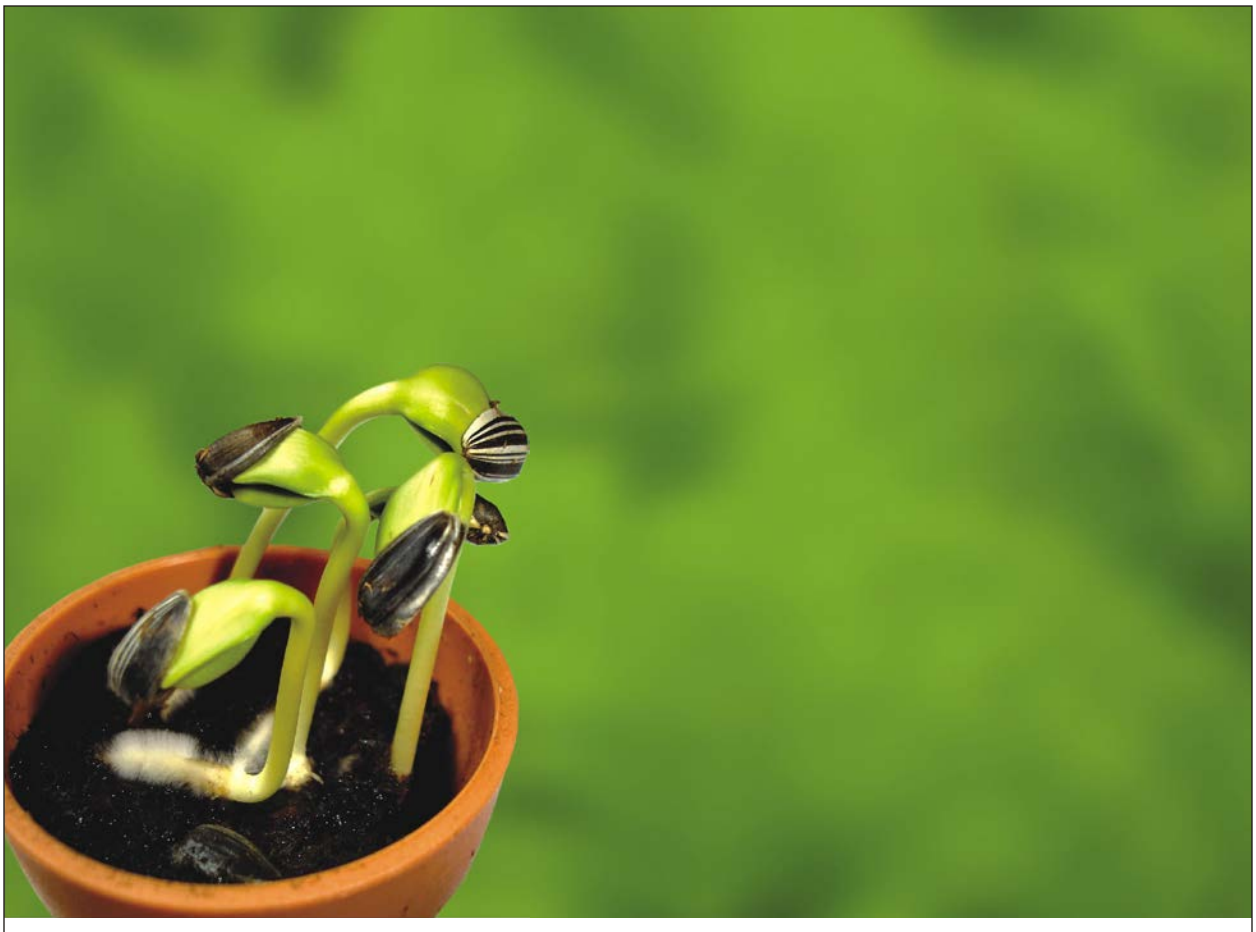

International Journal of Plant Breeding and Genetics

ISSN 1819-3595

Academic Journals Inc.

www.academicjournals.com

International Journal of Plant Breeding and Genetics 5 (1): 59-75, 2011
ISSN 1819-3595 / DOI: 10.3923/ijpbg.2011.59.75

GGE-biplot Analysis of Multi-environment Yield Trials of Barley (*Hordeium vulgare* L.) Genotypes in Southeastern Ethiopia Highlands

Zerihun Jalata
Department of Plant Science, Wollega University, P.O. Box 692, Nekemte, Ethiopia

ABSTRACT

The present study was conducted on 18 food barley genotypes across 11 environments in randomized complete block design with four replications in Bale highlands of Southeastern Ethiopia from 2001-2003 *Bona* cropping season with the objective of evaluating yield performance of barley genotypes and identification of mega environments. GGE (i.e., G = genotype and GE = genotype by environment, interaction) biplot methodology was used for graphical display of yield data after subjecting the genotypic means of each environment to GGE Biplot software. The analysis of variance revealed that environment accounted for 76.7% of the total variation while G and GE-interaction explained 2.3 and 9.7%, respectively. The first two principal components (PC1 and PC2) were used to display a two-dimensional GGE biplot. Thus, genotypic PC1 scores >0 classified the high yielding genotypes while PC1 scores <0 identified low yielding genotypes. Unlike genotypic PC1, genotypic PC2, scores near zero showed stable genotypes whereas large PC2 scores discriminated the unstable ones. The environmental PC1 were related to cross over type of GEI while PC2 scores were associated with non cross over GEI. Genotypes (A, G, E, H, L, B and R) were found to be desirable in high yielding and stability. The 11 test environments in the highlands of Bale were divided in to two distinct mega environments (Mega-1 and 2). Mega-1 constituted environments such as E1 (Sinana-01), E2 (Gassara-01), E3 (Sinja-01), E4 (Sinana-02), E5 (Gassara-02), E6 (Sinja-02), E8 (Sinana-03), E9 (Gassara-03) and E10 (Sinja-03) while *Biftu* cultivar being the best winner, on the other hand, Mega-2 contained two environments, E7 (Upper Dinsho-02) and E11 (Upper Dinsho-03) while *shage* cultivar being the best winner. The results of this study indicated that breeding for specific adaptation should be taken as a breeding strategy in Bale highlands to exploit positive GEI to increase production and productivity of barley.

Key words: Barley, GGE- biplot, GxE interaction, mega environment, cross over, yield

INTRODUCTION

Multi-Environment Yield Trials (MEYT) are conducted for different crops through out the world (Yan and Rajcan, 2002; Dehghani *et al*., 2006) not only to identify high yielding cultivars but also to identify sites that best represent the target environment (Yan, 1999; Yan *et al*., 2000, 2001). As usual in MEYT a number of genotypes are tested over a number of sites and years to see adaptation of the crop. But, it is often difficult to determine the pattern of genotypic responses across environments without the use of appropriate analytical tools such as GGEbiplot (Yan *et al*., 2001; Yan and Tinker, 2006) for graphical display of data. The measured yield of each cultivar in each test environment is a result of genotype main effect (G), an environment main effect (E) and genotype x environment (GE) interaction (Yan and Kang, 2003). Though, E is accountable for

about 80% of the total yield variation; however, it is only G and GE interaction that are relevant to cultivar evaluation and mega environment classification (Yan *et al.*, 2000; Yan, 2002; Yan and Rajcan, 2002; Kaya *et al.*, 2006). GE interaction is related to component of yield variation across environments for a genotype that can not be explained either by G or E alone (Yan and Hunt, 2001). GE interaction reduces the genetic progress in plant breeding programs through minimizing the association between phenotype and genotype (Comstock and Moll, 1963). Hence, GE interaction must be either exploited by selecting superior genotype for each a specific target environment or avoided by selecting widely adapted and stable genotype across wide range of environments (Ceccarelli, 1989). GxE interaction is used to determine if a genotype is widely adapted for a wide range of environmental conditions or selected for different subenvironments.

