20	58.08	-1.06	0.37	1.43

ICSB-1 (G1), ICSB-14 (G3), ICSB-1808 (G10) and ICSB-8003 (G12) that were among the top 5 yielding genotypes (51.30, 51.54, 54.40 and 55.43 g/plant, respectively), but had high ASV (2.45, 5.09, 2.15 and 4.10, respectively) were identified as good genotypes to validate for yield performance and specific adaptability. The results of ASV further confirmed that ICSB -14 (G3) was unstable and not adaptable and that ICSB -155 (G9) and ICSB -102 (G7) were consistent low yielders across environments. Odewale et al. [45] reported that two out of the five coconut genotypes grown across nine environments in southern Nigeria showed smaller ASV and thus better stability. Farshadfar [44] noted three out of the 20 bread wheat genotypes evaluated gave smaller ASV and higher grain yield than the grand mean and thus better relative stability. Lule et al. [31] identified three out of 32 genotypes of finger millet that had better grain yield, but with high ASV and thus good genotypes to validate for yield performance and specific adaptability. Stable genotypes follow genes that affect the trait in question and their expression relative to the environment being similar to average cultivar while unstable genotypes have genes that are challenged differently by a different environment [46].

### **3.2.3 Genotypes grain yield vs IPCA-1(AMMI plot)**

Genotypes or environments located on the right-hand side of the midpoint of the axis main effects have higher yields than those on the left-hand side [46]. In this study, genotypes No. 25, 12, 3, 10, 1, 14, 6, 24, 21 and 11 (Fig. 1) were generally high yielding as they were placed on right-hand side of midpoint representing grand mean. Similarly, Environments E5 and E6 were considered to be superior in grain yield (Fig. 1).

BTX TSC-20 (G25) followed by ICSB-1808 (G10) produced the best average yield (58.08 and 54.40 g/plant, respectively) and attained relatively small of IPCA-1 (-1.05 and -1.07, respectively), indicating that they were stable and widely adaptable genotypes (Table 6 and Fig. 1). Genotypic stability is crucial in addition to grain yield [47]. BTX -407 (G21), BTX -631 (G24) and ICSB -8001 (G11) attained the lowest IPCA-1 score (-0.11, -0.16 and 0.20, respectively) and average grain yield (47.92, 48.88 and 48.37 g/plant, respectively) (Table 6 and Fig. 1).

Genotypes with below average yield, such as ICSB -1003 (G19) and BTX 2-1 (G20) also

showed small values of IPCA-1, indicating consistence in yield performance across locations. ICSB -14 (G3) (51.54 g/plant) and ICSB -8003 (G12) (55.43 g/plant) were out of the best five genotypes in grain yield, but attained relatively high IPCA-1 scores (-3.40 and -2.91, respectively) (Table 6, Fig. 1). Although these results indicated inconsistent yield performance across environments, they demonstrated site specific adaptability for these genotypes. ICSB -155 (G9) yielded the least grain (37.96 g/plant) and attained relatively small IPCA-1 score (1.12) implying that it was average in adaptability (Fig 1; Table 6). Besides, ICSB -37 (G5) is among the low yielding genotypes, but attained relatively high IPCA-1 score (-1.46).

### **3.2.4 Relationship between genotypes and environments**

Fig. 2, gives vector view of relationship between genotypes and mega environments for grain yield, in which environments are connected with biplot origin *via* lines. They also show the relationship among genotypes. This view of biplot aids in the understanding of interrelationship among environments. The cosine of the angle between the vectors of two environments approximates the correlation coefficient between them.

Environments with a small angle between them are highly positively correlated, and they provide similar information on genotypes. Present investigations showed that E2 (Giza, 2<sup>nd</sup> planting date, 2012) and E4 (Giza, 2<sup>nd</sup> planting date, 2013) for grain yield (Fig. 3) were considered to be similar as they had small angle between them. In contrast, either E2 or E4 were dissimilar with E6 (Shandaweel, 2<sup>nd</sup> planting date, 2013), since the angle was obtuse.

