Genotype x environment interaction and stability analysis of grain yield in QPM hybrid varieties

Legesse Wolde[1]*, Tolera Keno [3], Abenezer Abebe[1],Demisew Abakemal [2], Worknesh Terefe[1]and Demoz Negera [2]

[1] Holetta Agricultural Research Center, Ethiopian Institute of Agricultural Research, Holeta, P. O. Box. 2003. Maize Breeder, Holeta, Ethiopia
[2] Ambo Agricultural Research Center, Ambo, Ethiopia
[3] Bako National Maize Research Center, Maize Breeder, Bako, Ethiopia
*Corresponding author: E-mail: legesse.wolde@gmail.com

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Abstract

Maize (*Zea mays L.*) is a major staple cereal widely cultivated in different agro-climatic environments of Ethiopia. Maize productivity in the tropical highland region of the country is known bylowaverage yield mainly due to the lack of high yielding and widely adapted improved cultivars. The objectives of this study were to determine G×E interaction and yield stability of quality protein maize (QPM) experimental hybrids,toidentify ideal genotype with high average yield depending on the differential genotypic responses to environment, and to form homogeneous grouping of environments. The study was conducted at seven environments representing the tropical-highland sub-humid maize growing agro-ecology of Ethiopia in 2015/2016. Thirty-three QPM hybrids and threecommercialhybrid checks were evaluated using a 4 ×9 alpha lattice design. Yield data was analyzed using AMMI and GGE bi-plot methods. Using AMMI analysis, four promising QPM hybrids designated asG31, G7,G19,G29, and G22 were identified based on combined stability and average yield.GGEbi-plotdisplayed that variety Jibatwas closest to the ideal genotype, can be considered as best hybrid whereas G29,G22were considered asdesirablystablegenotypes.GGE bi-plot also displayed Holeta as ideal environment and thus considered useful in discriminating the hybrids and representativeness as suitable environment. The GGE analysis delineated the test environments into three mega-environments useful for targeted evaluation of genotypes. The result of this study indicated specifically and widely adapted high yielding stable genotypes and also revealed homogeneous test environments.

Introduction

Maize is one of the cereal crops extensively grown worldwide being second in total area coverage and first in production and productivity. It is grown on more than 160 million hectares in the developing world, and many millions of people worldwide are dependent on maize as a staple food. In Africa, maize is a major staple, with more than 90% of the produce used for food and an average per capita consumption of about 50 kg. Africa consumes about 30% of world food maize, with Sub-Saharan Africa consuming the vast majority. Maize supplies at least one fifth of total daily calories consumed and accounts for 17 to 60% of people's total daily protein supply in 12 African countries (FAOSTAT-Agric. 2017).

Maize, despite its importance, is deficient in essential amino-acid contents, which are useful in nutrition for mono-gastric animals. In most developing countries where maize is the major staple, many people are chronically undernourished due to lack of supplemental diet which is observed from consumption of maize grainalone. The protein content of normal maize is relatively low, besides it lacks two important amino acids (lysine or tryptophan), essential for building proteins in humans and mono-gastric animals (Prasanna *et al.*, 2001).

Quality protein maize (QPM) contains the opaque-2 mutation, which increases the concentration of lysine and tryptophan in the grain endosperm and roughly doubles the biological value of maize protein, as well as additional modifier genetic systems to maintain tryptophan and lysine content in the endosperm and to make the endosperm vitreous which is similar to that of normal maize (Vasal, 1999). QPMcontains, in general, 55% more tryptophan, 30% more lysine and 38% less Leucine than that of normal maize (Prasanna *et al.*, 2001).

QPM is a valuable option as an animal product, especially for mono-gastric animals, since it can help reduce the requirement for additional protein sources in balanced feeds. Consequently, great interest has always been booming forQPM as a nutritionally enriched food source for impoverished people in regions of the world where maize is a primary source of energy. Infant feeding trials with QPM have repeatedly shown that QPM used as a weaning food reduces stunting and increases weight gain, thus improving child health(Graham *et al.*, 1990;Akalu*et al.*, 2010).From this perspective, the development of QPM varieties is very important for human diet.