In their investigation of Genotype x environment interaction (GEI), researchers have proposed and used different procedures to analyze GEI. For instance, regression coefficient (Finlay and Wilkinson, 1963), sum of squared deviations from regression (Eberhart and Russel, 1966), stability variance (Shukla, 1972), coefficient of determination (Pinthus, 1973), coefficient of variability (Francis and Kanneberg, 1978) and additive main effects and multiplicative interaction (AMMI) (Gauch and Zobel, 1988; Annicchiarico, 1997). Recently, Yan (1999) and Yan *et al.* (2000) proposed another methodology known as a GGE-biplot for graphical display of GEI pattern of MEYT data with many advantages. The GGE-biplot combines two concepts. First, although the measured yield is the combined effect of G, E and GE-interaction, only G and GE-interaction are relevant to and must be considered simultaneously, in genotype evaluation, hence the term GGE. Second, the biplot technique developed by Gabriel (1971) was employed for graphical display of the GGE of a MEYT data, hence the term GGE biplot. This GGE biplot is constructed by using the first two principal components (PC1 and PC2) also referred to as primary and secondary effects, respectively, derived from subjecting environment centered yield data (Yan, 1999; Yan *et al.*, 2000). The GGE biplot has been used effectively to identify the GEI pattern of the data. It clearly shows which genotype won in which environments simplifying mega environment identification. Another essential requirement for mega environment differentiation is repeatability of the which won where pattern (Yan and Hunt, 1998; Yan, 1999; Yan *et al.*, 2000) over years. Cross over GE interaction has been reported by (Ceccarelli, 1989; Ceccarelli and Grando, 1991; Jackson *et al.,* 1993; Van Oosterom *et al.,* 1993) in barley.

As barley is one of the most important cereal food crop in highlands of Ethiopia and Bale highlands in the Southeastern part of Ethiopia are among the major barley producing areas where barley is the second most important crop next to wheat in area coverage and production on small scale holdings (EASE, 2002). However, there is no available information or knowledge with regard to the nature and magnitude of GEI on barley in the study area so that the Sinana Agricultural Research Center barley breeding program used to select superior genotypes across environments, but environments vary in topography, climatic, biological and edaphic factors. Understanding GEI helps plant breeders to design better breeding strategy. Therefore, the objectives of this study were:

- To evaluate the yield performance of each genotype in relation to each environment
- To examine the possible existence of different mega environments
- To identify the winning genotype for each mega environment

MATERIALS AND METHODS

Breeding materials and testing locations: Eighteen food barley genotypes with inclusion of two cultivars *Aruso* (local) and *Shage* (standard cultivar) were evaluated across 11 barley growing

environments in randomized complete block design with four replications in Bale highlands of Southeastern Ethiopia from 2001 to 2003 *Bona* (season from July-December) cropping season. Barley genotypes were developed from barley collections from Bale areas and Institute of Biodiversity conservation through barley landrace enhancement program at Sinana Agricultural Researcher Center. These breeding materials were initially selected from preliminary and advanced nurseries in 1999 and 2000, thereafter evaluated in variety yield trials from 2001 to 2003 cropping season. Testing locations cover Sinana and Gassara with 2400 meters above sea level (masl), Sinja (2550 masl) and Upper Dinsho (3200 m.a.s.l) major barley growing areas. The former three locations receive biomodial type of rainfall, whereas, the later location with a long growing season receive monomodial rainfall. In general, testing areas comprise variable climatic, topographic, diseases, insect pests and edaphic conditions.

Planting: Barley seeds were planted at each location in a randomized complete block design with four replications. The plot size was 3 m^2 with six rows of 2.5 m long with spacing of 20 cm between rows. The recommended fertilizer rate of 50 kg ha^{-1} DAP (Diammonium phosphate) and 125 kg ha^{-1} seed rate was used at each location. The other important cultural practices were also applied uniformly.

Data collection and analysis: Grain yield data in kg $plot^{-1}$ was taken from four central rows (2 m^2) and converted in to tons $hectare^{-1}$ at 12.5% moisture content. Analysis of variance was done using system analysis software (SAS, 2004). The GGE Biplot methodology, which is composed of two concepts, the Biplot concept (Gabriel, 1971) and the GGE concept (Yan *et al*., 2000), was applied for visual examination of the GEI pattern of MEYT data by using GGE-biplot software (GGE-biplot, 2009). The GGE biplot shows the first 2 principal components (PC1 and PC2) derived from subjecting environment centered yield data (Yan *et al*., 2000). In this study, environment focused scaling was used in visualizing for environment comparison and genotype focused scaling for genotypic comparison. Beside this, the symmetric scaling was used in visualizing which won where pattern of MEYT data (Yan, 2002).

RESULTS AND DISCUSSION

Pooled analysis of variance indicated that genotype, environment and genotype x environment interaction showed significant ($p<0.01$) differences among barley genotypes tested. This result showed that barley yields were significantly influenced by environment (E) which accounted for 76.7% of the total yield variation, while G and GEI explained 2.3 and 9.7% of the variation, respectively (Table 1). The effect of GEI is more than three times that of G effect. The magnitude of GEI as compared to G suggested the possible existence of different mega environments. The partitioning of GGE through GGE biplot analysis showed that PC1 and PC2 accounted 52.2 and 16.9% of GGE sum of squares, respectively, explaining a total of 69.1% variation. This result revealed that there was a differential yield performance among barley genotypes across testing environments due to the presence of GEI. The presence of GEI complicates the selection process as GEI reduces the usefulness of genotypes by confounding their yield performance (Pham and Kang, 1988) through minimizing the association between genotype and phenotype (Comstock and Moll, 1963). Therefore, studying yield performances, patterns and GEI of barley genotypes in Bale highlands is paramount importance in genotype evaluation and mega environment investigation.

It is commonly reported that MEYT data may constitute a mixture of cross over and non-cross over types of GEI, the former indicate the change in yield ranking of genotypes across

Table 1: Analysis of variance for barley grain yield (t ha^{-1}) across 11 environments in Bale high lands of Southeastern Ethiopia, 2001-2003

Source of variation	Degree of freedom	Sum of squares	Mean squares	Explained variation (%)
Total	791	1059.046		
Replication	3	3.126	1.042**	
Environment (E)	10	812.553	81.255**	76.7
Genotype (G)	17	24.460	1.439**	2.3
GxE	170	102.647	0.604**	9.7
Error	591	116.260	0.197	11.0

Repeatability (R^2) = 0.890, Broad sense heritability (H^2) = 0.581, Coefficient of variation (%) = 24.40, Mean = 1.82 t ha^{-1}

Table 2: Genotype and environment code, mean grain yield (t ha^{-1}) and test environment mean (t ha^{-1}) of 18 barley genotypes tested across 11 environments in Bale highlands of Southeastern Ethiopia, 2001-2003