E1 (Giza, 1<sup>st</sup> planting date, 2012) and E3 (Giza, 1<sup>st</sup> planting date, 2013) lied closest to the origin and, therefore, contributed the least to GEI; these environments are the most representative (stable) environments, but with poor discriminating ability as indicated in Fig. 2. On the contrary, E5 (Shandaweel, 2<sup>nd</sup> planting date, 2012) exhibited the highest contribution; it indicated both good discriminating ability and representativeness, making it an ideal and best environment for testing the sorghum genotypes. Environment E6 is the least representative (unstable). Test environments which are discriminating but non-representative like E2, E4 and E6 are important under circumstances when

selecting genotypes that are specifically adapted if target environments can be divided into mega-environments. However, where the target environments cannot be divided into mega-environments such test environments like E2 can be useful for culling unstable genotypes.

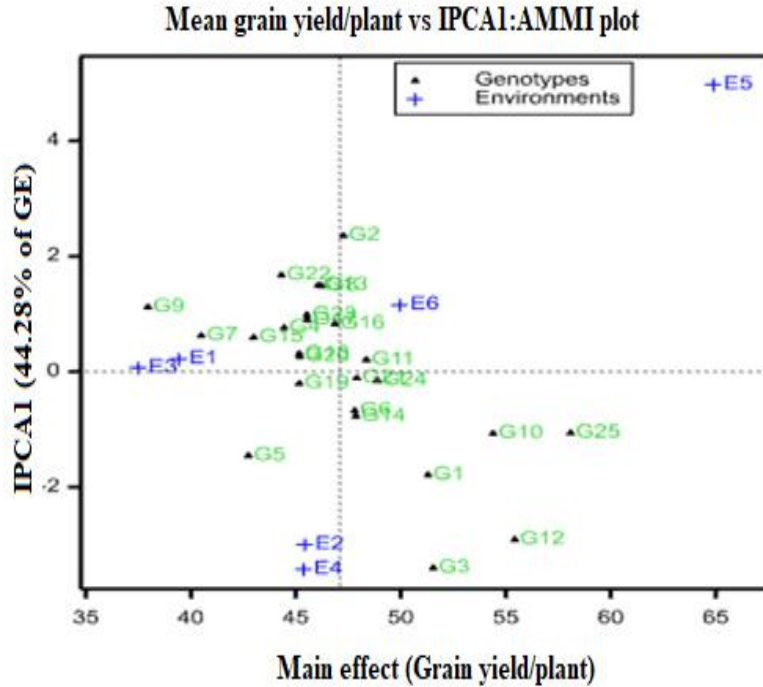


Fig. 1. The relationship between mean grain yield/plant (g) and IPCA-1 of 25 sorghum genotypes (G) evaluated under six environments (E)

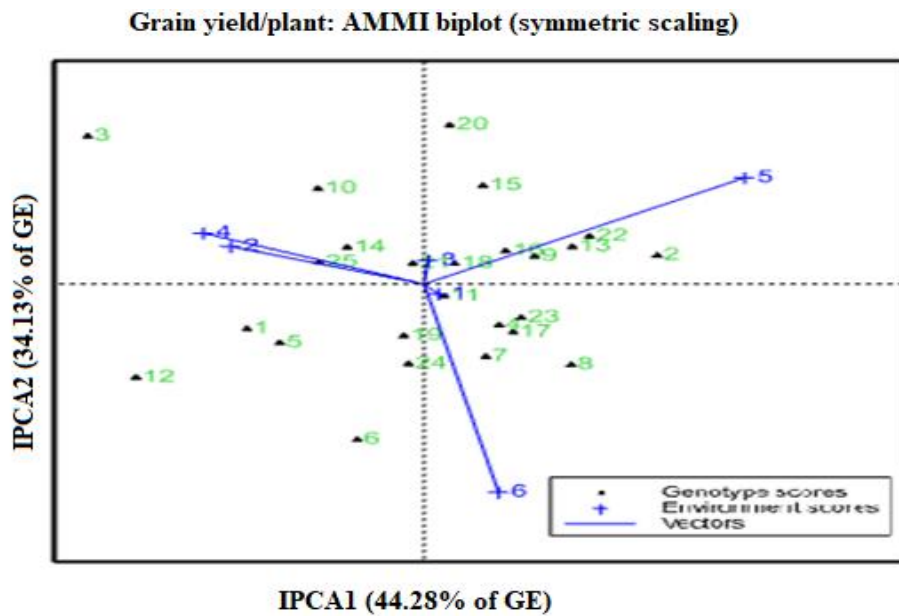


Fig. 2. The AMMI biplot showing relationship between genotypes and mega environments for grain yield