In Ethiopia maize receives significance place in terms of total production, productivity and possesses wide range of uses as human food, animal feed and industrial purposes. It is widely adapted across diverse agro ecological conditions. However, maize yields are considerably lower under the smallholders farming systems of the tropicalhighlandsof the country than other environments, predominantly due to lack of well-adapted and improved cultivars and due to genotype by environment (GE) interaction. Genotypes grown in different environments will frequently showsignificant fluctuations in yield performance. These changes are influenced by the different environmental conditions and are referred to as GE interaction occurring due to differential response of genotypes to different growing conditions (Bernardo, 2002). According to Comstock and Moll, (1963) GE interaction reduces the genetic progress in plant breeding programs through minimizing the association between phenotypic and genotypic values. As a result, it is not only average performance that is important in genotype evaluation in multi-location trials (MET) but also the magnitude of the interactions.

Stability of performance is also of special importance in Ethiopia and similar countries where environmental conditions vary considerably and means of modifying the environment are far from adequate.A stable genotype is the one giving higher or lower yield across all environments while showing consistency in yield performance across all locations. Thus, the study of GE interaction and stability analysis for genotype evaluated across different environments is very important to select superior genotype for each specific target environment or avoided by selecting widely adapted and stable genotype across wide range of environments (Lu'quez *et al.*, 2002; Najafian *et al.*, 2010). It is also useful to bring together homogeneous environmentsinto similar groups and identify the stable genotypes in each and everylocationandto recommend the appropriate environment for growing the plant (Gauch and Zobel, 1997).

In maize there are numerous methods employed to analyze multi environment trials(MET), among which AMMI has been commonly used to reveal pattern of GE interaction. It analyzes and interprets the effect of the genotype (G) and sites (E) as additive effects plus the GE as a multiplicative component and submits it to principal component analysis(PCA) (Zobel *et al.*, 1988; Gauch and Zobel, 1997). It is a multivariate technique used for assessing the phenotypic stability, adaptability of genotypes (Rashidi etal.,2013;Oliveira*et al.*, 2014) and to group test environments inmulti-environment variety trials (Yang *et al.*, 2005; Miranda *et al.*, 2009). On the other hand, GGE- bi-plot proposed by Yan *et al.* (2000) is aneffective method based on principal component analysis to fully explore MET data. It allows visual examination of the relationships among the test environments, genotypes and the GE interactions. It is an efficient tool for mega-environment analysiswhich enables to recommend specificgenotypes to specific mega-environments (Yan and Tinker, 2006; Legesse *et al.*, 2018), genotype mean performances and stabilityevaluation,and environmental evaluation (Bozović *et al.*, 2018,Chandel *et al.*, 2019). Selecting QPM hybrid cultivars for diverse maize growing tropical-highland areas of Ethiopia requires that maize breeders consider stability of performance in addition to an average or maximum performance.

The present investigation was therefore aimed to applyadditive main effects and multiplicative interaction(AMMI)andgenotype and genotype by environment(GGE)- bi-plots statistics to (i) assess GE interaction, the stability and adaptabilityofpromising experimental QPM hybrid varietiesrecently developed from tropical-highland adapted inbred lines across seven environments(ii) to determine ideal genotype with high average yield depending on the differential genotypic responses to environment and (iii) to form homogeneous grouping of environments and genotypes.

Materials and Methods

Study Material and experimental design

Thirty-three locally developed QPM three-way cross experimental hybrid varieties and three check hybrids considered to adapt under highland maizegrowingagro ecologies of Ethiopia wereevaluatedatsevenlocationsduring the main cropping season in 2015/2016 (Table 1). The experimental design employed was an alpha (0, 1) lattice (Patterson and Williams, 1976) with two replications at each location. The experimental unit consisted of a single row of five meters length spaced at 75 cm between rows. Planting was done using two seeds per hill and 25 cm apart between hills. Thinning was performed at three to five leaf stages to attain a final density of 53,333 plants ha^{-1}.

All other management practices including planting, fertilization, weeding and harvesting were performed as per the recommendations for each location. The sites where the experimentswereconducted are different in their altitude, geographic locations, weather conditions and soil types and hence regarded as individual environments (Table 2).Data for all relevant agronomic traits were collected, but only plot grain yield data converted into tonha-1were subjected to statistical analysis.

Statistical Analysis

ANOVA for grain yield for each environment from 36 hybrid varieties was analyzed using IRRI software (2009). The Bartlett's test of homogeneity of error variances gave a non-significant Chi-square, so the hypothesis of homogeneous error variance was accepted(Gomez & Gomez, 1984).The analysis of variance (ANOVA) was used and the G X E interaction estimated through stability analysis using the AMMI model (Zobel *et al.*, 1988). In this procedure, the contribution of each genotype and each environment to the GE interaction is assessed using the MATMODEL(Gauch, 1997). The results of the analysis were interpreted on the basis of tables and bi-plots that showed the main and first multiplicative axis term (PC1) of both genotypes and environments in terms of their mean production, and also to obtain a first look at their stability in terms ofGEinteraction with PC1. Also AMMI bi-plot with PCI and PC2 were constructed to evaluate genotypes in terms of their stability and specific adaptability to environments, and vice versa.