			Year											
			2001			2002				2003				Mean
Genotype		Collection												yield
code	Genotype	site	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	E11	(t ha^{-1})
A	*Garbu #46-1 (Sn98B)*	Bale	1.6	1.3	0.9	1.7	1.6	2.9	0.4	1.2	2.4	3.7	3.2	1.9
B	*Feresgama –2 (Sn98B)*	Bale	1.6	1.5	0.9	1.5	1.9	3.4	0.4	1.0	2.1	4.4	2.3	1.9
C	*Acc.4272 –3 (Sn98B)*	IBC	1.6	1.0	0.5	1.1	1.3	2.4	1.0	1.0	2.1	3.8	2.0	1.6
D	*Acc.3290 –1 (Sn98B)*	IBC	1.0	0.7	0.7	0.6	1.0	2.2	0.1	0.6	1.7	4.1	3.0	1.4
E	*Meskele –5 (Sn98B)*	Bale	1.8	1.8	1.1	1.6	1.6	2.5	1.0	1.4	2.2	3.8	2.4	1.9
F	*Burtuji –2 (Sn98B)*	Bale	1.5	1.7	0.8	1.6	1.4	3.2	0.3	0.9	2.1	4.9	3.0	1.9
G	*Balticha #15 Go-1(Sn98B)*	Bale	1.6	1.5	0.9	1.6	2.1	2.6	0.6	1.3	2.7	3.8	3.0	2.0
H	*Aruso #74 –4 (Sn98B)*	Bale	1.5	1.7	0.9	1.4	2.0	2.9	0.5	1.0	2.0	4.0	2.9	1.9
I	*Shasho # 22 Go- 1(Sn98B)*	Bale	1.5	1.8	1.5	1.5	1.5	3.2	0.7	1.2	2.5	4.8	2.8	2.1
J	*Acc.1718 –2 (Sn98B)*	IBC	0.8	0.9	0.9	1.0	1.0	2.6	0.3	0.4	2.2	4.3	2.8	1.6
K	*Balticha #15 Go-5(Sn98B)*	Bale	1.7	1.7	1.0	1.4	1.7	3.0	0.8	1.1	2.3	4.6	3.0	2.0
L	*Acc.3284- 14 #2-1 (Sn98B)*	IBC	1.7	1.7	0.6	1.7	1.8	3.1	1.3	1.1	2.4	4.1	2.6	2.0
M	*Acc.3234- 15 -1 (Sn98B)*	IBC	1.3	0.9	0.6	1.2	1.1	2.8	0.7	0.7	2.0	3.3	3.4	1.6
N	*Aruso #3 Ad(b) –1 (Sn98B)*	Bale	1.7	2.1	0.2	1.4	1.6	2.5	1.1	1.4	2.1	3.4	2.6	1.8
O	*Acc.235236-1 (Sn98B)*	IBC	0.9	1.8	0.8	1.2	0.7	2.9	1.1	0.6	2.2	4.4	4.1	1.9
P	*Feresgama #26 Ro-1(Sn98B)*	Bale	1.2	1.3	0.9	1.1	1.0	2.9	0.6	0.7	2.0	4.0	2.8	1.7
Q	*Shage*	Cultivar	0.7	0.7	0.7	0.4	0.4	2.6	1.5	0.5	1.0	4.4	5.1	1.6
R	*Aruso*	local	1.8	1.4	0.7	1.5	1.6	3.1	0.6	1.4	2.4	3.6	2.5	1.9
Mean			1.42	1.42	0.81	1.31	1.41	2.82	0.72	0.97	2.13	4.08	2.97	

E1: Sinana-01, E2: Gassara-01, E3: Sinja-01, E4: Sinana-02, E5: Gassara-02, E6: Sinja-02, E7: Upper Dinsho-02, E8: Sinana-03, E9: Gassara-03, E10: Sinja-03 and E11: Upper Dinsho-03; IBC: Institute of biodiversity conservation, Ethiopia

environments and the later term shows constant yield rankings of genotypes across environment (Yan and Hunt, 2001; Matus-Cadiz *et al*., 2003; Kaya *et al*., 2006). Accordingly, different genotypes which performed maximum grain yield in different environments include genotypes A (Garbu # 46-1 (Sn98B)) and L (Acc.3284- 14 #2-1 (Sn98B) (in E4), B (Feresgama -2 (Sn98B)) (in E6), F (Burtuji -2 (Sn98B)) (in E10), I (Shasho # 22 Go- 1(Sn98B))(in E3) and R (Aruso) and M (Acc.3234- 15 -1 (Sn98B) (in E8) environments (Table 2). Thus, such inconsistent yield ranking from environment to environment indicates the presence of possible cross over GEI as described by Baker (1988), Crossa (1990), Yan and Hunt (2001) and Kaya *et al.* (2006). This study agrees with cross over GEI reports of Ceccarelli (1989), Ceccarelli and Grando (1991), Jackson *et al.* (1993),

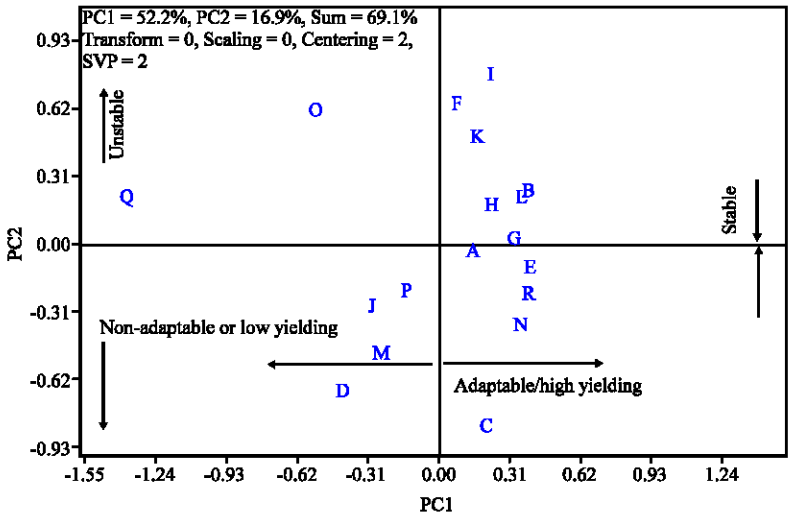

Fig. 1: GGE-biplot based on genotype focused scaling for genotypes

Van Oosterom *et al.* (1993) and Dehghani *et al.* (2006) in barley crop, Asfaw *et al.* (2008) in small red beans. The presence of cross over GEI shows the existence of different mega environment in which different winning genotypes can be selected. On the other hand, some genotypes had maximum yield in some environments. For instance, E (Meskele -5 (Sn98B)) had highest yield in E1(Sinana-01) and E8 (Sinana-03) environments, G (Balticha #15 Go-1(Sn98B)) in E5 (Gassara-02) and E9 (Gassara-03), N (Aruso #3 Ad(b) -1 (Sn98B)) in E2 (Gassara-01) and E8 (Sinana-03) and Q (Shage) cultivar had highest yield in E7 (Upper Dinsho-02) and E11 (Upper Dinsho-03) environments (Table 2). This suggests that there exist also another possible GEI known as non cross over GEI.

To graphically visualize the locations of genotypes on a biplot, a GGE-biplot based on genotype focused scaling is shown in Fig.1. The requirement for near perfect correlation (r = 0.949) (data not shown) between genotype PC1 scores and genotype main effects for the dataset has been met, so that, the yielding ability, genotype stability, discriminating and representativeness of environments can be efficiently visualized on the graph (Yan, 1999; Yan *et al.*, 2000). Thus, genotypes that had PC1 scores greater than zero were high yielding (except genotype C) while genotypes that had PC1 less than zero scores were identified as lower yielding or non adaptable (except genotype O) (Table 2).

Some inconsistencies were observed because the biplot did not explain 100% GGE variation (Yan, 2002). PC2 is associated with genotypic stability or instability on the biplot graph. Thus, the high yielding genotypes can be divided in to stable and unstable groups. Based on this, genotypes A(*Garbu #46-1 (Sn98B)*, G (*Balticha #15 Go-1(Sn98B)*), E (*Meskele –5 (Sn98B)*), H (*Aruso #74 -4 (Sn98B)*), L (*Acc.3284- 14 #2-1 (Sn98B)*), B (*Feresgama -2 (Sn98B)*) and R (*Aruso*) were high yielding as well as stable, since their absolute PC2 score is near zero. Whereas, the other group, consisted of five high yielding but unstable genotypes, i.e., I (*Shasho # 22 Go- 1(Sn98B)*), F (*Burtuji -2 (Sn98B)*), K (*Balticha #15 Go-5(Sn98B)*), O (*Acc.235236-1 (Sn98B)*) and N (Aruso #3 Ad(b) -1 (Sn98B)) as they had larger absolute PC2 scores.

