Genotype x Environment Interactions for Seed Yield in Sesame in Western Ethiopia

Chemeda Daba[1*], Amsalu Ayana[2], Habtamu Zeleke[2], and Adugna Wakjira[3]

[1]Bako Agricultural research Center P. O. Box 03, Bako, West Shewa, Ethiopia
[2] Haramaya University, P. O. Box 138, Dire Dawa, Ethiopia
[3]Ethiopian Institute of Agricultural Research, P. O. Box 2003 Addis Ababa, Ethiopia

Abstract: As sesame is a short day plant and sensitive to light, heat, and moisture stress the yield is not stable. The selection of stable genotypes that interact less with the varying environment in which they are to be grown is required. The extent of genotype by environment interaction indicates the likelihood of adaptation of a given genotype to a particular agro-ecology and helps to design a breeding strategy for developing varieties suitable for cultivation in a target area. The objective of the study was to assess the significance and magnitude of GEI effect on sesame seed yield and to evaluate the efficiency of the combined use of AMMI and GGE techniques to study GEI. The treatment consisted of ten sesame genotypes grown in four locations (Angar, Uke, Wama and Bako) in western Ethiopia during the 2011 and 2012 main cropping seasons (June to October). The experiment was laid out as a randomized complete block design with three replications. The seed yield data were analysed using additive main effects and multiplicative interaction (AMMI) and the genotype and genotype x environment interaction effect (GGE) biplot. The AMMI analysis showed that environment, genotype, and genotype by environment interaction significantly ($P \leq 0.01$) influenced seed yield. Both AMMI stability value and the GGE–biplot indicated that EW002 (G1) and BG006 (G2) were the most stable genotypes with high seed yields. The result showed that Uke could be used as the best test location for sesame yield trial in the future. The GGE-biplot model showed that eight environments used for the study belong to three different environments. Four genotypes viz. EW002 (G1), BG006 (G2), Obsa (G8) and Dicho (G9) were identified as desirable. In conclusion, the results of the study revealed that EW002 and BG006 are the best genotypes for high seed yield and stability, and could be recommended for production in western Ethiopia. Both AMMI and GGE-biplot produced similar results, suggesting that either of the two can be used at a time.

Keywords: AMMI; GGE-biplot; Seed yield; *Sesamum indicum* L. Stability; Test environment

1. Introduction

Genotype by environmental interaction (GEI) is generally considered a hindrance to crop improvement in most cases (Kang, 1998). It may also, however, offer an opportunity for selecting and using genotypes that show positive interactions with locations and the prevailing environmental conditions (exploiting specific adaptability or yield stability) (Ceccarel1, 1996; Annicchiarico, 2002). Evaluation of genotypic performances at a number of environments provides useful information on genotypic adaptation and stability (Crossa, 1990; Ceccarell, 1996). Such a strategy provides the means for exploitation of GEI as an advantage rather than considering it as a hindrance to crop variety development.

Analysing the magnitude of GEI by proper techniques rather than neglecting them is useful for exploiting the opportunities and or limiting the disadvantages that these effects may cause. Several statistical models have been proposed for studying the GEI effect and exploiting its advantage. The two frequently used statistical analyses are the additive main effects and multiplicative interaction (AMMI) model, the genotype main effect, and the genotype x environment interaction effect (GGE) model (Gauch, 2006).

AMMI model combines the analysis of variance, geno type and environment main effects with principal component analysis of GEI into a unified approach (Gauch and Zobel, 1996). However, the GGE biplot method, which is always close to the best AMMI model in most cases (Ma *et al.* 2004), was developed to use some of the functions of these methods jointly. Purchase *et al.* (2000) developed a quantitative stability value known as the AMMI stability value (ASV) to rank genotypes through the AMMI model. The developed ASV was considered to be the most appropriate single method to describe the stability of genotypes. Gruneberg *et al.* (2005) showed that AMMI, as a multivariate tool was highly effective for the analysis of multi-environment trials (MET).

The GGE- methodology, which is composed of two concepts- the biplot concept (Gabriel, 1971) and the GGE concept (Yan *et al.*, 2000) was used to visually analyse the multi-environment yield trial (MEYTs) data. The GGE concept is based on the understanding of genotype by environment interaction (GE) and genotype (G) and they are the two sources of variation that are relevant to genotype evaluation and that they must be considered simultaneously (Yan, 2002).

The GGE-biplot model provides breeders with a more complete and visual evaluation of all aspects of the data

*Corresponding Author. E-mail: Chemeda2012@gmail.com

ISSN 1992-0407

by creating a biplot that simultaneously represents mean performance and stability as well as identifying mega environments (Yan and Kang, 2003; Ding *et al.,* 2007). The difference of AMMI from GGE is that GGE-biplot analysis is based on environment centered PCA whereas AMMI analysis is based on double centered PCA. For the research purpose of gaining accuracy AMMI and GGE are still equally useful (Gauch *et al.,* 2008).

Sesame (*Sesamum indicum* L.) is an indigenous crop widely produced in the lowlands receiving high rainfall in western Ethiopia. Breeding sesame to develop high-yielding varieties for the western part of the country was started in 2005. As a result, two varieties were officially released in 2010 for the area and some advanced breeding lines were identified (Dagnachew *et al*., 2011). As sesame is a short day plant and sensitive to light, heat, and moisture stress the yield is not stable (Mohammed, 2015). The information on GEI is required to recommend released varieties and select elite breeding lines. However, this type of genetic information is lacking for sesame varieties recommended or being cultivated in western Ethiopia.

Seed yield of sesame can vary considerably between genotypes and seasons due to GEI (Suvarna *et al*., 2011). Hagos and Fetien (2011) reported that 13 sesame genotypes grown at different sites in the northwestern Ethiopia showed significant genotype by location interactions for seed yield. A study conducted to assess the oil contents of 20 sesame varieties for stability and adaptation at six locations in southern Ethiopia indicated highly significant GEI (Zenebe and Hussein, 2011). Several studies were carried out on GEI on sesame by Bo-Shim *et al.* (2003), Kumaresan and Nadarajan (2010), Ahmed and Ahmed (2012), and Mirza *et al.* (2013), who reported highly significant genotypes, environment, and GEI for seed yields of sesame genotypes.