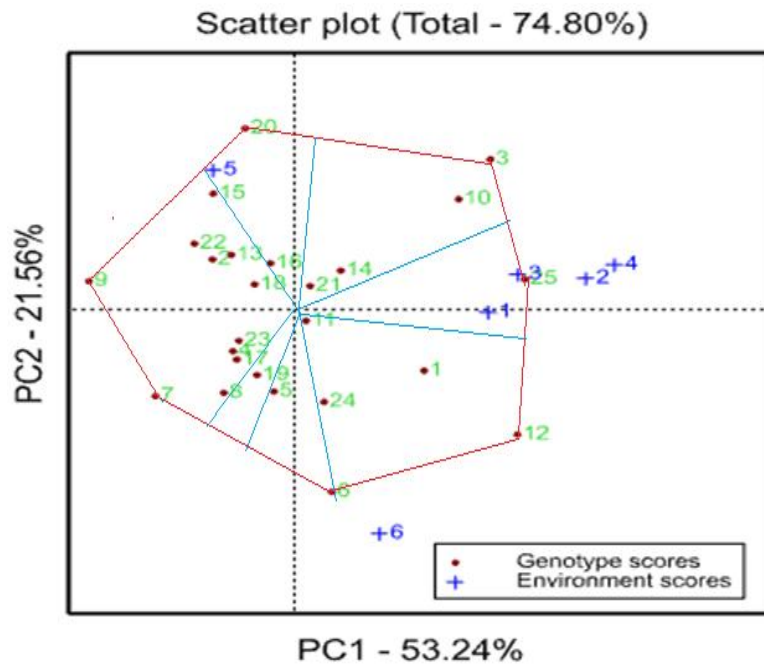


Fig. 3. Polygon view of GGE biplot (which-won-where) showing the (G+G×E) interaction effect for grain yield of 25 sorghum genotypes in 6 environments

### 3.3 GGE Biplot Analysis

#### 3.3.1 Polygon view

The polygon view of GGE biplot for grain yield (Fig. 3) indicates the best genotypes (s) for each environment(s). The genotypes located on the vertex of a polygon are best or poorest genotypes in some or all environments, except left bottom quadrant [43]. The genotype G25 was found promising in E3 and E1 followed by G10, G12 and G3, in descending order. The genotype G12 followed by G3 were promising in E2 and E4 environments. In E5, the promising genotypes were G20, G2, G22 and G13. In E6, the promising genotypes were G12 and G6. The polygon reflects that G9 is poor grain yielding and not suitable to either of the environments.

#### 3.3.2 Mega-environments (which-won-where)

An important feature of the GGE biplot (which-won-where) was also predicted. In mega-environment identification process, further genotypes are connected together to form a polygon, and perpendicular lines are drawn to form sectors which will make it easy to visualize the mega-environments. Environments in one sector having best-performing genotype can be considered as mega-environments for that genotype [48]. These results are in conformity

with the findings of Reddy et al. [40] who observed high yielding and stable genotypes. Biplots were divided into seven sectors in Fig. 3; genotypes which fall in same sector as with environment are said to be adapted to those locations.

The results (Fig. 3) indicated four mega-environments thus two environments, E1 (Giza, 1<sup>st</sup> planting date, 2012) and E3 (Giza, 1<sup>st</sup> planting date, 2013) formed one mega-environment, E2 (Giza, 2<sup>nd</sup> planting date, 2012) and E4 (Giza, 2<sup>nd</sup> planting date, 2013) formed another mega-environment, while E5 (Shandaweel, 2012) and E6 (Shandaweel 2013) formed two separate mega-environments, respectively. The winning genotypes for each mega-environment are those positioned at the vertex. G25 is the winning genotype for the mega-environment which consists of E1 and E3, G3 is the winning genotype for E2 and E4, while G20 is the winning genotype for E5 mega-environment and G12 and G6 are the winning genotypes for the E6 mega-environment. These genotypes are the most adapted to the respective environments.