Table 1 - Genotypic coding, their identification pedigree, and selection history for genotypes originated from Ambo highland Maize Research Program and CIMMYT in Ethiopia studied across 7 environments in 2015/2016.

Entry	Genotype code	ID
1	G*1	AMH5020-1
2	G2	AMH5020-2
3	G3	AMH5020-3
4	G4	AMH5020-4
5	G5	AMH5020-5
6	G6	AMH5020-6
7	G7	AMH5020-7
8	G8	AMH5020-8
9	G9	AMH5020-9
10	G10	AMH5020-10
11	G11	AMH5020-11
12	G12	AMH5020-12
13	G13	AMH5020-13
14	G14	AMH5020-14
15	G15	AMH5020-15
16	G16	AMH5020-16
17	G17	AMH5020-17
18	G18	AMH5020-18
19	G19	AMH5020-19
20	G20	AMH5020-20
21	G21	AMH5020-21
22	G22	AMH5020-22
23	G23	AMH5020-23
24	G24	AMH5020-24
25	G25	AMH5020-25
26	G26	AMH5020-26
27	G27	AMH5020-27
28	G28	AMH5020-28
29	G29	AMH5020-29
30	G30	AMH5020-30
31	G31	AMH5020-31
32	G32	AMH5020-32
33	G33	AMH5020-33
34	JIBAT+	AMH5020-34
35	WEBI+	AMH5020-35
36	WENCHI+	AMH5020-36

*G= experimental genotypes which are referred fromno.G1- G33,
+ =No. 34-36 are check hybrids

The GGE bi-plots were constructed (SYSTAT Software Inc., 2006) from the first two principal components (PC1 and PC2) derived by subjecting the environment-centered yield data (which contains G and GE) to singular valued composition (Yan, 2002; Yan *et al.*, 2000). GGE bi-plot used to rank the genotypes on the bases of yield and stability and correlation vector among environments was done. Also, the test location vector length, the cosine value of the angle between the location and the average location, and the distance between the positions of a location and the "ideal" test location were used as measures for the location discrimination ability, representativeness, and desirability indices for each test location for grain yield was generated. Graphs showing "which won where" pattern to reveal the presence or absence of different mega-environments weregenerated using GGE bi-plot analysis(Yan 2001;Yan and Rajcan, 2002).

Results and Discussion

AMMI Model Analysis

The results of combined ANOVA and AMMI analysis of variance for maize grain yield of 33QPM experimental hybrids varieties tested along with three check hybrids at seven locations is presented inTable 3.Considering the additive component of the result, it appeared that grain yields of the QPM hybrids were significantly affected by environment which explained 57.57% of the total variation(G+E+GEI) while genotype and genotype x environment interaction accounted for 24.03 % and 18.40 %, of the total variation, respectively. The analysis also showed highly significant ($p < 0.01$) difference among environments (E), genotypes (G) and genotype by environment interaction (GE).Large sum of squares for environment indicates that the contribu-

Table 2 - Environment Sites orientations, altitude, rainfall&temperature

SN	Environment	Altitude (m.asl)	Latitude	Longitude	Annual Rainfall (mm)	Minimum Temp (0c)	Maximum Temp (0c)
1	Ambo	2225	80° 57' N	38° 7' E	1115	11.7	25.4
2	Holeta	2400	9° 00' N	38° 30' E	1065	6.4	22.1
3	Kulmsa	2200	8° 5' N	39° 10' E	1078	10.0	23
4	Adet	2240	11° 17' N	37° 43' E	1091	18.2	25.3
5	Haremaya	2020	9° 26' N	42° 3' E	728	8.99	25.15
6	Hawassa (Anegecha)	2381	7° 0' N	38° 29' E	1656	14.0	24.0
7	Jimma (Dedo)	2300	7° 40' N	36°50' E	1700	13.4	23.2

tion of environmental effect was much higher than the effect of genotype for the variation of grain yield of QPM hybrids due to diverse environmental conditions of the testing locations.Yan and Hunt (2002) indicated that usually, E explains most of the total yield variation, while G and GE are normally small. This is specifically true to traits like yield that has low heritability (Brar et al.,2010).The results of AMMI analysis was supported by several authors who reported significant interactions of genotypes x environments and the predominance of environment effect than other factors on soybean (Asratet al., 2009) on wheat (Shetaye, 2015)and maize (Kassaet al., 2013; Demissewet al., 2016, Legesseet al., 2018).