A crop variety is best if it has a high mean yield and a consistent performance when grown across diverse locations and years (Gauch *et al*., 2008). Plant breeders usually evaluate a series of genotypes across environments before a new improved genotype is released for production (Naghavi *et al*., 2010). Therefore, identification of genotypes that perform consistently better across environments should be emphasized (Annicchiarico, 2009). Studying the underlying factors of the GEI effect and quantifying unexplained variations are of prime importance for selection and recommendation of environmentally stable crop varieties (Signor *et al*., 2001). Therefore, this research was conducted to assess significance and magnitude of genotype x environment interaction effects on seed yield of sesame and to evaluate the efficiency of the combined use of AMMI and GGE techniques to study GEI.

2. Materials and Methods

2.1. Experimental Locations

Ten sesame genotypes were grown in four locations in 2011 and 2012 crop seasons (Table 1). The four locations, namely, Anger, Uke. Wama, and Bako, represent major sesame growing agro-ecologies for sesame production in western Ethiopia. Two of the locations, namely Angar and Uke are found 50 km apart in Angar and Didessa valleys. Wama is found in the valley of Wama while Bako is found in the basin of Gibe. The four locations are also used as testing sites for sesame breeding by Agricultural Research Center. The environments were given codes for ease of data handling and analysis. Years were considered as environments.

2.2. Planting Material

The planting material consisted of ten sesame genotypes. The genotypes comprised two released sesame varieties for western Ethiopia, seven advanced breeding lines, and a local check (Table 2). They were selected based on their high yield, good agronomic characters and disease resistance in western Ethiopia. All genotypes have determinate growth habit with a white seed color. The genotypes were also given codes for data analysis (Table 3).

2.3. Treatments and Experimental Design

The treatments consisted of ten sesame genotype (EW002s, BG006, EW023-2, EW003-1, EW0011-4, EW008-1, EW011-2, Obsa, Dicho, and Wama) (Table 1). The genotypes were planted from June 13 to 16 each year at each location. The experiment was laid out as a randomized complete block design with three replications. The seed was drilled in each row at seeding rate of 5 kg ha^{-1} in plot consisting of 6 rows of 5 meter length each with the spacing of 40 cm.

2.4. Experimental Procedure

First plowing was done by tractor in May 12 to 17 each year at all locations. At planting the land was prepared manually. Sowing was done at all locations on June 13 to 16 both years. Nitrogen fertilizer in the form of urea was applied at the rate of 46 kg N ha^{-1} at planting. Twenty days after planting, thinning was done to 10 cm spacing between plants. Hand weeding was done four times at a fortnightly interval starting 15 days after planting. The genotypes were harvested on October 14 to 18 each year. Seed yield per plot of the middle four rows were taken and reported in kg ha^{-1}.

2.5. Data Analysis

The AMMI model, which combines the standard analysis of variance with principal component analysis (Zobel *et al*., 1988), was used to estimate the magnitude of G x E interaction. Bartlett's test (Steel and Torrie, 1980) indicated heterogeneity error variance for the trait seed yield in each of the four locations for two years and then the data log transformed to proceed further for pooled analysis. The AMMI analysis and the IPCA were performed using Agro base 20. The AMMI's stability value (ASV) was calculated to rank genotypes in terms of yield stability using the formula suggested by Purchase *et al.* (2000) as shown below.

AMMI Stability Value:

$$(ASV) = \sqrt{\left[\frac{SSIPCA1}{SSIPC2} IPCA1score\right]^2 + (IPCA2\ score)^2}$$

Where: SS= sum of squares, IPCA1= Interaction principal component analysis axis one, IPCA2= Interaction principal component analysis axis two.

In general, an absolute stability value (ASV) was determined using a procedure that combines IPCA1 and IPCA 2. The GGE-biplot shows the first two principal components (PC1 and PC2, also referred to as primary and secondary effects, respectively) derived from subjecting environmental centered yield data (yield variation due to GGE) to singular value decomposition (Yan *et al.*, 2000).

For raw data of seed yield biplots of the first two principal components were constructed using Genstat 15th edition and used to illustrate the relation among genotypes, environments and between the genotypes and environments.

In the present study, genotype-focused scaling was used to compare genotypes, while environment focused, scaling was used to compare environments. Furthermore, symmetric scaling was preferred in visualizing the which–won-where pattern of the multi-environment trial yield data (Yan, 2002).

Table 1. Description of four locations used for evaluation of sesame genotypes.

Location	Soil type	Temperature(mean)	Rainfall (mm)	Latitude	Longitude	Altitude m.a.s.l.
Angar	Humic nitosol	22^{0}C	1699	09^0 32'N	0360 37'E	1355
Uke	Humic nitosol	22 ^{0}C	1730	09^0 22'N	0360 31'E	1383
Wama	Vertisol	21 ^{0}C	1680	08^0 58'N	0360 48'E	1436
Bako	Humic nitosol	20 ^{0}C	1465	09^0 04'N	0370 02'E	1597

Note: Agro climatology and Geospatial Research Division, EIAR, 2016' m.a.s,l = Metres above sea level.

Table 2. Description of 10 sesame genotypes evaluated in four locations during the 2011 and 2012 cropping season.

Entry	Genotype	Category	DM	PH	BP	YP
1	EW002	Elite breeding line	124	140	9	17
2	BG006	Elite breeding line	123	138	7	16
3	EW023 -2	Elite breeding line	125	142	5	12
4	EW003-1	Elite breeding line	122	145	7	17
5	EW0011-4	Elite breeding line	124	140	8	14
6	EW008-1	Elite breeding line	121	137	7	16
7	EW011-2	Elite breeding line	124	139	7	16
8	Obsa	Released in 2010	119	135	7	14
9	Dicho	Released in 2010	120	140	8	16
10	Wama	Local (farmers' cultivar)	121	137	6	15

Note: DM = days to maturity, PH = plant height (cm), branches per plant and YP = yield per plant.