#### 3.3.3 Comparison plot for genotypes based on the concentric circle

An ideal environment is the one which is on the intrinsic circle (Fig. 4). So E1 (Giza, 1<sup>st</sup> planting

date, 2012) is considered the ideal environment. However, E5 (Shandaweel, 2012) and E6 (Shandaweel, 2013) cannot be ideal environment for selecting genotypes which can be adaptable for the whole region. Fig. 4 shows the comparison plot for genotypes, and an ideal genotype is one which is near or at the center of the concentric circle. Hence in the study, the plot reflected that G25 (BTX TSC-20) is the most ideal genotype as shown by its position and followed by G1 and G10. This also reflects that the genotype has high mean and it is stable. Good genotypes are those which are closer to the ideal genotype, thus G12, G14, G21, G11, G3 and G24. They are positioned closer to the ideal genotypes. However, G9 (ICSB-155), G7, G20, G15, G22, G2 and G8 are the worst genotypes as their position in the plot are located far from the concentric circle.

As the pooled ANOVA showed the presence of GEI for the sorghum grain yield, it means a breeder faces challenge of selection genotypes for advancement and or release, hence further testing for genotypes with wider and specific adaptation and locations with good discriminating ability and representativeness was done. This is similar to the study which was done by Gasura et al. [49], where they tested 20 sorghum varieties and there was a large effect of GEI about seven times larger than the effect of genotypes. AMMI ANOVA showed that IPCA1 accounted for 44.29% and IPCA2 accounted for 34.12%, both accounting for a sum of 78.41% (Table 4) and

this showed similarity with study of Gasura et al. [49], where PC1 and 2 explained 36.8 and 29.5%, respectively. The biplot analysis identified the discriminating ability and representativeness as well as the correlation of environments [50] and genotype average performance. The results showed the importance of testing and comparing genotypes so as to select the ones with specific and wide adaptation accordingly and environments which are representativeness to reduce experimenting costs by discarding unrepresentative locations and those with poor discriminating abilities. The greater IPCA-1 shows greater discriminating ability of an environment. This gives the importance of determining the discriminating ability to enhance separation through differences in performances of different genotypes. The results revealed that E1 though low yielding but gave more information on the tested genotypes than the other environments. So this study provides important information on selecting and releasing best and ideal genotypes which are good for production in specific and widely adapted environments as well as determine the most effective and necessary environments which gives more information on varieties in future breeding trials. Identification of mega-environments (Fig. 3) was studied also and very important information on which-won-where was unveiled in the results obtained. The mega-environment identification involved a situation whereby one or more environments with similar or homogenous characteristics were

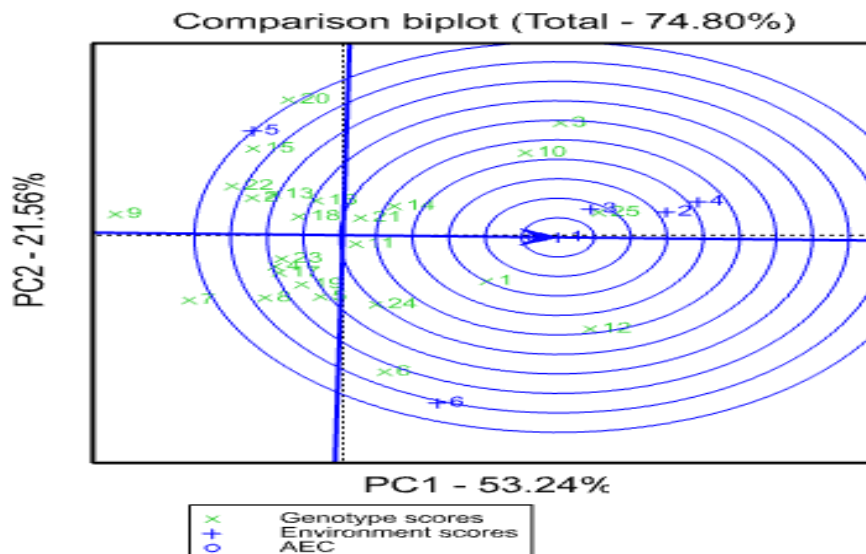


Fig. 4. The average environmental coordination (AEC) view to rank genotypes and environments relative to the center of the concentric circles