Furthermore, GEI was partitioned into four interaction principal components analysis axes (IPCA) and all thefour multiplicative components terms of AMMI revealed significant using an approximate F-statistic (Gollob, 1968).The percentage contributions of the PC1 and PC2 were 28.20% and 24.16%, respectively and together explained 52.3% of variability.PC3 &PC4 also explained 20.74% and 10.79 of the variability, respectively, and thus brining cumulative total to83.79%, the remaining 16.21% of the interaction effect being the residual or noise, therefore, not interpreted (Purchaseet al., 2000). The variation contributed by these four IPCAs showed differential performance of genotypes for grain yield across the locations. However, the variability contributed byPC1&PC2 wasconsidered for further analysis, as the simplicity of the two-dimensional analysis would be maintained.AccordingtoGauch and Zobel, 1997,AMMI, with the first two multiplicative terms of the genotype and environment, was the best predictive model and confers relatively factual interaction pattern of genotypes with given test environments.

Table 3 - AMMI analysis of variance of grain yield of 33 experimental QPM hybrid varieties along with 3 check hybrids grown across 7 environments in 2015.

Source	D.F.	S.S.	M S.	% Treatment's	% G x E pr
Total	755	2798.3	3.71		
Treatments	251	2074.8	8.27***		
Genotypes	35	498.5	14.24***	24.03	
Environments	6	1194.4	199.07***	57.57	
Block	14	72.4	5.17***		
Interactions	210	381.8	1.82**	18.40	
IPCA 1	40	107.3	2.68**		28.20
IPCA 2	38	92.5	2.44**		24.16
IPCA 3	36	79.2	2.20**		20.74
IPCA 4	34	41.2	1.21*		10.79
Residuals	62	61.5	0.99		16.11
Error	490	651.1	1.33		

Mean grain yield value of the 36QPMhybrids is shown in Table 4.Grain yield among the maize varieties ranged from 4.753 th-1(G 14) to 8.504 th-1 (Jibat). Of the varieties, G31 (-0.00078), G7 (0.02786), G19 (-0.03702), G29 (0.04110), and G22 (-0.04355) showed the least G X E interaction as measured by first IPCA 1(Table 4), which took 28.02% of the GXE interaction SS,and are apparently considered as stable genotypes, whereas G24(1.21019) followed by G21 (-1.03125) had the largest interaction and are responsive to environmental change and thus not stable. Among the five genotypes

Table 4 - Mean grain yield performances of QPM hybrid genotypes along with IPCA scores analyzed across seven locations

Genotype	Mean	IPCAg1	IPCAg2
G1	6.452	0.23932	0.30275
G2	6.165	0.20968	0.62972
G3	6.806	-0.31287	0.59845
G4	6.966	-0.19299	0.1809
G5	6.813	-0.25733	0.17699
G6	6.923	0.36877	0.70268
G7	7.137	0.02786	-0.17987
G8	7.345	0.33992	-0.16667
G9	6.353	-0.26774	-0.75409
G10	5.428	-0.34594	-0.52614
G11	6.921	0.46185	0.21899
G12	7.197	-0.7168	0.29255
G13	6.672	-0.37412	0.06462
G14	4.753	-0.54449	-0.71043
G15	7.106	-0.2395	0.06295
G16	8.461	-0.3998	-0.07224
G17	7.35	-0.18476	-0.42223
G18	8.029	0.59468	-0.77186
G19	7.234	-0.03702	0.02851
G20	7.321	0.27698	0.05929
G21	6.145	-1.03125	-0.07343
G22	7.934	0.06207	0.49802
G23	7.483	0.27429	-0.52419
G24	6.421	1.21019	-0.09357
G25	5.247	-0.43276	-0.06636
G26	6.85	0.11733	-0.53644
G27	6.352	0.34189	-0.11262
G28	5.74	0.2244	0.11203
G29	7.846	0.0411	-0.30006
G30	6.89	-0.04355	0.16457
G31	7.391	-0.00078	0.32337
G32	6.332	-0.08846	0.30905
G33	6.309	0.16923	-0.09871
JIBAT	8.504	0.39818	0.32984
WEBI	6.865	0.37878	-0.30352
WENCHI	7.476	-0.26635	0.65714

depicted stable across testing environments, G31 is the most stable and widely adapted genotype due to its low contribution to the interaction effects. The IPCA score of the genotype in the AMMI analysis are indication of stability or adaptation over environment. The greater the IPCA score, the more specifically adapted is the genotype to a specific location. The more IPCA score approximate to zero, the more stable or adapted is the genotypein overall environment tested(Gauch and Zobel, 1997; Alberts, 2004).