Table 3. Genotypes and environments and their codes

No	Genotype	Genotype code	No	Environments	Env. code
1	EW002	G1	1	Angar 2011	E1
2	BG006	G2	2	Uke 2011	E2
3	EW023- 2	G3	3	Wama 2011	E3
4	EW003-1	G4	4	Bako 2011	E4
5	EW0011-4	G5	5	Angar 2012	E5
6	EW008-1	G6	6	Uke 2012	E6
7	EW011-2	G7	7	Wama 2012	E7
8	Obsa	G8	8	Bako 2012	E8
9	Dicho	G9			
10	Wama	G10			

3. Results and Discussion

3.1. AMMI Analysis

The AMMI analyses of variance showed that seed yield was significantly ($P \leq 0.01$) influenced by environment, genotype, and genotype-environment interaction (GEI) (Table 4). The significant effect of GEI on seed yield implied differential responses of the genotypes across the environments. This suggestion is consistent with that of Primomo *et al.* (2002) who found similar results in soybean. Significant GEI complicates selection since the variety with the highest mean yield may not be the best genetically (Signor *et al.*, 2001).

In the present study, GEI, environment and genotype explained 45.11%, 38.64%, and 16.25% of the total variation, respectively (Table 4). The magnitude of GEI sum of squares was close to two-third of the variation due to genotype as a main effect, indicating that there were differences in genotypic responses across the environments. This is in agreement with the results of Yan and Kang (2003), who indicated that large GEI, relative to genotype effect suggests the possible existence of different mega-environments with different top-yielding genotypes. It was reported that multi-environment trial data may constitute a mixture of crossover and non-crossover types of GEI. Crossover type of GEI indicates change in the yield ranking of genotypes across environments and the non-crossover types of GEI shows a constant yield ranking of genotypes across environments (Yan and Hunt, 2001; Matus-Cadiz *et al.*, 2003). According to Gauch and Zobel (1996, 1997), in normal multi-environment yield trials, environment accounts for about 80% of the total variation, while G and GEI each accounts for about 10%, which is in contrast to the results of the present study (Table 4).

The AMMI analysis partitioned the sum of squares of GEI into seven interaction principal component axes (IPCA), of which the first five IPCA were significant (Table 4). The results from the AMMI model showed that, the first IPCA captured 42.26% of the interaction sum of squares. Similarly, the second and the third (IPCA2 and IPCA3) explained 30.36% and 16.19% of the GEI sum of squares, respectively. The sum of squares for the first five IPCAs cumulatively contributed to 98.50 % of the total GEI. In this line, Zobel *et al.* (1988) proposed that two interaction principal component axes for AMMI model were sufficient for a predictive model. Other interaction principal component axes captured were mostly non-predictive random variation and did not fit to predict validation observations. Therefore, in general, the model chosen by predictive criterion consists of two IPCA (Kaya *et al.*, 2002).

Table 4. Analysis of variance (ANOVA) for seed yield (2011 and 2012).

Sources	DF	SS	MS	Total variation explained (%)	G x E Explained (%)	Cumulative (%)
Total	239	6.835				
Environments	7	2.355	0.336***	38.64		
Reps within Env.	16	0.268	0.017			
Genotypes	9	0.990	0.110***	16.25		
Genotype x Env.	63	2.749	0.044***	45.11		
IPCA1	15	1.161	0.077***		42.26	42.26
IPCA2	13	0.834	0.064***		30.36	72.62
IPCA3	11	0.445	0.040***		16.19	88.81
IPCA4	9	0.164	0.018***		5.97	94.78
IPCA5	7	0.102	0.015***		3.72	98.50
IPCA6	5	0.028	0.006		1.02	99.52
IPCA7	3	0.013	0.004		0.48	100.0
Residual	144	0.473	0.003			

*Note: Grand mean = 2.811; R-squared = 0.9308; C.V. = 2.04%; **P<0.01; *** P<0. 001; IPCA=Interaction principal component axis.*

Purchase (1997) reported that the IPCA scores of genotypes in the AMMI analysis are an indication of the stability of a genotype over environments. The greater the absolute value IPCA scores, the more specifically adapted a genotype is to a particular environment. The more IPCA2 scores approximate to zero, the more stable or adapted the genotype is over all environments sampled (Gauch and Zobel, 1996; Ferney *et al.*, 2006).

The genotype G2 (BG006) and G1 (EW002) showed the lowest absolute scores for the IPCA1 and they were the most stable followed by G9 (Dicho) (Table 5). The more the IPCA score approximates to zero in absolute terms, the more stable or adapted the genotype is over all the environments sampled (Alberts, 2004). When IPCA2 was considered, G5 (EW0011-4) was the most stable followed by G8 (Obsa). Stability rank of genotypes varied for IPC1 to IPC2. This means that the two IPCA have different values and meanings. Therefore, the other option is to calculate ASV to get estimated value between IPCA1 and IPCA2 scores as ASV was reported to produce a balance measurement between the two IPCA scores (Purchase, 1997).

In the present study, Genotype G2 (BG006), G5 (EW0011-4) and G1 (EW002) were found to be stable (Table 5). Although EW0011-14 was the second stable genotype for ASV, it was ranked 9th for mean seed yield. As per the value of ASV the most unstable genotypes were G7 (EW011-2), G10 (Wama) and G3 (EW023-2). It is to note that a genotype with low ASV values is considered more stable than a genotype with high ASV (Purchase, 1997).

Table 5. Mean yield (kg ha^{-1}) rank, IPCA1 and 2 scores and ASV sesame genotypes tested across four locations of western Ethiopia in 2011 and 2012.