bunched into one big location, like in this study where (E1 and E3) and (E2 and E4) were bunched into two separate mega environments meaning in the future, costs of raising multi-locational trials will be reduced by putting that effect into consideration. Which-won-where [12] identified best winners for the mega-environment or sector. This enables the researcher to have specific and valid justification to recommend genotypes which are good for that particular environment [49]. This also means the genotypes can be tested in those few mega-environments and still good yield data results can be obtained. The GGE biplot also gave information which is important if a researcher has to make decisions and conclusions about specific correlations among environments and genotypes. The study results gave a better understanding of how biased a researcher can be if there is GEI and fails to do further GEI biplot analysis. The GGE have a lot of information which validates appropriate environment for testing and appropriate genotypes for selection and recommendation [50]; there was effective evaluation of environments and genotypes and evaluation of genotypes based on the mean performance and stability across environments which is important required information for a researcher.

#### 4. CONCLUSIONS

The results showed that the grain yield performance of the 25 genotypes was significantly influenced by environment, genotype and their interaction. A further analysis on the adaptability and stability across the 6 environments was done. BTX TSC-20 (G25) followed by ICSB-1808 (G10) showed both high yielding and stability across the test environments. These have been identified as possible candidates for use as good seed parents in future breeding programs. E1 (Giza, 1<sup>st</sup> planting date, 2012) though low yielding but gave more information on the tested genotypes than the other environments. ICSB-1808 (G25) is the winning genotype for the mega-environment which consists of E1 and E3, ICSB-14 (G 3) is the winning genotype for E2 and E4, while BTX 2-1 (G20) is the winning genotype for E5 mega-environment, ICSB-80003 (G12) and ICSB-70 (G6) are the winning genotypes for the E6 mega-environment. These genotypes are the most adapted to the respective environments. Considering the great influence of the environment and genotype x environment interaction on grain yield of grain sorghum

parental lines, further testing in additional locations over more seasons and locations is encouraged.

#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

#### REFERENCES

1. FAO STAT. Food and Agriculture Organization of the United Nations. Statistics Division; 2017. (Accessed on 02/08/2017) Available:<http://faostat3.fao.org/>
2. Al-Naggar AMM, El-Nagouly OO, Abo-Zaid Zeinab SH. Differential responses of grain sorghum genotypes to water stress at different growth stages. *Egypt. J. Plant Breed.* 2002a;6(1):111–124.
3. Al-Naggar AMM, El-Nagouly OO, Abo-Zaid Zeinab SH. Genetics of some grain sorghum traits under different water stress conditions. *Egypt. J. Plant Breed.* 2002b;6(1):125–141.
4. Al-Naggar AMM, El-Kadi DA, Abo-Zaid Zeinab SA. Genetic analysis of drought tolerance traits in grain sorghum. *Egypt. J. Plant Breed.* 2007a;11(3):207-232.
5. Al-Naggar AMM, El-Kadi DA, Abo-Zaid Zeinab SA. Inheritance of nitrogen use efficiency traits in grain sorghum under low-and high-N. *Egypt. J. Plant Breed.* 2007b;11(3):181-206.
6. Lin CS, Binns MR. Concepts and methods of analyzing regional trial data for cultivar and location selection. *Plant Breeding Reviews.* 1994;12:271-297.
7. Gauch HG, Zobel RW. Identifying mega-environments and targeting genotypes. *Crop Sci.* 1997;37:311-326.
8. Crossa J, Gauch HG, Zobel RW. Additive main effects and multiplicative interaction analysis of two international maize cultivar trials. *Crop Sci.* 1990;30:493-500.
9. Ebdon JS, Gauch HG Jr. Additive main effect and multiplicative interactions analysis of national turf grass performance trials: I. Interpretation of Genotype x Environment Interaction. *Crop Sci.* 2002;42:489-496.
10. Blanche SB, Myers GO, Kang MS. GGE biplot and traditional stability measures for interpreting genotype by environment interactions. *J. Crop Improve.* 2007;20: 123-135.