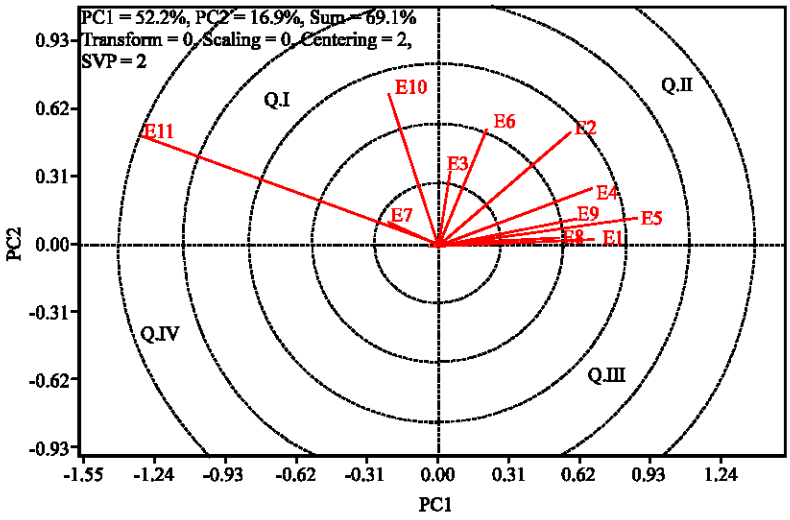

Fig. 2: GGE- biplot based on environment focused scaling for environments to show relationship among test environments in discriminating genotypes. Q = quadrant

Environment evaluation based on GGE-biplot

Relationship among test environments: GGE-biplot which depends on environment focused scaling was portrayed to estimate the pattern of environments (Fig. 2). Environment PC1 scores had both negative and positive scores indicating that there was a difference in rankings of yield performance among genotypes across environments leading to cross over GEI. Unlike PC1, the environmental PC2 scores had only positive scores. This give rise to non cross over GEI, leading to consistent genotype yield performance across environment. Environment PC1 and PC2 scores in this study showed GEI components against the reports of (Yan and Hunt, 2001; Yan *et al*., 2000) that indicated PC1 for non cross and PC2 for crossing over.

To visualize the relationship between environments, lines are drawn to connect the test environments to the biplot origin known as environment vectors. The cosine of the angle between the two environments is used to approximate the relation between them (Kaya *et al*., 2006; Yan and Tinker, 2006). The correlation coefficients among 11 test environments are indicated in Table 3 while the vector view of the GGE- biplot (Fig. 2) gives a succinct summary of the correlation among the environments. Thus, all environments which are found in the quadrant II were positively correlated to each other as the angle between them was less than 90° (i.e., acute angle) which was also true for environments in quadrant I. In addition to this, E10, E11 and E7 were positively correlated with E3 of quadrant II and there was also positive relation between E10 and E3, E6 and E2. However, since the angle between E11 or E7 and E6 was nearly 90°, hence the correlation between them was close to 0. Similarly, the correlation between E10 and E4 approaches to 90° indicating near 0 associations. This weak association was also shown in Table 3. However, there were some inconsistencies. For instance, Fig. 2 showed the existence of very close correlation between E11 and E7, but the actual correlation was of course not highly significant (Table 3). Like wise, Fig. 2 suggested positive correlation between E7 and E10, as opposed to this, Table 3 indicated negative correlation. These inconsistencies were due to GGE biplot was not 100% efficient (Yan, 2002; Kaya *et al*., 2006). Figure 2 showed that there were negative correlation between E11 or E7 and all the remaining environments (except with E10, E3 and E6) and there exist also

Table 3: Correlation coefficients among 11 test environments in Bale highlands of Southeastern Ethiopia, 2001-2003

	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	E11
E1	1.00										
E2	0.626**	1.00									
E3	0.009	0.123	1.00								
E4	0.819**	0.760**	0.218	1.00							
E5	0.841**	0.581**	0.167	0.804**	1.00						
E6	0.295	0.463*	0.401	0.540*	0.348	1.00					
E7	-0.043	0.137	-0.307	-0.157	-0.250	-0.157	1.00				
E8	0.924**	0.623**	0.064	0.754**	0.820**	0.185	0.026	1.00			
E9	0.633**	0.551*	0.261	0.833**	0.682**	0.351	-0.257	0.609**	1.00		
E10	-0.314	0.113	0.522*	-0.111	-0.156	0.434	-0.112	-0.341	-0.125	1.00	
E11	-0.687**	-0.307	0.004	-0.548*	-0.633**	-0.081	0.378	-0.530*	-0.606**	0.236	1.00

Correlation (r) at probability **p<0.01 = 0.596 and *p<0.05 = 0.478

negative correlation between E10 and each E9, E5, E8 and E1 environments as the angle between them is greater than 90° (i.e., obtuse angle). The presence of wide obtuse angles (angle >90°) (i.e., strong negative correlations) among test environments is an indication of high cross over GEI (Yan and Tinker, 2006).

As Yan and Tinker (2006) and Kaya *et al.* (2006) reported, the presence of close associations between testing environments reveals that similar information about the genotype could be obtained from fewer test environments and hence there could be better potential to reduce testing cost under limited resources. When there are no correlations of error effects among testing environments, the phenotypic correlation between environments may be used to study indirect response to selection (Cooper and Delacy, 1994). Hence, indirect selection may be carried out for the same character if measured on the same genotypes in different environments. Test environment E9 was significantly positively correlated with E1, E2, E4, E5 and E8 environments; similarly, E_8 correlated well with E1, E2, E4 and E5 environments. Beside this, E_5 was also significantly positively correlated with E1, E2 and E4 and E1 and E2 with each other and with E4 and E5 (Table 3). This suggests that indirect selection could be effective for grain yield in testing environments showing significant positive correlation. The existence of significant correlation between environments showed that the obtained information was very similar so that testing environment may be reduced to minimize cost with out significantly affecting the validity of information.

Discriminating ability and representativeness of test environments: Discriminating power and representativeness view of the GGE- biplot is an important measure of testing environment (Dehghani *et al.*, 2006). The length of concentric circles on the biplot helps to visualize the length of the environment vectors which is proportional to standard deviation with in the respective environments on the biplot and also shows the discriminating ability of the environments (Yan and Tinker, 2006). Thus, among the 11 testing environments (Fig. 2), E11(Upper Dinsho-03) with long vector was the most discriminating, while E7 (Upper Dinsho-02) was the least discriminating environment. The test environments which are consistently non-discriminating provide little information on the genotype differences (Yan and Tinker, 2006) and/or the performances of all genotypes in testing environment were uniform.

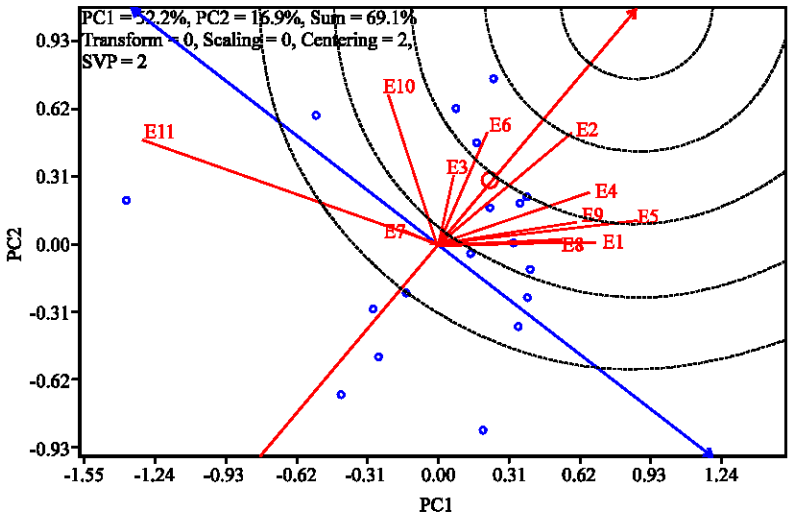

Fig. 3: The discriminability and representativeness view of the GGE-biplot to show the discriminating ability and representativeness of the test environments

On the other hand, Fig. 3 shows Average Environment Axis (AEA) (Yan *et al.*, 2001) view of biplot. Average Environment Axis (AEA) is the line that passes through the average environment (represented by small circle) and biplot origin. The average environment has the average coordinates of all test environments. A test environment that has a smaller angle with the AEA is more representative of other test environments according to Yan and Tinker (2006). Thus, E2 (Gassara-01) was the most representative environments, where as E11 (Upper Dinsho-03) and E7 (Upper Dinsho-02) with the large deviation from AEA were the least representative. Test environments that are both discriminating and representative is good test environment for selecting generally adapted genotypes (Yan and Tinker, 2006).

