Mega-Environment Targeting of Maize Varieties using Ammi and GGE Bi-Plot Analysis in Ethiopia

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በቆሎ በኢትዮጵያ ከሚመረቱ የምግብ ሰብሎች መካከል በምርትና ምርታማነቱ ግንባር ቀደም ስፍራን የያዘ ሰብል ነው፡፡ የስብስን ምርታማነት ከሚደግፉ የተለያዩ መንስዔዎች ውስጥ በዋነነት ከፍተኛውን ቦታ የሚይዘት ከጥናትና ምርምር የተገኙ የተሻሻሉ ዝርያዎች በጊኑም ሁሉም ዝርያዎች   በበቆሎ አብቃይ ስነ-ምህዳሮች ላይ ተዘርተው በምርታማነታቸው ወጥነት የማያሳዩ መሆናቸው ይታወቃል፡፡ እንደየካባቢው የአየር ፀባይ፤ የአፈር ዓይነትና የዝናብ መጠን እንዲሁም የመሬት ከባር ወለል ከፍታ ልዩነት የተነሳ በምርታማነታቸው ለየካባቢው ተመራጭና ተመራጭ ያልሆኑ ዝርያዎችን መለየት ይቻላል፡፡ በዚህ ምክንያት ለተለያየ ዝርያዎች ምርታማነት ተስማሚና ወካይ የሆነ ስፍራዎችን ሊይቶ በማወቅ የትኛው ዝርያ በየትኛው ስፍራ ላይ ቢዘራ ሀለንትናዊ የአካባቢ ባሀሪያትን ተባብሶ ከፍተኛ ምርት ሊሰጥ ይችላል? እንዲሁም የትኛቹ ስፍራዎች በአየር ንብረት ተቀራራቢነት በጥቅል ተደምረው አንድ ዝርያ በወጥነት በሁሉም ስፍራ ዘርቶ ምርታማ የሚያደርጓቸውን አካባቢዎች ሊይቶ ለማወቅ ጥናቱ ተደረገ፡፡ ጥናቱ ለምርት በምርምር የተለቀቁ 19 ዲቃላ የበቆሎ ዝርያዎችን በማካተት ወይናደጋማና ደጋማ ስፍራዎች ላይ ተዘርተው የተለያዩ መረጃዎችን በማሰባሰብ እንዲጠናቀር ከተደረገ በኋላ ለጥናቱ ስኬት ከፍተኛ ትኩረት ተሰጥቶት ለውሳኔ እንደየመጠን ከየካባቢው የተሰበሰበ የዝርያዎቹ ምርት አግባብ ባላቸው ሳይንሳዊ ዘዴዎች እንዲሰ ተደረገ፡፡ በስሌቱ መሰረት ከዝርያዎቹ በአማካይ በሄክታር 4.47 (BH545) እስከ 7.49 (BH546) ቶን ምርት ተመዘበ፡፡ እንዲሁም በተደረገው ስሌት G14 እና G1 ተበለው የተለየ ዝርያዎች ለአዝበዣኞቹ የጥናቱ ስፍራዎች ተስማሚ እንዲሆኑ ቢታወቅም BH546 በሚባል ስያሜ የሚለየው ዝርያ በከፍተኛ ደረጃ ተመራጭ እንደሆነ ለመረገጥ ተችሷል፡፡ በሌላ በኩል E9 በተባለ ምህያር-ቃል የሚለይ ስፍራ በአብዛኛው ዝርያዎች ተመራጭ እንደሆነ ስሌቱ ሲያሳይ ፤ E1 የተባለው ግን ተመራጭ እንደልሆነ ታውቋል፡፡ ሆኖም ግን 11 የጥናት ስፍራዎች በሶስት ዋና ዋና ፤ እያንዳንዳቸው በዝርዎቹ ምርታማነት የጎላ ልዩነት በሚታይበትበው ወጥ ክፍሎች እንደተከፈሉ የስሌቱ ውጤት ለይቶ አሳይቷል፡፡ በዚህ መሰረት E9 በሚል ስያሜ የሚለየው ስፍራ በበዘችንትን እንደ አንድ ዋና ክፍል የተከፈለ ሲሆን በሁለተኛ ክፍል ውስጥ በጥቅል ዘጠኝ አካባቦች E1, E2, E3, E5, E6, E7, E8 እና E11 በአንድነት ተደመሩ፤ እንዲሁም E4 እና E10 በሶስተኛው ክፍል ውስጥ ተመደቡ፡፡ E3, E5 and, E7 በተባለ ምህያር-ቃል የተለየ ስፍራዎች ለዝርዎቹ ምርታማነት ወካይና ተመራጭ መሆናቸውን ጥናቱ አሳየ፡፡ ነገር ግን E4, E9 and E10 የተባሉ አካባቢዎች በውስን ስፍራዎች ውሰጥ ምርታማ የሚሆኑ ዝርዎችን መለየት የሚችሉ መሆናቸውን ጥናቱ ደረጋባል፡፡ በሌላ በኩል E8 and E11 የተባሉ ስፍራዎች የዝርዎችን ምርታማነትና ተመራጭነት በጉልህ ለማሳየት ምንም አስተዋፅዖ ያለበርከቱ መሆናቸውን ጥናቱ አሳይቷል፤ በመጨረሻም የዚህ ጥናት ውጤት ወገነት ያላቸው ሶስት ዋና ዋና ስነ-ምህዳራትን ለይቷል፤ ዝርዎች በምርታማነታቸው ተመራጭነት የሚኖራቸውንና የማይኖራቸውን ሊይተው የሚያሳዩ ስፍራዎችን ጠቁሟል እንዲሁም በምርታማነትና ለአብዛኛው አካባቢዎች በወጥነት ተስማሚነቱን የሚያሳይ ዝርያ ለይቶ አሳይቷል፡፡