No	Genotype	Yield	Rank	IPCA1	IPCA2	ASV	Rank
1	EW002	881	1	0.0281	-0.2684	0.27	3
2	BG006	750	3	-0.002	-0.0852	0.09	1
3	EW023- 2	556	10	-0.3322	0.0818	0.47	8
4	EW003 -1	735	4	-0.1997	0.3797	0.47	7
5	EW0011-4	608	9	-0.1219	0.0076	0.17	2
6	EW008-1	625	8	0.2112	0.3499	0.46	6
7	EW011-2	710	5	0.4572	0.1466	0.65	10
8	Obsa	847	2	-0.2845	-0.0729	0.40	5
9	Dicho	704	6	-0.0925	-0.3056	0.33	4
10	Wama	646	7	0.3364	-0.2335	0.52	9

Where: IPCA1= Interaction principal component analysis axis one; IPCA2= Interaction principal component analysis axis two; ASV = AMMI stability value.

Site mean can easily define whether the environment is favorable or not for a crop to perform well. In the present study, the site mean observed ranged from the lowest of 400 (kg ha^{-1}) at E4 (Bako) to the highest 888 kg ha^{-1} at E2 (Uke), with a grand mean of 706 kg ha^{-1} (Table 6). Thus, environments E2 (Uke in 2011), E3 (Wama in 2011), E5 (Anger in 2012), E6 (Uke 2012), and E8 (Bako in 2012) were rich; E1 (Anger in 2011) and E7 (Wama in 2012) were moderate; and E4 (Bako in 2011) was poor. G1 (EW002) and G8 (Wama) gave the highest yields across the environments and G2 (BG006), G4 (EW003-1) and G7 (EW011-2) produced above average seed yield. G1 (EW002) ranked first at four environments: at E2 (Uke in 2011), E5 (Anger in 2012), E7 (Wama in 2012 and E8 (Bako in 2012). The other high yielding genotype G8 (Obsa) performed best at the two environments: E4 and E6. This differential yield ranking of the genotypes across the environments revealed that the G x E interaction effect was a crossover type (Yan and Hunt 2001; Matus-Cadiz *et al.,* 2003). Based on the combination of mean seed yield, ASV and IPCA1 values, BG006 (G2) and EW002 (G1) were the two best genotypes.

Table 6. Mean seed yield (kgha^{-1}) of 10 sesame genotypes tested in eight environments.

Genotype	E1	E2	E3	E4	E5	E6	E7	E8	Mean
G1	662	1185	781	340	963	954	1038	1123	881
G2	774	748	695	409	867	721	808	978	750
G3	383	880	533	489	403	651	500	608	556
G4	867	909	690	621	748	727	341	975	735
G5	454	833	643	372	782	591	511	678	608
G6	774	821	714	372	623	817	578	302	625
G7	1266	808	896	245	784	541	622	514	710
G8	515	892	881	664	899	977	960	983	846
G9	512	964	838	307	552	638	818	1005	704
G10	691	843	838	184	671	512	802	622	645
Site mean	*690*	*888*	*751*	*400*	*729*	*713*	*698*	*779*	*706*

Where: E1 = Angar 2011; E2 = Uke 2011; E3 = Wama 2011; E4 = Bako 2011; E5 = Angar 2012; E6 = Uke 2012; E7 = Wama 2012 and E8 = Bako 2012.

3.2. GGE-Biplot Analysis

3.2.1. Ranking of Genotypes Based on Yield and Stability

Based on the scores of PC1 and PC2, the sesame genotype in this study area can be divided into three groups (Figure1). The first group included four stable genotypes (G1=EW002; G2=BG006; G8= Obsa; and G9=Dicho) that were high yielding as near zero PC2 scores showed genotypic stability. Group two included two unstable and low yielding genotypes (G3 = EW023-2; and G7 = EW0011-2) and group three consisted of four genotypes (G4 = EW003-1; G5 = EW0011-4, G6 = EW008-1; and G10 = Wama) that were low yielding but stable. A position in either direction away from the biplot origin indicated greater GEI and reducing stability (Yan, 2002). Unlike PC1, PC2 which was related to genotypic stability, divided the genotypes of interest into different groups.

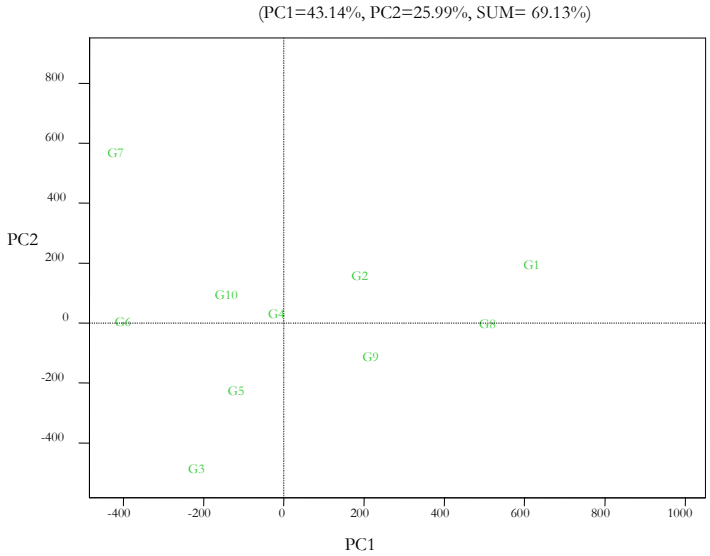

Figure 1. GGE-biplot based on genotype-focused scaling for comparison the genotypes.

GGE-biplot based on genotype focused scaling is shown to detect the locations of genotypes. It has been reported that when PC1 in GGE- biplot approximates the genotype (mean performance), PC2 must approximate the G x E associated with each genotype which is the measure of stability or instability (Yan *et al.*, 2000; Yan, 2002). Kaya *et al.* (2006) reported that the genotypes having PC1 > 0 were recognized as high yielding while those genotypes having PC1 score < 0 were identified as low yielding.