11. Sharma RC, Morgounoy AI, Braun HJ, Akin B, Kesser M, Kaya Y, Khalikulov Z, Ginkel MV, VSN International. GenStat for Windows 17th Edition. VSN International, Hemel Hempstead, UK; 2014. Available:<http://www.GenStat.co.uk>
12. Yan WK, Kang MS, Ma B, Woods S, Cornelius PL. GGE Biplot vs. AMMI analysis of genotype-by-environment data. *Crop Sci.* 2007;47:643-655.
13. Gauch HG, Piepho HP, Annicchiarico P. Statistical analysis of yield trials by AMMI and GGE: Further considerations. *Crop Sci.* 2008;48:866-889.
14. Yan W, Hunt LA, Sheng Q, Szlavnicz Z. Cultivar evaluation and mega-environment investigation based on the GGE biplot. *Crop Sci.* 2000;40:597-605.
15. Yan W, Hunt LA. Biplot analysis of multi-environment trial data. In: Quantitative Genetics, Genomics and Plant Breeding. Kang, M. S., (Ed.), CABI Publishing, New York. 2002;289-303.
16. Butran A, Velasco P, Ordas A, Malvar RA. Yield evaluation of maize cultivars across environments with different levels pink stem borer infestation. *Crop Sci.* 2004;44: 741-747.
17. Yan WK. GGE biplot - A windows application for graphical analysis of multi-environment trial data and other types of two-way data. *Agronomy Journal.* 2001;93(5):1111-1118.
18. Yan WK, Rajcan I. Biplot analysis of test sites and trait relations of soybean in Ontario. *Crop Sci.* 2002;42:11-20.
19. Gabriel KR. The biplot graphic display OF matrices with application to principal component analysis. *Biometrika.* 1978;58: 453-467.
20. Yan W, Kang MS. GGE biplot analysis: A graphical tool for breeders, geneticist and agronomist. CRC Press LLC, Boca Roton, Florida, USA; 2003.
21. Kaya Y, Aksura M, Taner S. GGE-biplot analysis of multi-environment yield trials in bread wheat. Bahari Dağdaş International Agricultural Research Institute, Turk. J. Agric For. 2006;30:325-337.
22. Yan W, Tinker NA. Biplot analysis of multi-environment trial data: Principles and applications. *Can. J. Plant Sci.* 2006;86: 623-645.
23. Yan W. Singular-value partitioning in biplot analysis of multi-environment trial data. *Agron. J.* 2002;94:990-996.
24. Steel RGD, Torrie GH, Dickey DA. Principles and procedures of statistics: A biometrical approach. 3<sup>rd</sup> Ed. McGraw-Hill, New York, USA. 1997;450.
25. Gauch HG, Zobel RW. AMMI analysis of yield trials. In: Kang, M.S. and Gauch, H.G., Eds., *Genotype by Environment Interaction*, CRC Press, Boca Raton. 1996;85-122.
26. Purchase JL. Parametric analysis to describe G X E interaction and stability in winter wheat. PhD Thesis. Department of Agronomy, Faculty of Agriculture, University of the Orange Free State, Bloemfonten, South Africa; 1997.
27. Rono JK, Cheruiyot EK, Othira JO, Njuguna VW, Macharia JK, Owuoche J, Oyier M, Kange AM. Adaptability and stability study of selected sweet sorghum genotypes for ethanol production under different environments using AMMI analysis and GGE biplots. *Scientific World Journal.* 2016;1-14. Article ID: 4060857.
28. Sial MA, Arain MA, Ahmad M. Genotype x environment interaction on bread wheat grown over multiple sites and years in Pakistan. *Pak. J. Bot.* 2000;32(1):85-91.
29. Panhwar RN, Keerio HK, Khan MA, et al. Relationship between yield and yield contributing traits in sugarcane (*Saccharum officinarum* L.). *Journal of Applied Sciences.* 2003;3(2):97-99.
30. Misra RC, Das S, Patnaik MC. AMMI model analysis of stability and adaptability of late duration finger millet (*Eleusine coracana*) genotypes. *World App. Sci. J.* 2009;6(12):1650-1654.
31. Lule D, Fetene M, DeVilliers S, Tesfaye K. Additive main effects and multiplicative interactions (AMMI) and genotype by environment interaction (GGE) biplot analyses aid selection of high yielding and adapted finger millet varieties. *Journal of Applied Biosciences.* 2014;76(1):6291-6303.
32. Przulj N, Miroslavljevic M, CaNak P, Zoric M, Boca Nski J. Evaluation of spring barley performance by biplot analysis. *Cereal Research Communications.* 2015;43(4): 692-703.
33. Kiliç H. Additive main effects and multiplicative interactions (AMMI) analysis of grain yield in barley genotypes across environments. *Journal of Agricultural Sciences.* 2014;20:337-344.