Hence, E2 (Gassara-01) was good test environment for selecting widely adapted genotypes. Testing environments that are discriminating but non representatives are useful for selecting specifically adapted genotypes if the target environment is divided in to mega environments (Yan and Tinker, 2006). Hence, E11 (Upper Dinsho-03) was useful for selecting specifically adapted genotypes like *Shage* cultivar. Non-discriminating testing environments are those with very short vectors and are less useful (Yan and Tinker, 2006). Thus, E7 (Upper Dinsho-02) was less useful test environment may be due to unfavorable rainfall condition. The ideal test environment (the center of concentric circles) should be both highly discriminating and most representatives of the target environments (Kaya *et al.*, 2006; Yan and Tinker, 2006).Of course under natural condition such environment does not exist but could be used relatively as a reference. Thus, the ideal test environment was E2 (Gassara-01) (Fig. 4) and it is an environment in which best genotypes could be most easily identified. The concentric circles following ideal test environment (except E11 and E7) were favorable environments. For instance, E6 (Sinja-02) was more favorable than E3 (Sinja-01).This was may be due to better yielding condition at Sinja in 2002 than 2001 cropping season. In his report, Yan *et al.* (2001) indicated that favorable test environments must have large PC1 scores (more discriminating genotypes) and near zero PC2 scores (more representative of an average environment).

Performance of barley genotypes in all environments: To visualize the performance of each genotype in each environment, both the genotype and environmental vectors are drawn (Fig. 5).

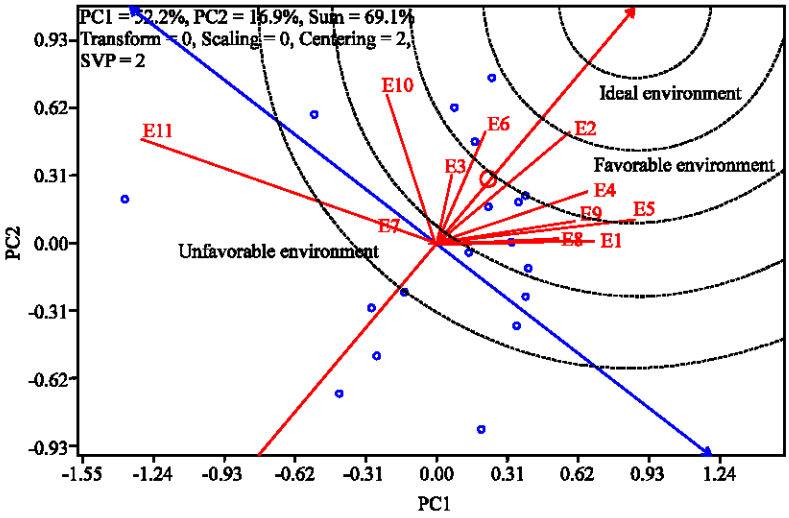

Fig. 4: GGE-biplot based on environment focused scaling for comparison of the environments in relation to ideal environment

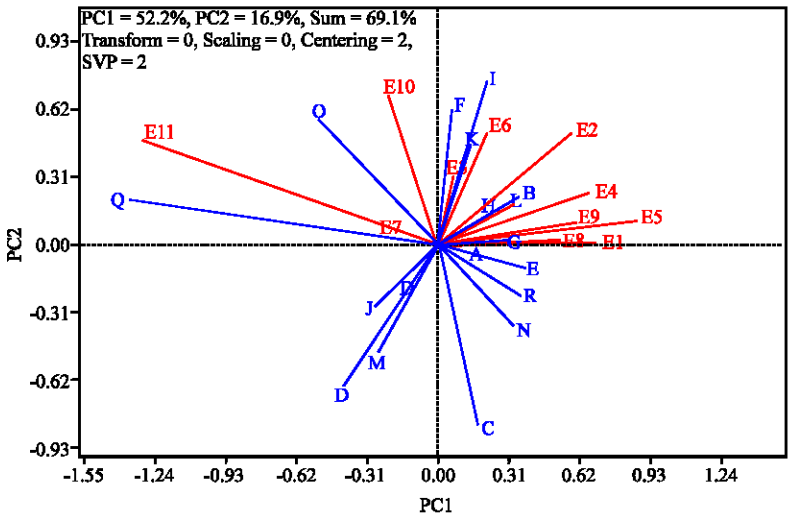

Fig. 5: The GGE-biplot view showing the performance of each genotype in each environment Barley genotype evaluation based on GGE-biplot

The performance of the genotype in an environment is better than average if the angle between its vector and the environment's vector is less than 90°. And, it is less than average if the angle is greater than 90° and near average if the angle is about 90° (Yan and Tinker, 2006). In this regard, genotype I and K performed well in E6 and E3 than in others. Where as the cultivar Q performed specifically better in E11 than in others. Genotype C, D and M had poor performances in most of the environments. Thus, different genotypes showed different responses in different environments. A genotype located nearer to the biplot origin has an average value in each of the environments. Such genotype has very minimum contribution to both G and GE interaction. Beside this, the length of genotype vector measures the contribution of the genotype to either G or GEI or both (Yan and Tinker, 2006). Thus, genotype I with the longest vector is the best genotype, while

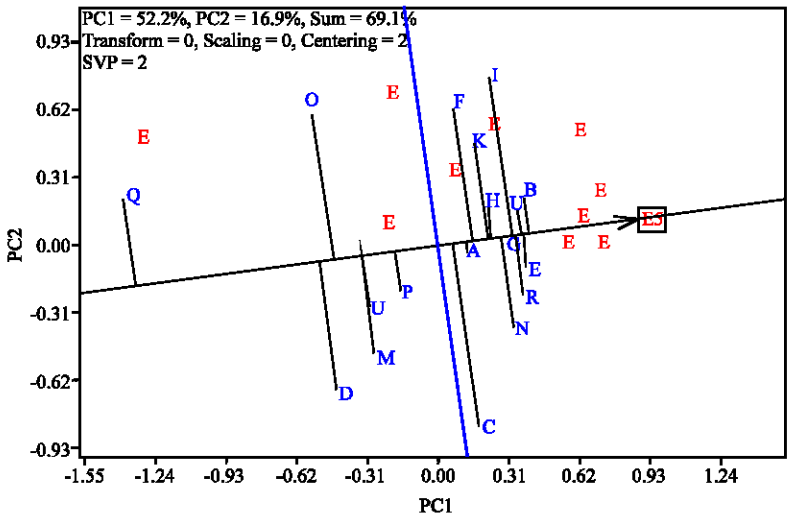

Fig. 6: Ranking genotypes based on performance in E5 (Gassara-02) environment

genotype Q with the longest vector is the poorest or the most unstable. This conforms to Yan and Tinker (2006) report. On the other hand, genotype A having very short vector and nearer to the biplot origin has very minimum contribution to both G and GEI.

Ranking genotypes based on performance in environment (E5): In ranking genotypes based on their performance in an environment, a line is drawn that passes through the biplot origin and the environment. This line is called the axis for this environment (Yan and Tinker, 2006) and along it is the ranking of genotypes. Thus, Fig. 6 shows ranks of genotypes based on their yield performance in E5 (Gassara-02). From the graph, genotypes ranging from P to Q below the perpendicular line to the axis had lower than the average yield in this environment, while genotype C showed nearly average yield performance. The highest yielder in E5 was genotype B followed by I, in contrast to this, genotype Q gave inferior yield. This difference in response among genotypes is mainly due to genotypic and genotypic and environmental interaction.