Further, environmental grain yield averaged over locations varied from 4.893 tha-1 (Hawasa) to 8.79 tha-1(Adet) (Table 5).AMMI analysis also showed that the least first IPCA value of 0.05885 was recorded for Haramaya while the highest IPCA value (1.36440) was observed forAdet. This indicated low interaction of the climatic conditions atHaramaya and high interaction atAdet. Haramaya is, therefore, more stable in evaluating the performance of thegenotypes. However, the average performance of the genotypes atHaramaya is below overall mean performances oftheseven locations indicating that Haramayais considered to be poor potential environment. On the contrary, Adet compared to overall value of testing locations gave above average mean performances despite is unstable conditions. According to Yan et al.(2011) for an environment to become desirableitshould have more discriminating ability of the genotypes in terms of genetic main effects andahigh stability index, which implies more representativeness of the overall environment.

AMMI-Bi-plot

The relative magnitude and direction of genotypes along the abscissa and ordinate axis in bi-plot is important to understand the response pattern of genotypes across environments. The best genotype should combine high yield and stable performance across range of production environments and the genotypes withPC1 score close tozeroexpressed general adaptationwhilethe larger scores with PC1 score of the same sign depicted more specific adaptation to environment (Ebdon and Gauch, 2002;Tadesse, et al., 2017).

In Figure 1 of AMMI biplot, the Y-axis represents the IPCA1 score, while the x-axis represents the yield of the variety which is the main effect of the genotype. Accordingly, Jibat,G16 and G18are high yielding butare far from the origin of the biplot which indicated their unstable performances to adapt across test locations. However, these hybrids will have good potential to adapt in specific location. On the other hand, G14, G10 and G25 have low average yield performances and less adapted to the testing locations as they are far away from the origin of the biplot. Conversely G31, G7, G20 and G22 are closer to the origin and revealed better performances than the overall mean yield of the genotypes,and these genotypes are less responsive to the environmental changes and thus could exhibit wide adaptation across the testing locations.This finding corroborated with Demissewet al.,2016andTadesseet al., 2017.

With regard to the locations indicated in Figure 1,AdetandAmboare high yielding environments but more responsive to the environmental change due to the expression of largest IPCA score. Similarly, Hawassa and Kulumsa,expressed greater negative IPCA2score but

Table 5 - Environmental mean grain yield (tha-1) values along with their IPCA scores

Number	Environment	Mean	IPCAe1	IPCAe2	IPCAe3	IPCAe4
1	Adet	8.790	1.36440	0.48160	1.20685	-0.70152
2	Ambo	7.299	-1.30439	0.00361	0.39010	0.67236
3	Haramaya	5.628	0.05885	-1.69894	-0.03580	-0.29906
4	Hawassa (Angecha)	4.893	0.89535	-0.58397	-1.28000	0.32455
5	Holeta	7.863	0.55277	1.18257	-0.43234	0.93262
6	Jimma (Dedo)	7.406	-0.58357	-0.19583	0.99550	0.33043
7	Kulumsa	6.190	-0.98341	0.81096	-0.84432	-1.25939

with poor yielding environments. Accordingly,allthese environments are not stable to test the varieties for broad adaptation; however, it could be suitable to test

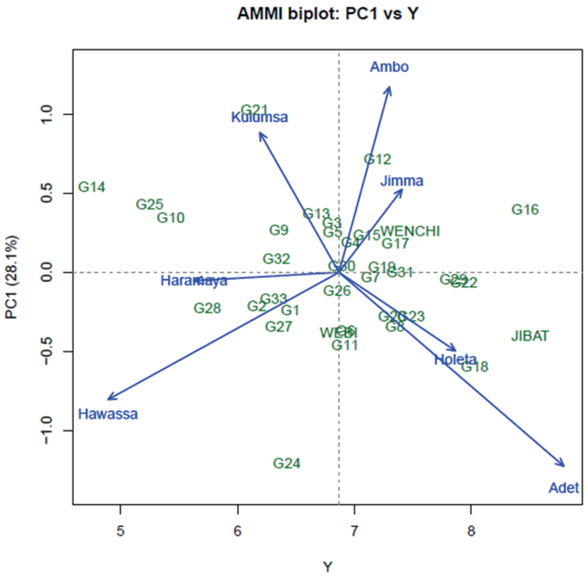

Fig. 1- AMMI- bi-plot for mean grain yield of 36 genotypes grown at seven locations. The genotypes are indicated in block letter while the locations are indicated by their identification names.