34. Sousa LB, Hamawaki OT, Nogueira APO, Batista RO, Oliveira VM, Hamawaki RL. Evaluation of soybean lines and environmental stratification using the AMMI, GGE biplot, and factor analysis methods. *Genet. Mol. Res.* 2015;14(4): 12660-12674.
35. Wonde Abera, Labuschagne M. Stability analysis of Ethiopian maize varieties using AMMI model. *Ethio. J. Agric. Sci.* 2005;18(2):173-180
36. Asnake W, Henry M, Temesgen Z, Girma T. Additive main effects and multiplicative interactions model (AMMI) and genotype main effect and genotype by environment interaction (GGE) biplot analysis of multi-environmental wheat variety trials. *African J. Agric. Res.* 2013;8(12):1033-1040.
37. Abeya T, Chemed D, Girma M, Dagnachew L, Negash G. Regression and additive main effects and multiple interactions (AMMI) in common bean (*Phaseolus vulgaris* L.) genotypes. *Ethiop. J. Biol. Sci.* 2008;7(1):45-53.
38. Girma M, Chemed D, Abeya T, Dagnachew L, Negash G. Genotype x environment interaction for yield in field pea (*Pisum sativum* L.). *East Afri. J. Sci.* 2011;5(1):6-11.
39. Adugna A. Assessment of yield stability in sorghum. *African Crop Science Journal.* 2007;15(2):83-92.
40. Reddy PS, Reddy BVS, Rao PS. Genotype by sowing date interaction effects on sugar yield components in sweet sorghum (*Sorghum bicolor* L. Moench). *SABRAO Journal of Breeding and Genetics.* 2014;46(2):241-255.
41. Mortazavian SMM, Nikkiah HR, Hassani FA, Sharifal-Hosseini M, Taheri M, Mahlooji M. GGE biplot and AMMI analysis of yield performance of barley genotypes across different environments in Iran. *Journal of Agricultural Science and Technology.* 2014;16(3):609–622.
42. Eberhart SA, Russell WA. Stability parameters for comparing varieties. *Crop Sci.* 1966;6(1):36–40.
43. Hagos GH, Abay F. AMMI and GGE biplot analysis of bread wheat genotypes in the northern part of Ethiopia. *Journal of Plant Breeding and Genetics.* 2013;1(1):12–18.
44. Farshadfar E. Incorporation of AMMI stability value and grain yield in a single non parametric index (Genotype Selection Index) in bread wheat. *Pakistan J. Biol. Sci.* 2008;11:1791-1796.
45. Odewale JO, Ataga CD, Agho C, Odiowaya G, Okoye MN, Okolo EC. Genotype evaluation of coconut (*Cocos nucifera* L.) and mega environment investigation based on additive main effects and multiplicative interaction (AMMI) analysis. *Res. J. Agric. and Envi. Management.* 2013;2(1):1-10.
46. Ngeve JM, Bouwkamp JC. Comparison of statistical methods to assess yield stability in sweet potato. *Journal of American Society Horticultural Sciences.* 1993;118: 304–310.
47. Naroui Rad MR, Abdul Kadir M, Rafii Hawa MY, Jaafar Naghavi MR, Farzaneh Ahmadi. Genotype × environment interaction by AMMI and GGE biplot analysis in three consecutive generations of wheat (*Triticum aestivum*) under normal and drought stress conditions. *Aust. J. Crop Sci.* 2013;7(7):956-961.
48. Gebre W, Mohammed H. Study on adaptability and stability of drought tolerant maize varieties in drought prone areas of South Omo Zone, SNNPRS. *International Journal of Research in Agriculture and Forestry.* 2015;2(7):9–13.
49. Gasura E, Setimela PS, Souta CM. Evaluation of the performance of sorghum genotypes using GGE biplot. *Can. J. Plant Sci.* 2015;95:1205-1214.
50. Sujay R, Ganapathy KN, Gomashe SS, Rathore A, et al. GGE biplot analysis to evaluate genotype, environment and their interactions in sorghum multi-location data. *Euphytica.* 2012;185:465-479.

© 2018 Al-Naggar et al.; This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Peer-review history:

The peer review history for this paper can be accessed here:  
<http://www.sciencedomain.org/review-history/22970>