Ranking environments based on the performance of a genotype: Figure 7 shows the rank of the test environments in relative to the performance of a genotype I. To study the specific adaptation of a genotype, a line is drawn that passes through the biplot origin and the genotype. On the axis, genotype and environments are ranked along it. Thus, the graph indicates that genotype I had higher than the average in all environments, but nearly average in E7. Among this, it performed best in E2, E10 and E6 environments than the other remaining environments.

Mean performance and stability of barley genotypes: Figure 8 shows the Average Environment Coordination (AEC) view of the GGE biplot. With in a single mega environment, genotypes should be evaluated based on both mean performance and stability across environments. The single arrowed line is the AEC abscissa which points to higher mean yield across environments or to greater genotype main effect and the AEC ordinate is indicated by double arrows in either direction away from the biplot origin indicating greater GEI effect and reduced stability (Kaya *et al*., 2006; Yan and Tinker, 2006). Thus, across environments, I had the highest mean

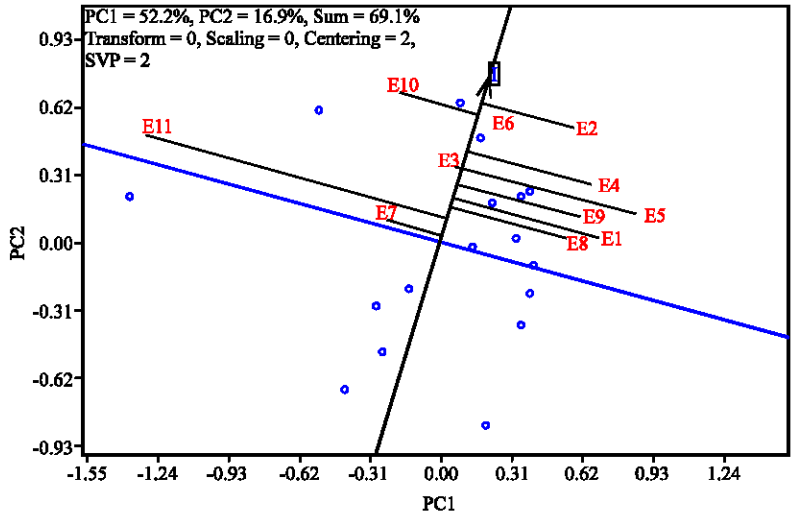

Fig. 7: Ranking genotypes on genotype I (Shasho # 22 Go- 1(Sn98B))

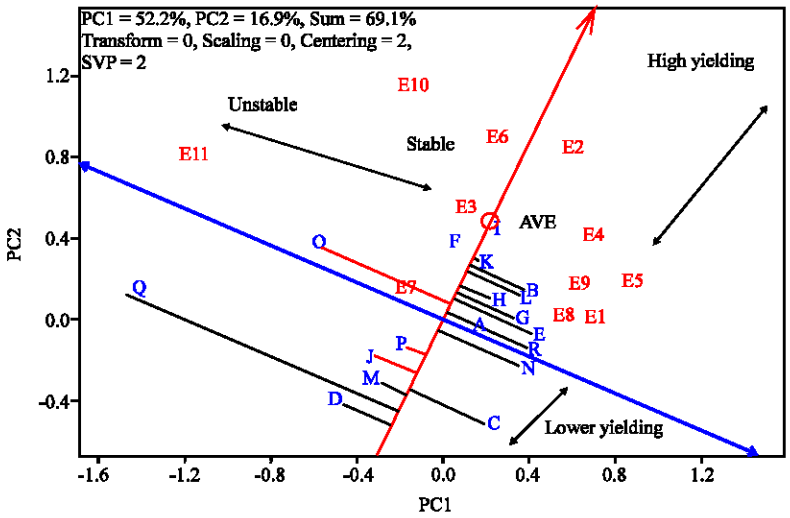

Fig. 8: Average Environment Coordination (AEC) views of the GGE biplot based on environment focused scaling for the mean performance and stability of genotypes. AVE = Average environment

yield, whereas, genotype Q with a longest genotype vector was highly unstable (poorly stable). On the other hand, genotype K with shortest vector length was highly stable and high yielding. According to Yan and Tinker (2006), stability is meaningful only when associated with high mean performance. High yielding and stable genotypes should have large PC1 scores but near zero absolute PC2 scores and such genotypes are more easily identified at locations with large PC1 scores but near zero PC2 scores (Yan *et al.*, 2000). The AEC ordinate separates genotypes with above average means from below average means. Therefore, genotypes with above average means were from I to R (except genotype C) on the graph, while genotype from N to D (except genotype N) indicate genotypes with below average means (Fig. 8). The length of the average environment

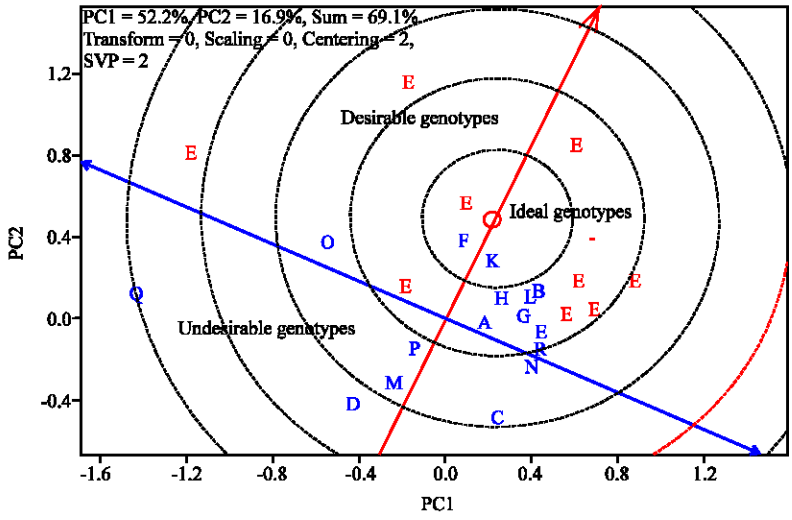

Fig. 9: GGE-biplot based on genotype-focused scaling for comparison of the genotypes with ideal genotype

vector relative to the biplot is the measure of the relative importance of genotype main effect and GEI such that the longer it is, the more important is the genotype main effect indicating the more meaningful the selection based on mean performance (Kaya *et al*., 2006). Thus, such genotype with above average mean performance could be selected for future breeding where as the remaining genotypes was rejected.

An ideal genotype should have both high mean yield performance and high stability across environments (Kaya *et al*., 2006; Yan and Tinker, 2006). It is a genotype to be on Average Environment Axis (AEA) on positive direction and has vector length equal to the longest vectors of the genotypes on the positive side of AEA with the largest vector length of high yielding genotypes and indicated by an arrow pointed to it (Kaya *et al*., 2006; Yan and Tinker, 2006). In this study (Fig. 9), I, F and K were ideal genotypes (the center of concentric circles) and genotypes located closer to the ideal genotype are more desirable than the others. Genotypes grouped in the concentric circle next to ideal genotype were more desirable. However, genotype 'Q' was undesirable.

Comparison between two barley genotypes: On the GGE biplot, the performance of two genotypes can be visually compared by connecting their markers with a straight line and drawing perpendicular line/equality line that passes through the biplot origin. The distance between two genotypes estimates the euclidean distance between them which is a measure of the overall dissimilarity. Genotypes had better yield in environments that are located on its side of the equality line (Yan *et al*., 2000; Yan and Tinker, 2006). When genotype I and Q (shage) are compared (Fig. 10), the performance of genotype 'I' was better than shage at almost all test environments except E7 and E11 while genotype shage had best performance in E11. The two genotype gave similar yield in E7. This indicates the presence of cross over interaction. The differences between the two genotypes vary by environment. This may be due to the difference in rainfall, temperature, shoot fly effect, maturity and disease. Similar report has been indicated by Dehghani *et al*. (2006) on rain fall and temperature difference, Saeed and Francis (1984) on relative humidity which had significant effect on yield and high contribution to GEI.