genotypes for specific adaptation.On the other hand, Holeta and Jimma showed modest expression of IPCA values with above average performance as compared to the overall mean yield. These locations are less responsive to environmental interaction and thus could be potentially useful for evaluation of maize genotypes.

As for specific adaptation of genotypes, Figure 2 showed G24, G8 and G27 with medium yield performance atAdet and Hawassa, G18with higher yield performance, andG26, G23andWebi with moderate tohigher yield performances at HaramayaandHawassa.Jibat and G11 with higher yield performance at Adet whereas G6, G2, Wenchi and G3 with moderate yield performance at Holeta and Kulumsa. Most of the genotypes whichportrayed high performance in the specified environments are considered revealinginferior performances in the unspecified environments. This result is in agreement with the findings of several researchers who studied interaction of genotypes with environments and genotype adaptation over testing locations (Demissewet al.,2016 and Tadesseet al., 2017, Legesseet al., 2018, Chandelet al, 2019)

Furthermore, when a test environment marker falls close to the bi-plot origin, that is, if the test environment has a very short vector, it means that all genotypes performed similarly and therefore it provided little or no information about the genotype differences. Test environments with long vectors and small angles with the AEC abscissa are more discriminating of the genotype and representative of the test environments and consequently are ideal for selecting superior genotypes. While test environments with long vectors and large angles with the AEC abscissa, cannot be used in selecting superior genotypes, but are useful in culling unstable genotypes (Yanet al., 2013). According to Figure 2 biplot of this study,theenvironmentHaramaya is identified to be the most discriminating as indicatedby the longest distance of these environments from the

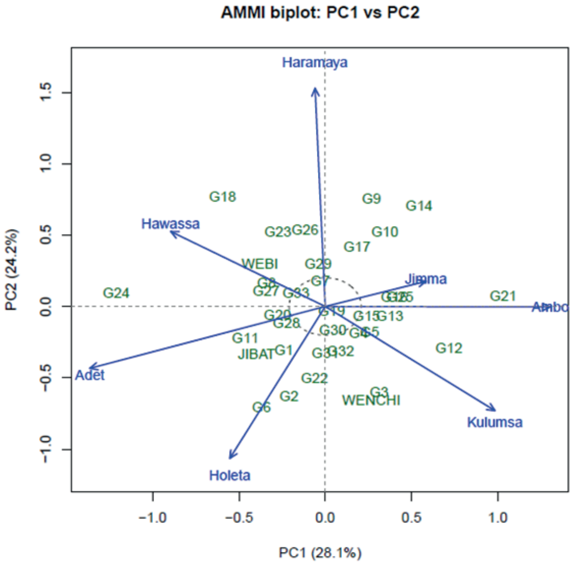

Fig. 2 - AMMI-bi-plot(PC1 vs PC2) for mean grain yield of 36 maize genotypes grown at seven environments. The genotypes are indicated in block letter while the location are identified by their identification names

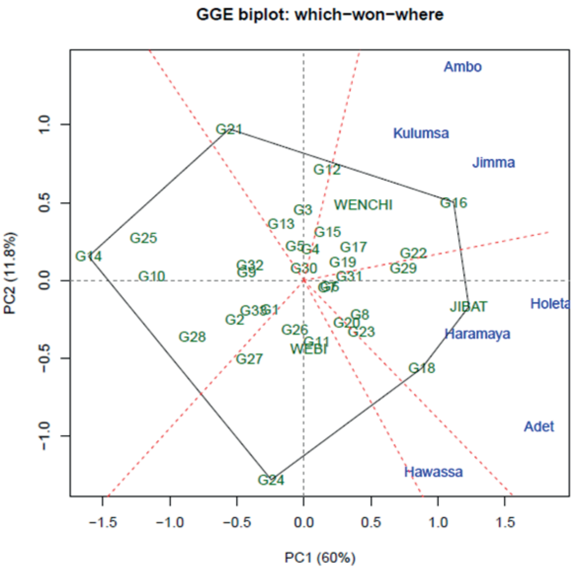

Fig. 3 - Genotype plus genotype by environment interaction of GGE bi-plot for grain yield in 36 QMP maize genotypes tested based on environment focused scaling for the polygon view exhibiting 'which won where' and environment grouping

origin point. In contrast,environmentJimmamay have little discriminating power and genotypicdifferences at Jimmaremains to be highly consistent with those averaged yield overenvironments, because it had less IPCA 1 and IPCA2 scores(Table 5) compared tothe rest of environments.