3.2.2. Relationships among Test Environments

A GGE-biplot, which was based on environment scaling, is shown to estimate the pattern of environments (Figure 2). Environment PC1 scores were obtained in both positive and negative scores. This case exhibited that PC1 scores present proportional genotypic yield differences across environments which were caused by both crossover and non-crossover GEI. Similar to PC1, PC2 had both positive and negative scores. It gives rise to the crossover GEI, leading to disproportionate genotypic yield differences across environments (Yan *et al.*, 2000). A genotype may, on one hand, have large positive interaction with some environments; it may, on the other hand, have large negative interaction with some other environments.

Favorable test environments should have large PCA1 scores (more discriminating of genotypes) and near zero PC2 scores (more representative of an average environment) (Yan *et al.,* 2001). Test environment with larger vectors like E8 (Bako in 2012), E7 (Wama in 2012) and E5 (Anger 2012) were more discriminating for the genotypes. These environments may be better test environments under limited resources and whenever there is a need to conduct multi-environment yield trials in a limited number of locations.

The correlation coefficients among the eight test environments (locations by year combination) are presented in Table 7. The vector view of the GGE biplot (Figure 2) illustrates a summary of the interrelationship among the environments and base the line that connects the biplot origin and the marker of the test environment are called environment vectors (Yan and Tinker, 2006) . The 28 correlation coefficients were calculated and six of which were found to be significant. Five pairs of the environments were significantly positively correlated because the angles between them were less than 90^0 (acute angle). On the other hand, E3 and E4 were highly negatively correlated. The presence of strong negative correlation (wide obtuse angle) among locations is an indication of a strong crossover which means genotype by environment interaction (Yan and Tinker, 2006). The angle between the vectors of two environments is related to their correlation coefficient (Kaya, *et al.*, 2006). The cosine of an angle between the vectors of two environments approximate the genetic correlation between them (Kroonenberg, 1995; Yan 2002, 2001) and allows visualization of similarity between environments in ranking genotypes (Yan, 2001). According to the theory, an acute angle indicates a positive correlation, an obtuse angle indicates a negative correlation and a right angle shows existence of no correlation (Yan and Kang, 2003; Yan and Tinker, 2006; Kandus *et al.,* 2010).

Environments E2 and E5, E2 and E4, E2 and E6, E4 and E6, E5 and E6 were similar in their discrimination of the genotypes being significantly positively correlated (Table 7). Such significant correlations among test environments suggest that an indirect selection for seed yield can be practical across the test environments. For instance, the genotype adaptable to or high yielding in the environment E6 may also show a similar response to environments E4 and E5. An indirect selection can be applied in the case where the same character is measured on the same genotypes in different environments. Where there are no correlation error effects among environments, the phenotypic correlation between environments may be used to investigate indirect responses to selection (Cooper and Delacy, 1994).

The presence of close association among test locations suggests that the same information about the genotypes could be obtained from fewer test locations and hence the potential to reduce the testing costs. If two locations are closely correlated consistently across years one of them can be dropped without loss of much information about the genotypes.

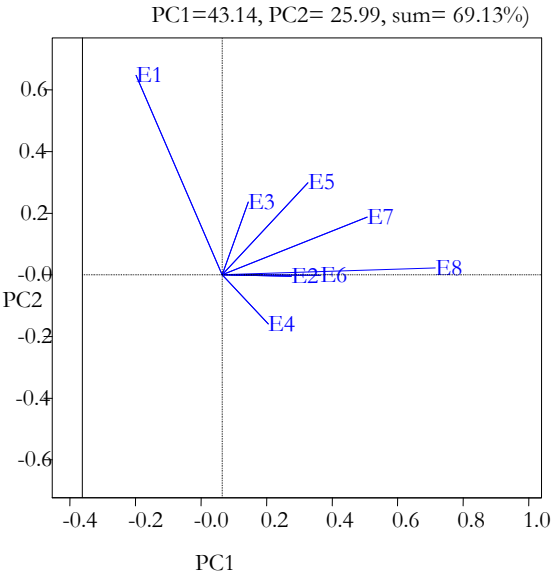

Figure 2. GGE-biplot based on environment-focused scaling for environments. PC and E stand for principal component and the environments, respectively.

Table 7. Correlation coefficient among the eight test environments.

	E1	E2	E3	E4	E5	E6	E7
E2	-0.1428						
E3	-0.6659	-0.4903					
E4	0.4211	0.6977*	-0.8784**				
E5	-0.2808	0.7003*	-0.1195	0.3931			
E6	-0.1428	1.0000***	-0.4903	0.6977*	0.7003*		
E7	-0.2111	0.3936	0.2337	0.2082	0.1593	0.3936	
E8	-0.2905	0.1158	0.2612	0.0594	0.2251	0.1157	0.0865

*Where: E1 = Angar 2011; E2 = Uke 2011; E3 = Wama 2011; E4 = Bako 2011; E5 = Angar 2012; E6 = Uke 2012; E7 = Wama 2012 and E8 = Bako 2012; *, ** and *** indicate significance at P < 0.05, P < 0.01 and P < 0.001 respectively*

3.2.3. Which–Won–Where Pattern of Genotypes

The genotypes that are located far away from the biplot origin are connected with straight lines, so that a polygon or vertex hull is formed with all other genotypes contained within the vertex hull (Figure 3). The vertex genotypes are G1, G8, G3, G6 and G7. These genotypes are the most responsive; they are either the best or the poorest genotypes in some or all of the environments. The rays are perpendicular lines between adjacent genotypes on the polygon which facilitates a visual comparison among them. For instance, Ray1 is perpendicular to the side that connects genotype G7 and G1; Ray 2 is perpendicular to the side that connects genotype G8 and G3; Ray 3 is perpendicular to the side that connects genotype G3 and G6; Ray 4 is perpendicular to the side that connects genotype G6 and G7.