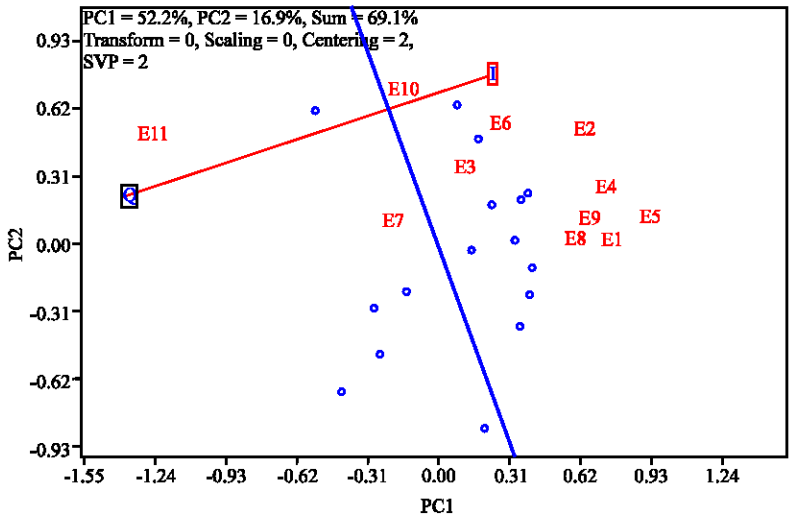

Fig. 10: Comparing two barley genotypes I and Q of their performances in different environments

Mega environment classification and winning genotype: Visualization of the which won where pattern of MEYT data is necessary for studying the possible existence of different mega environments in the target environment (Gauch and Zobel, 1997; Yan *et al*., 2000, 2001). The polygon view of a biplot is the best way to visualize the interaction patterns between genotypes and environments (Yan and Kang, 2003) to show the presence or absence of cross over GEI which is helpful in estimating the possible existence of different mega environments (Gauch and Zobel, 1997; Yan and Rajcan, 2002; Yan and Tinker, 2006). The polygon is formed by connecting the markers of genotypes that are further away from the biplot origin such that all genotypes are contained in the polygon (Kaya *et al*., 2006). The genotypes which are located on vertices of the polygon formed are either the best or poorest in one or more environments (Yan *et al*., 2000; Yan and Rajcan, 2002; Yan and Tinker, 2006). The vertex genotypes in each sector is also the best genotype for sites whose markers fell in to the respective sector so that sites with in the same sector share the same winning genotype (Yan, 1999, 2002; Yan *et al*., 2000). On the biplot, rays or lines that are drawn perpendicular to the sides of the polygon divide it in to sectors. The polygon view of a biplot is indicated in Fig. 11. Nine rays divide the biplot in to 9 sectors, out of these; environments fall only in to 3 of them. Five environments {E2, E3, E4, E6 and E10} fell in sector 1 delineated by ray 1 and ray 2. And, the vertex genotype for this sector was I (*Shasho # 22 Go-1(Sn98B)*) implying that this genotype was the winning genotype for these environments. Sector 2 delineated by ray 2 and 3 contained four environments {E1, E5, E8 and E9}. The remaining two environments, E11 and E7 were contained in sector 8 and Q (*Shage*) cultivar being the winner for this sector.

Depending on the mega environment definition of different winning cultivars (Gauch and Zobel, 1997) and the presence of high cross over GEI, it appears that there exist two possible mega environments. The first mega environment (Mega-1) was consisting of nine environments which are found in sector 1 and 2 with the genotype I (*Shasho # 22 Go- 1(Sn98B)*) being the best winner in these environments. And, the second mega environment (Mega-2) was small as compared to the first containing two environments, E11 and E7 with *Shage* cultivar being the winner. The environments found in sector 2 was intentionally combined with sector 1 to constitute mega-1 as

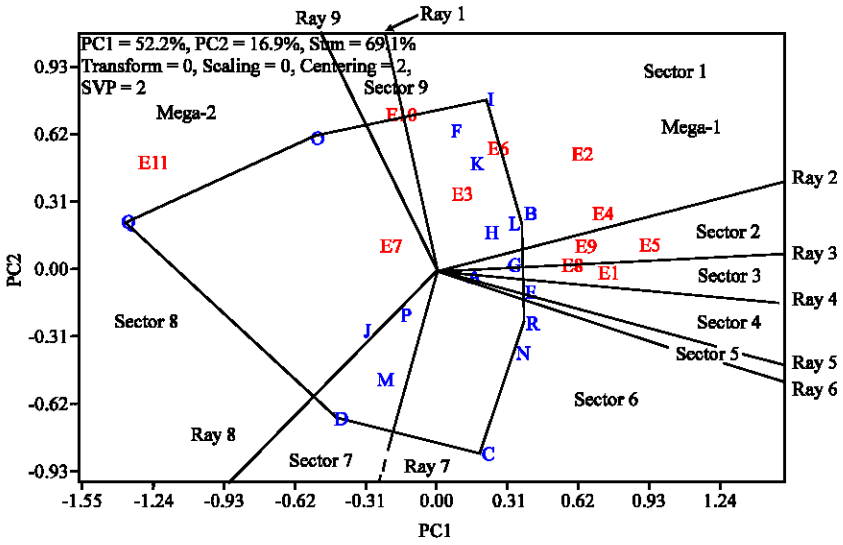

Fig. 11: Polygon views of the GGE biplot based on symmetrical scaling for the which won where pattern of genotypes and environments

these environments were similar to each other except the difference in yearly effects for the locations in sector 1 (Fig. 2, Table 2) and had also strong positive correlation (Fig. 2, Table 3).

When the two winning genotypes are compared, each genotype had contrasting performances in each specific mega environment (Table 2). For instance, *Shage* has shown best yield performance in Mega-2 very cool highland environments (3200 masl) with long growing season, but performed poorest in the other environments. In contrast to this, genotype 'I' performed poorly in mega-2, however, showed best performance in mega-1 (Fig. 5, 11, Table 2). The other contrasting feature of these two cultivars is that, *Shage* is known for its very susceptibility to barley shoot fly and very late maturing when grown in mega-1 where there is high prevalence of shoot fly and short cropping season so that gives low yield. On the other hand, genotype I being highly tolerant or resistant to shoot fly and early maturing (Variety Registration Bulletin, 2007) is well adapted and high yielder in Mega-1. Resistance to shoot fly could be considered as one of their secrets of adaptation differences. In addition to this, maturity and temperature difference may be suggested as another causes of cross over GEI in these areas. The results of this findings were in accordance with the reports of Van Oosterom *et al.* (1993) and Yan and Hunt (2001) with respect to maturity as cause of GEI in barley and wheat, respectively. In another report, Yan and Hunt (2001) indicated temperature difference and plant height as main causes of GEI in wheat. This result also coincides with reports of Kang (1998) which indicated large GE-interactions can be expected when there is wide variation between genotypes for morphophysiological characters possessing resistance to stresses or wide variations of environments for the incidence of the same stresses. The utilization of environmental and physiological data of different variables is very important to characterize the genotypes and target region to explain the main causes of GEI (Crossa, 1990). The differences in temperature, humidity, disease and insect pests and rainfall between the different test environments in the study area needs to be explored further to put more clearly the magnitude and causes of cross over GEI.

Selection in the target environment increase production and productivity of the crop through reducing yield loss that could happen by growing the variety where it would have been inferior.

For instance, if we consider this trial, by producing barley genotype I only in Mega-1, yearly an advantage of 15 to 130% yield hectare^{-1} would be obtained over *Shage* cultivar. But, by producing the same genotype I in Mega-2 environment, we would lose yield amount ranging from 45-53% hectare^{-1} as compared to the yield that could be obtained from *Shage* cultivar. This indicates how much specific adaptation is more important than wide adaptation in barley growing areas of Bale high lands to exploit repeatable GEI. Generally, the findings of this study showed that favorable environments were more discriminating and representative of the overall environments and in addition to this, the presence of high heritability (H^2 = 0.581) (Table 1) for grain yield shows environments were high yielding. Beside this, high heritability is useful in the selection of high yielding genotypes. This coincides with Kaya *et al.* (2006) report in wheat. Similarly, Ceccarelli (1994, 1996) reported heritability is higher in high yielding environment than low yielding environment in barley (*Hordeum vulgare* L.). Atlin and Frey (1990) and Abdelmula *et al.* (1999) found the similar report in Oat (*Avena sativa* L.) and Faba bean (*Vicia faba* L.), respectively.