Besides, angles between the genotype and environment vectors determine the natureof the interaction as it is positive for acute angle, negligible for right angle, and negative for obtuse angle (Hagos andAbay, 2013). Similarly, the angle between the vectors of two environments determines the relationships between pair of environments. Thus, the cosine of the angle between the vectors of two environments approximates the correlation coefficient between them (Yan, 2002).According to Figure 2 of this study, the angles between seven of the environments were less than 90 degree indicating high correlations amongst them. Thus, Ambo and Jimma, Ambo andKulumsa sites were identified as relativelyredundant test environments because they had small angles revealing strong positive association suggesting that these environments tend todiscriminate among genotypes in a similar manner. Thus, genotypes in these environments will reveal stable performances, while the performances of the genotypes in uncorrelated environments would imply poor and unstable performances.Similar observation was noted byDemissewet al. (2016) whoreported the same locations to have been closely correlated and information generated in any of these environments could serve for theotherlocation.

GGE Bi-plot

The GGE bi-plot of the best genotypes in each of the environments for seed yield is presented in Figure 3. The polygon view of the GGE-bi-plot explicitly displays 'which-won-where' i.e. (best genotype in each environment) and it is a summary of the GEI pattern of a multi-environment seed yield trial data (Yan, 2011; Hongyuet al., 2015). The polygon is formed by connecting the genotypes that are further away from the bi-plot origin such that all other genotypes are contained within the polygon. To each side of the polygon, a perpendicular line, starting from the origin is drawn and extended beyond the polygon so that the bi-plot is divided into several sectors, and the different environments were separated into different sectors. In this polygon there were six sectors. Accordingly, the following genotypes namely, Gibat, G18, G24, G14, G21 and G16 located at the corner of a polygon are vertex genotypes with longest vectors. The vertex cultivar in each sector represents the highest yielding cultivar in the location that falls within that particular sector (Yan et al.,2007; Aduet al.,2013).

Further, the environment group within each sector and the cultivar at the polygon's boundary characterize the mega-environment (Yan &Rajcan, 2002). Thus,thepresence of mega-environment is justified by different genotypes performing best in different test locations, and the large variation due to environment indicates strong influence of environments and existence of mega-environment among trial conducting locations; (Gauch and Zobel, 1997; Yan and Kang, 2003). The analysis in this study indicated the existence of

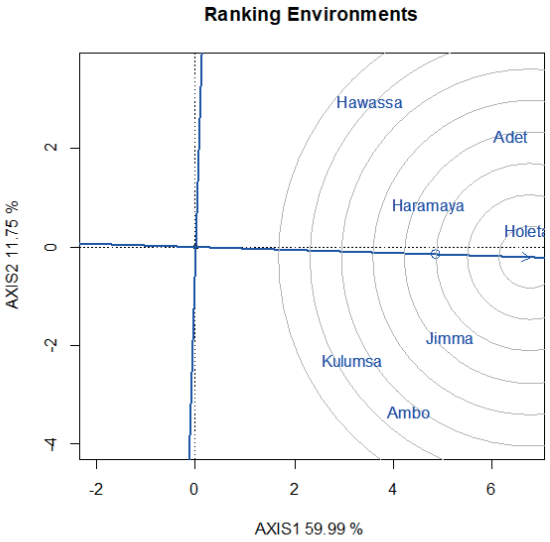

Fig. 4 - Genotype plus genotype by environment interaction of GGE bi-plot for grain yield in 36 maize hybrids tested based on environment focused scaling for environment comparison

three mega-environments which areidentifiedas; G18 winning niche for Hawassa environment, Jibat winning niche for Adet, Haramaya and Holeta environments and G16 winning niche for Ambo, Kulumsa and Jimma environments. The genotype of the vertex of the polygon, contained in a mega-environment, had the highest yield in at least one environment and was one of the best-performing genotypes in the other environments.These genotypes have the largest vectors in their respective directions; the vector length and direction represent the extent of the response of the genotypes to the tested environments (Yan and Rajcan, 2002).The three other corner genotypes, G24, G14 and G21, were the poorest-yielding. These genotypes were located far away from all of test locations, reflecting the fact that they yielded poorly at each location. All other genotypes are contained within the polygon and have smaller vectors, implying that these genotypes are less responsive in relation to the interaction with the environments within that sector (Yan and Rajcan, 2002).