The "which–won- where" view of the GGE-biplot is an effective visual tool in mega environment analysis (Yan *et al.,* 2007). The visualization of the which–won-where pattern of multi-environment yield trial data is important for studying a possible existence of different mega–environments in a region (Gauch and Zobel 1997; Yan *et al.*, 2000, 2001). The four rays divided the biplot into four sectors and the environments fell into three of them (Figure 3). The falling of all environments into a single sector indicates that a single genotype has the highest yield in all environments. The falling of all environments into different sectors means that different genotypes win in different sectors (Yan *et al.,* 2007). The vertex genotypes for each quadrant (sector) are the one that gave the highest yield for the environment that fall within that quadrant (Yan, 2002). G1 and G8 are the vertex genotypes for sector 1 in that they produced the highest yields. The vertex genotype G7 produced the highest yields at E1 and E3 whereas the remaining other two vertex genotypes G6 and G3 produced poor yields in almost all of the environments. Actually, they were the poorest genotypes in some or most of the environments.

Figure 3 biplot analysis suggests 3 mega-environments. The first mega contained five environments viz., E2, E5, E6, E7 and E8 with genotype G1 and G8. The second mega-environment contained only one environment E4 whereas the third mega was with two environments namely E1 and E3. According to the section 'visual comparison of two genotypes in different environments'

the line perpendicular to the polygon side that connects G7 and G1 facilitates the comparison between G7 and G1, G1 yielded higher than G7 in most of the environments because six environments were on the side of G1. Similarly, the line perpendicular to the polygon side that connects genotypes G8 and G3 facilitates the comparison between G8 and G3; G8 yielded higher than G3 in six environments that fall into the G8 sector because they are on the side of G8. Figure 3 indicates that there were three test environments (mega- environments) for evaluation of sesame genotypes in western Ethiopia. These mega environments were represented by genotype G1, G8 and G7. The results of this study may be confirmed by findings of multi-year experiments.

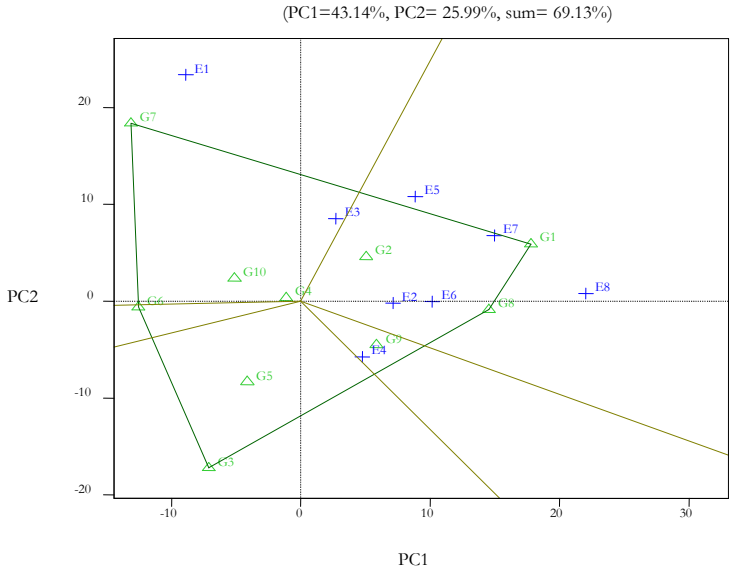

Figure 3. The polygon view of the GGE- biplot based on symmetrical scaling for which -won -where pattern for genotypes and environments. PC, G and E stands for principal component, genotype and environments, respectively.

3.2.4. Comparison of Genotypes

In the present study, genotype G1 was a desirable genotype for seed yield and stability followed by G2, G8 and G9 which are located in the next concentric circle. The low yielding genotype G7 and G10, G5, G6 and G3 are undesirable because they are far away from the ideal genotype (Figure 4). An ideal genotype is a one that has both high mean seed yield and high stability; it is defined as a one that is the highest yielder in all test environments (Yan and Kang, 2003; Farshadfar *et al.*, 2012). Although an ideal genotype may not exist in reality, it can be used as a reference for evaluating genotypes (Mitrovic *et al.*, 2012). A genotype is desirable if it is closer to the ideal genotype (Yan and Hunt, 2002; Kaya *et al.*, 2006).

The centre of concentric circle in Figure 4 represents the position of an ideal genotype which is defined by a projection on the mean environment axis that equals the longest vector of the genotype that had above average yield and by a zero projection on the perpendicular line (zero variability across environments). Because the unit of both PC1 and PC2 for the genotype is the original unit of yield in a genotype-focused scaling (Figure 4), the unit of AEC abscissa (mean yield) and ordinate (stability) should also be the original unit of yield. The unit of distance between genotypes and an ideal genotype, in turn, is the original unit of yield. Therefore, the ranking based on the genotype-focused scaling assumes that stability and mean yield are equally important (Yan, 2002).

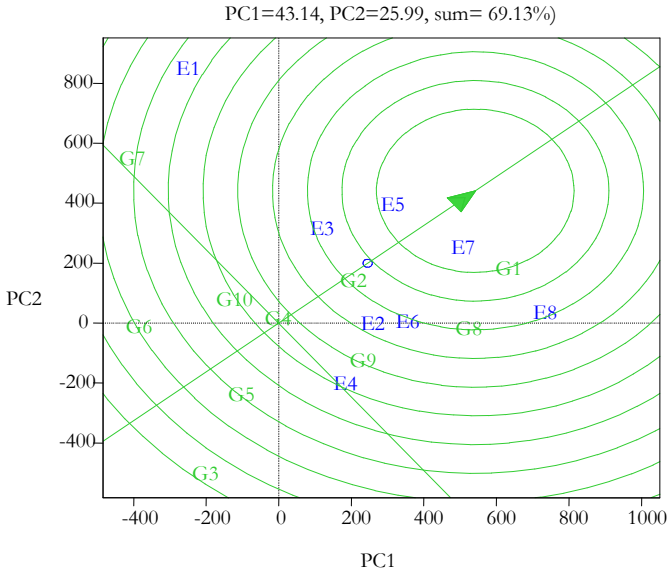

Figure.4. GGE–biplot based on genotype focused scaling for comparison of the genotypes. PC, G and E stand for principal component, genotypes, and environments, respectively. Details of the genotypes and environments are given in Tables 1 and 2.