CONCLUSION

The results of this study indicated that barley grain yield performances were highly influenced by environmental effect followed by the magnitude of GEI and genotype contributed the least effect. The magnitude of GEI effect was about more than three times that of genotype. Barley genotypes showed cross over GEI across environment and among genotypes tested there were desirable genotypes in terms of high mean yield. That is why genotype I (Shasho # 22 Go-1(Sn98B)) was officially released in 2005 for commercial production in Bale highlands and similar agroecology with a common name *Biftu*. It was developed from landrace population through pure line selection by Sinana Agricultural Center barley breeding program. This variety is six rowed type with high yielding potential, high shoot fly tolerance and/or resistance and uniformity. It showed 23.8% and about 10% overall yield advantage over standard cultivar (*shage*) and local (*Aruso*), respectively. Regarding testing environments, there exist two possible mega environments (Mega-1 and 2) in Bale highlands of Southeastern Ethiopia. Thus, barley breeding program of Sinana Agricultural Research center of Bale region should consider these two different mega environments separately to maximize yield potential of barley through exploitation of positive GEI. Beside this, additional barley yield trials may be launched to better clearly identify the magnitude of GEI and the causes of GEI by considering necessary environmental and biological variables.

ACKNOWLEDGMENT

I would like to thank the Oromia Agricultural research Institute: Sinana Agricultural research center for funding and provision of facilities to conduct the trials. I am also grateful to Prof. Yan W. for his free provision of GGE-Biplot, 2009 Version 5.2 software for data analysis. Amare Biftu and Badada Legesse are also acknowledged for their technical assistance in field data collection.

REFERENCES

Abdelmula, A.A., W. Link, E. Von Kittlitz and D. Stelling, 1999. Hetrosis and inheritance of drought tolerance in faba bean, *Vicia faba* L. Plant Breed., 118: 485-490.

Annicchiarico, P., 1997. Joint regression vs. AMMI analysis of genotype-environment interactions for cereals in Italy. Euphytica, 94: 53-62.

Asfaw, A., T. Assefa, B. Amsalu, K. Negash and F. Alemayehu *et al.*, 2008. Adaptation and yield stability of small red bean elite lines in Ethiopia. Int. J. Plant Breed. Genet., 2: 51-63.

Atlin, G.N. and K.J. Frey, 1989. Selecting oat lines for yield in low productivity environments. Crop Sci., 30: 556-561.

Baker, R.J., 1988. Tests for cross over genotype-environment interactions. Can. J. Plant Sci., 68: 405-410.

Ceccarelli, S., 1989. Wide adaptation: How wide. Euphytica, 40: 197-205.

Ceccarelli, S. and S. Grando, 1991. Selection environment and environmental sensitivity in barley. Euphytica, 57: 157-167.

Ceccarelli, S., 1994. Specific adaptation and breeding for marginal conditions. Euphytica, 77: 205-219.

Ceccarelli, S., 1996. Adaptation to low or high input cultivation. Euphytica, 92: 203-214.

Comstock, R.E. and R.H. Moll, 1963. Genotype x Environment Interactions. Symposium on Statistical Genetics and Plant Breeding. National Academy Science National Research Council, Washington, D.C., pp: 164-196.

Cooper, M. and I.H. Delacy, 1994. Relationships among analytic methods used to study genotypic variation and genotype x environment interaction in plant breeding multi-environment trials. Theor. Applied Genet., 88: 561-572.

Crossa, J., 1990. Statistical analysis of multilocation trials. Adv. Agron., 44: 55-85.

Dehghani, H., A. Ebadi and A. Yousefi, 2006. Biplot analysis of genotype x environment interaction for barley yield in Iran. Agron. J., 98: 388-393.

Eberhart, S.A. and W.A. Russell, 1966. Stability parameters for comparing varieties. Crop Sci., 6: 36-40.

EASE, 2002. Federal democratic republic Ethiopia: Central agricultural census commission. Ethiopian Agricultural Sample Enumeration, 2001/02. (1994 E.C). Report on the Preliminary Results of Area, Production and Yield of Temporary Crops (Meher Season, Private Peasant Holdings), Part I. October, 2002.

Finlay, K.W. and G.N. Wilkinson, 1963. The analysis of adaptation in a plant breeding programme. Aust. J. Agric. Res., 14: 742-754.

Francis, T.R. and L.W. Kannenberg, 1978. Yield stability studies in short season maize. I. A descriptive method for grouping genotypes. Can. J. Plant Sci., 58: 1029-1034.

GGE-biplot, 2009. GGE-biplot software version 5.2. The Complete Biplot Analysis System: GGEbiplot Pattern Explorer. Copy Right Weikai Yan, 2001-2009, USA.

Gabriel, K.R., 1971. The biplot graphic display of matrices with application to principal component analysis. Biometrika, 58: 453-467.

Gauch, H.G. and R.W. Zobel, 1988. Predictive and postdictive success of statistical analyses of yield trials. Theor. Applied Genet., 76: 1-10.

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

Jackson, P.A., D.E. Byth, R.P. Johnston and K.S. Fischer, 1993. Genotype x environment interactions in progeny from a barley cross. 1. Patterns of response among progeny genotypes for grain yield and time to anthesis. Aust. J. Exp. Agric., 33: 619-627.

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

Kaya, Y., M. Akcura and S.Taner, 2006. GGE-Biplot analysis of multi-environment yield trials in bread wheat. Turk J. Agric., 30: 325-337.

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

Pham, H.N. and M.S. Kang, 1988. Interrelationships among respectability of several stability statistics estimated from international maize trials. Crop Sci., 28: 925-928.

Pinthus, J.M., 1973. Estimate of genotype value: A proposed method. Euphytica, 22: 121-123.

SAS., 2004. System Analysis Software. Version 9.1.2. SAS Institute Inc., Cary, North Carolina, USA.

Saeed, M. and C.A. Francis, 1984. Association of weather variable with genotype-environment interaction in grain Sorghum. Crop Sci., 24: 13-16.

Shukla, G.K., 1972. Some statistical aspects of partitioning genotype environment components of variability. Heredity, 29: 237-245.

Van Oosterom, E.J., D. Klejin, S. Ceccarelli and M.M. Nachit, 1993. Genotype by environment interactions of barley in the Mediterranean region. Crop Sci., 33: 669-674.

Variety Registration Bulletin, 2007. Report equitable and sustainable finance for agriculture rural development. Ministry of Agriculture and Rural Development: Crop Development Department. http://www.isgmard.org.vn/Information%20Service/Special%20Events/Plenary%20Meeting%202007/Documents/MARD/Bao%20cao%20-%20Vu%20Tai%20chinh%20-%20Final-E.pdf.

Yan, W. and L.A. Hunt, 1998. Genotype by environment interaction and crop yields. Plant Breed. Rev., 16: 135-178.

Yan, W., 1999. Methodology of cultivar evaluation based on yield trial data-with special reference to winter wheat in Ontario. Ph.D. Thesis, University of Guleph, Guleph, ON., Canada.

Yan, W., L.A. Hant, S. Qinglai and Z. Szalvincs, 2000. Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop Sci., 40: 597-605.

Yan, W. and L.A. Hunt, 2001. Interpretation of genotype X environment interaction for winter wheat yield in Ontario. Crop Sci., 41: 19-25.

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

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

Yan, W. and I. Rajcan, 2002. Biplot analysis of test sites and trait relations of soybean in Ontario. Crop Sci., 42: 11-20.

Yan, W. and M.S. Kang, 2003. GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists and Agronomists. 1st Edn., CRC Press LLC., Boca Roton, Florida, pp: 271.

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