Figure 4 shows the graphical evaluation of the test environments for their power to discriminate between the environments that have both high mean yield and high stability is called an idealenvironment. Such environment for experimental evaluation is one with high IPCA1 value (higher cultivar discrimination power) and IPCA2 value close to zero (more representative of the overall environment mean) (Miranda et al., 2009, Yan et al., 2007). In the same taken, anenvironment is more desirable if it is located closer to the ideal environment. Thus, using the ideal environment as the centre, concentric circles were drawn to help visualize the distance between each environment and the ideal environment (Yan et al., 2011).This helped to identify the best environment, and thus in our case'Holeta' was found the best for being close to the ideal environment both in discriminating the hybrids and representativeness as suitable environment forselecting superior genotypes, which implies that varieties selected in that location would have high probability to also perform well in other locations of the same region (Yan and Tinker 2006; Nai-Yin et al., 2013). Contrary tothesefindingsDemissewet al. (2016) identified 'Kulumsa' as most desirable environment.

An ideal genotype should have an invariably high average yield in all environments concerned. A genotype that is located at the center of the circles or is the genotype closest to the hypothetical genotype is considered a superior genotype with higher grain yield and good yield stability(Yan and Kang, 2003,Yan,and, Tinker, 2006, Yan et al., 2017). As displayed in As displayed in Figure 5, Jibat was the closest to the hypothetical ideal genotype and therefore identified as the best and G29,G22 in the second and G16, G17,G19 in the third desirability category of hybrid varieties in terms of their higher yielding performance and stability. Therefore, these genotypes can be closely followed and recommended for commercial production in terms of their high grain yield and broad adaptability. G14 G25 and G10were extremely far away from the concentric circle and thus not in the ideal hybrid category. They are also poor yielding and highly responsive to environmental change mainly because of their distance from the concentric circle. In line with these findings several researchers reported the relative contribution of stability and mean grain yield for the identification of desirable genotype following the GGE bi-plot procedure of ideal genotypes (Demisewet al.,2016;Oral, et al., 2018).

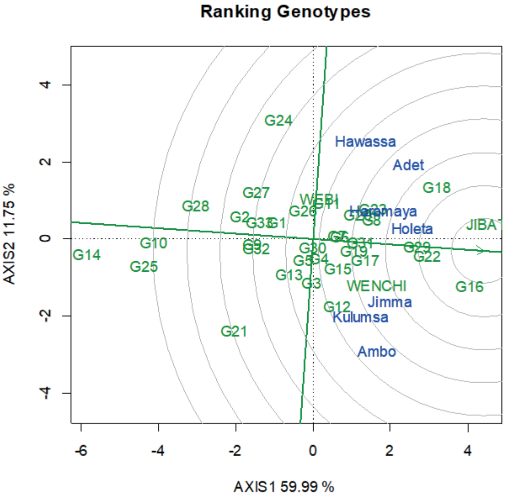

Fig. 5 - Genotype plus genotype by environment interaction of GGE bi-plot for grain yield in 36 QPM maize genotypes tested based on environment focused scaling for genotype comparison

Conclusion

The current analysis of multi-environment field experiment trial data on grain yield of QPM maize hybrids revealed the presence of GEI with the largest variation accounted bylocation followed by GEI and genotypes, respectively. Grain yield among the maize varieties ranged from 4.751 tha-1 (G 14) to 8.504 tha-1. AMMIanalysisdepicted G31, G7, G30 and G19 as stable genotypes with better performances than the overall mean yield of the genotypes. AMMI also displayed that Ambo and Kulumsa and Ambo andJimma have close associations with minimum response to environment change, thus genotypes in these environments could reveal stable performances. GGE bi-plot displayed Holeta as ideal environment and thus considered useful both in discriminating the hybrids and representativeness as suitable environment forselecting superior genotypes. GGE bi-plot also displayed thatvarietyJibat, was closest to the ideal genotype may be considered as best hybrid whereas G29, G22considered desirable genotypes. Three homogeneous environments were identified based on GGE-Bi-plotanalysis;however, this subdivision pattern of homogeneous grouping of environments can only be considered as a suggestion as it is based exclusively on one-year MET dataset.

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