4. Conclusions

The study has demonstrated that EW002 (G1), BG006 (G2), Obsa (G8), and Dicho (G9) are desirable genotypes for seed yield and stability. These genotypes can be used as parents in sesame breeding programs in the future. Furthermore EW002 and BG006 are the best stable genotypes with high seed yield and could be recommended for commercial production for western Ethiopia. Environments viz., Uke 2011 (E2), Angar 2012 (E5), Uke 2012 (E6), Wama 2012 (E7) and Bako 2012 (E8) were identified as favorable test environments for sesame production. Among the test sites, Uke is the best and it is recommended as a test location for sesame breeding in the future. Both AMMI and GGE-biplot tools produced similar results and could be used alternatively rather than simultaneously.

5. Acknowledgements

The authors acknowledge the financial support provided by Rural Capacity Building Project and also Bako Agricultural Research Center for all supports provided during the time of executing of the experiments.

6. References

Ahmed, S. B. M. and Ahmed, A. F. 2012. Genotype x season interaction and characters association of some sesame (*Sesamum indicum* L.) genotypes under rain fed conditions of Sudan. *African Journal of Plant Science,* 6 (1): 39-42.

Alberts, M. J. A. 2004. A comparison of statistical methods to describe Genotype x Environment interaction and yield stability in multi-location maize trials. MSc. Thesis. Department of Plant Sciences/Plant Breeding, University of the Free State, Bloemfontein, South Africa.

Annicchiarico P. 2002. Genotype x Environment interaction: Challenges and opportunities for plant breeding and cultivar recommendation. FOA, Rome. 150 pp.

Annicchiarico P. 2009. Coping with and exploiting genotype-by-environment interactions. P. 519–564. Plant breeding and farmer participation Edited by Ceccarelli, S., E.P. Guimarães, E. Weltizien, Food and Agriculture Organization of the United Nations FAO. Rome, Italy.

Bo-Shim, K., Churl-Whan, K., Dong-Hee, K. and Jang-Whan, P. 2003. Interpretation of genotype x environment interaction effects on yield in sesame. Sesame and Safflower Newsletter, 18: 20-24.

Ceccarelli, S. 1996. Positive interpretation of genotype by environment interaction in relation to sustainability and biodiversity. In: Cooper, M. and Hammer. G. L. (Eds) Plant Adaptation and Crop improvement .CAB International Wallingford, UK. pp. 467-486.

Cooper, M. and Delacy, I. H. 1994. Relationship among analytic methods used to study genotypic variation and genotype-by-environment interaction in plant breeding multi-environment trials. Theory Applied Genetics 88: 561-572.

Crossa, J. 1990. Statistical analyses of multi-location trials. Advances in Agronomy, 44: 55-86.

Crossa, J., Gauch, H. G. and Zobel, R. W. 1990. Additive main effects and multiplicative interaction analysis of two international maize cultivar trials. Crop Science 30: 493-500.

Dagnachew, L., Girma, M., Abeya, T., Chemeda, D., Aschalew, S., Kasa, M., Zerihun, A., Teshome, B., Shiferaw, T. and Abdulaziz, T. 2011. Progress and prospects of sesame breeding in Western Ethiopia. pp. 129-140. In: Geremew Terefe., Adugna

Wakjira and Dereje Gotfu. (Eds.), Oilseeds: Engine for Ethiopian Economic Development. EIAR, Addis Ababa, Ethiopia.

Ding, M., Tier, B. and Yan, W. 2007. Application of GGE- biplot analysis to evaluate genotypes (G) environment (E) and G x E interaction on P.radiata. Case study. Australian Forest Genetics Conference, 11-14 April 2007, the old wool store, Hobart, Tasmania, Australia.

Farshadfar, E., Mohammadi, R., Aghaee, M. and Vaisi, Z. 2012. GGE-biplot analysis of genotype x environment interaction in wheat-barley disomic addition lines. Australian Journal of Crop Science, 6 (6): 1074- 1079.

Ferney G. B., Alexei, M. and Aigul, A. 2006. Evaluation of grain yield stability, in spring wheat from Kazakhstan and Siberia. Journal of Central European Agriculture, 7: 649-660.

Gabriel, K. R. 1971. Biplot display of multivariate matrices with application to principal components analysis. Biometrika, 58: 453-467.

Gauch, H. G. statistical analysis of yield trials by AMMI and GGE-biplot. Crop Sci., 46: 1488-1500.

Gauch, H. G. and Zobel, R. W. 1996. AMMI analysis of yield trials. In: Genotype by environment interaction. Kang & Gauch (Eds). CRC Press, Boca Raton, New York.

Gauch, H. G. 1982a. Noise reduction by eigenvector ordinations. Ecology, 63: 1634-1649

Gauch, H. G. and Zobel, R. W. 1997. Identifying mega-environments and targeting genotypes. Crop Science 37: 311-326.

Gauch, H. G., Piepho, H. P. and Annicchiarico, P. 2008. Statistical analysis of yield trials by AMMI and GGE: Further considerations. Crop Science. 48: 866–889.

Gruneberg W. J., Manrique K., Zhang, D. and Hermann, M. 2005. Genotype x environment interactions for a diverse set of sweet potato clones evaluated across varying ecographic conditions in Peru. Crop Science, 45: 2160-2171.

Hagos, T. and Fetien, A. 2011. Additive Main Effects and Multiplicative Interactions Analysis of yield Performance of sesame genotypes across environments in Northern Ethiopia. Journal of the Dry lands, 4: 259-266.

Kandus, M. Almorza, D. Ronceros, R. B. and Salerno, J. C. 2010. Statistical models evaluating the genotype-environment interaction in maize (Zea mays L.). International Journal of Experimental Botany, 79: 39-46.

Kang, M. S. 1998. Using genotype by environment interaction for crop cultivar development. Advances in agronomy, 62: 199-252.

Kaya, Y., Ackura and M., Taner, S. 2006. GGE-biplot analysis of multi-environment yield trials in bread wheat. Turkish Journal of Agriculture 30: 325-337.

Kaya Y. K., Palta, E., Taner, S. 2002. Additive Main Effects and Multiplicative Interactions Analysis of Yield Performances in Bread Wheat Genotypes across Environments. Turkish Journal of Agriculture, 26: 275-279.

Kroonenberg, P. M. 1995. Introduction to biplots for G × E tables. Centre for Statistics. Research Report 51. The University of Queensland, Brisbane, Australia. 22 pp.

Kumaresan, D. and Nadarajan, N. 2010. Genotype x Environment interactions for seed yield and its components in sesame (Sesamum indicum L.). Electronic Journal of Plant Breeding, 4: 1126-1132.

Ma, B. L., Yan, W., Dwyer, L. M., Frégeau-Reid, J., Voldeng, H. D., Dion, Y. and Nass, H. 2004. Graphic analysis of genotype, environment, nitrogen fertilizer, and their interactions on spring wheat yield. Agronomy Journal, 96:169-180.

Matus-Cadiz, M. A., Hucl, P., Perron, C. E., and Tyler, R. T. 2003. Genotype x environment interaction for grain color in hard white spring wheat. *Crop Science,* 43: 219-226.

Mirza, M. Y., Ahmad, K. M., Amjad, M. and Nawaz, M. S. 2013. Stability analysis for economic traits in sesame (Sesamum indicum L.) Pakistan Journal of Agricultural Research, 26 (3): 168-177.

Mitrovic, B., Stanisavljevi, D., Treski, S., Stojakovic, M., Ivanovic, M., Bekavac G., Rajkovic, M. 2012. Evaluation of experimental Maize hybrids tested in Multi-location trials using AMMI and GGE biplot analysis. Turkish Journal of Field Crops., 17 (1): 35-40.

Mohammed Abate. 2015. Genetic diversity, association of traits and Genotype x Environment interaction of sesame (Sesamum indicum L.) in Ethioipia. PhD Thesis Haramaya University, Haramaya Ethiopia. pp. 71-89.

Naghavi, A., Sofalian, O., Asghari, A., Sedghi, M. 2010. Relation between freezing tolerance and seed storageproteins in winter bread wheat (Triticum aestivum L.). Turkish Journal of Field Crops, 15: 154–158.

Primomo, V. S., Falk, D. E., Ablett, G. R., Tanner, J. W. and Rajican, I. 2002. Genotype x Environment interactions, stability, and agronomic performance of soybean with altered fatty acid profile. Crop Science 42: 37-44.

Purchase, J. L. 1997. Parametric analysis and genotype x environment interaction and yield stability in winter wheat. PhD Thesis, Department of Agronomy, Faculty of Agriculture, of the University of the Free State, Bloemfontein, South Africa.

Purchase, J. L., Hatting, H. and Van Deventer, C. S. 2000. Genotype x Environment interaction of winter wheat (Triticum aestivum L.) in South Africa: II. Stability analysis of yield performance. South African Journal of Plant and Soil nutrition, 17: 101-107.

Signor, C. E., Dousse, S., Lorgeous, J., Denis, J. B., Bonhomme, R., Carolo P. and Charcosset, A. 2001. Interpretation of genotype x environment

interactions for early maize hybrids over 12 years. Crop Science, 41: 663-669.

Suvarna, M. H., Nehru, M. S. D. and Manjunath, A. 2011. Stability analysis of sesame varieties during early kharif. Indian Journal of Agricultural Research, 45 (3): 244-248.

Steel, R. G. and Torrie, J. H. 1980. Principles and procedures of statistics. McGraw-Hili, New York.

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.

Yan, W. 2002. Singular-value partitioning in biplot analysis of multienvironment trial data. Agronomy Journal 94: 990-996.

Yan, W. and Hunt, L. A. 2001. Genetic and Environmental causes of genotype by environment interaction for winter wheat yield in Ontario. Crop Science, 41: 19-25.

Yan, W. and Hunt, L. A. 2002. Biplot analysis of multi-environment trial data, In: Kang, M. S. (Ed.) Quantitative Genetics, Genomics and Plant Breeding. CAB International, Willingford.

Yan, W. and Kang, M. S. 2003. GGE biplot analysis: a graphical tool for breeders, In: Kang M.S. (Ed.) Geneticists, and Agronomist. CRC Press, Boca Raton, FL, pp. 63-88.

Yan, W. and Tinker, N. A. 2006. Biplot analysis of multi-environment trial data: Principles and applications. Canadan Journal of Plant Science, 86: 623-645.

Yan, W., Cornelius, P. L., Crossa, J. and Hunt, L. A. 2001. Two types of GGE biplots for analyzing multi-environment trial data. Crop Science 41: 656-663.

Yan, W., Hunt, A. L., Sheng, Q. and Szlavnics, Z. 2000. Cultivar evaluation and mega-environment investigation based on GGE- biplot. Crop Science, 40: 596-605.

Yan, W., Kang, M. S. Ma, B., Woods, S., and Cornelius, P.L. 2007. GGE-biplot vs. AMMI analysis of genotype –by- environment data. Crop Science, 47: 643-655.

Yan, W. and Hunt, L. A. 1998. Genotype by environment interaction and crop yield. Plant Breeding Reviews, 16: 135-178.

Zenebe Mekonnen and Hussien Mohammed. 2011. Study on genotype x environment interaction of oil content in sesame (Sesamum indicum L.). World Journal of Fungal and Plant Biology, 1 (1): 15-20.

Zobel, R. W., Wright, M. J. and Gauch, H. G. 1988. Statistical analysis of yield trial. Agronomy Journal, 80: 388-393.