Abstract

In multi-location experimental trials, test locations must be selected to properly discriminate between varieties and to be representative of the target regions. The objective of this study were to evaluate test locations in terms of discrimination ability, representativeness, and desirability, and to investigate the presence of mega-environments using AMMI and GGE models and to suggest representative environments for breeding and variety testing purposes. Among 19 maize varieties tested across 11 environments, mean grain yield ranged between 4.47 t/ha (BH545) to 7.49 t/ha (BH546). Both AMMI and GGE models identified G14 and G1 as desirable hybrids for cultivation because they combined stability and higher average yield. Nonetheless, as confirmed by GGE analysis BH546 was most closest to the ideal genotype hence, considered as best hybrid. Environment wise, E9 and E4 were the most stable and unstable test environments, respectively. The 11 test environments fell into three apparent mega-environments. E9

formed one group by its own, E1, E2, E3, E5, E6, E7, E8 and E11 formed the second group and E4 and E10 formed the third group. E3, E5 and, E7 were both discriminating and representative therefore are favorable environments for selecting generally adapted genotypes. E4, E9 and E10 were discriminating but non-representative test environments thus are useful for selecting specifically adapted genotypes. E8 and E11 were non-discriminating test environments hence little information about the genotypes. The results of this study helped to identify mega-environments, also representativeness and discriminating power of test environments better visualized with the GGE bi-plot model.

Introduction

Maize (*Zea mays* L.) is the world's most widely grown cereal and is the primary staple food in many developing countries. In Ethiopia, maize is one of the major cereals widely cultivated across diverse ecologies. These include lowland moist, lowland and highland moisture stress, mid altitude and highland sub-humid moist agro-ecologies. As each of these agro-ecologies are differing in altitudes, rainfall and soil properties, they possess their own characteristic limitations and opportunities revealed in production and productivity of maize varieties under the influence of prevailing weather conditions (LEGESSE *et al.*, 2012).

Under these heterogeneous environments, allocating a variety that can successfully adapted to a certain location or across locations is difficult due to the interaction effects of genotypes with the environment. In order to solve this problem, experimental research need to be carried out in multi-environment variety trials to identify and analyze the major factors that are responsible for genotype adaptation (De LACY *et al.*, 1996). In multi-location experiments the influence of environment is basically attached to the expression of complex characteristics and reveals high influence of environment. The result is changes in the relative behavior of the genotype in different environments. This phenomenon is called genotype by environment interaction (GEI) occurring due to differential response of genotypes to different growing conditions (BERNARDO, 2002). The GEI makes it difficult to select genotypes that produce high yield and that are more stable in breeding programs. This, of course, reduces the selection progress (YAN, *et al.*, 2000). A cultivar, to be commercially successful, it must perform well across the range of environments to which it is grown. The presence of GEI reduces the correlation between phenotype and genotype, and makes it difficult to judge the genetic potential of a genotype (SAMONTE *et al.*.2005)

Because of difference in cultivar ranking from place to place due to GEI, it is necessary to subdivide growing regions into several relatively homozygous mega-environments. A mega-environment is defined as a portion of a crop species growing region with fairly homogeneous environments that cause similar

genotypes to perform best. Such classification will enable breeders to breed and target adapted genotypes for each mega-environment (YAN *et al.*, 2007).

There are a number of statistical packages for effective analysis of yield data obtained from evaluation of genotypes across locations and targeting of genotypes into mega-environment. The additive main effects and multiplicative interaction model (AMMI) has been extensively applied to assess the stability of varieties (BETRAN *et al.,* 2003; BERTOIA *et al.,*2006; FAN *et a*l.,.2007) or to group test environments in the case of multi-environment variety trials (GAUCH and ZOBEL, 1997; TERASAWA JÚNIOR *et al.*, 2008; BALESTRE *et al.*,2009). Nevertheless, test location evaluation requires incorporating the genotype main effect (G) with genotype by environment interaction (GEI) as in the genotype main effect plus genotype by environment interaction (GGE) bi-plot method (YAN and KANG, 2003; YAN and HOLLAND, 2010). YAN *et al.*(2007) pointed out that the GGE bi-plot is the most appropriate type of bi-plot for mega-environment investigation, genotype evaluation and test location evaluation. YAN and TINKER. (2006) employed AMMI and GGE to target genotypes into mega-environment. They concluded the complementarities of both models and gave high emphasis on the role of GGE in mega-environment analysis and genotype evaluation.YAN *et al.* (2000) stated that GGE bi-plot is an effective visual tool in mega-environment analysis as it is able to capture more G + GE than the AMMI's bi-plot. EBDON AND GAUCH(2002) claimed that mega-environment classification based on AMMI model are virtually the same as that based on a GGE bi-plot. On the other hand YAN *et al.* (2007) claimed that GGE bi-plots are superior to AMMI bi-plots for showing mega-environments, even in case for which both methods happen to delineate the same mega-environment. SETIMELA *et al.*(2007) analyzed grain yield data of 35 early to intermediate maturing open-pollinated maize varieties (OPVs) for five seasons across 59 locations of the Southern African Development Community. The GGE bi-plot analysis of these data showed that ideal test environments could discriminate superior performing maize OPVs from poor ones, and identified six mega-environments in the target areas.

The GEI may be reduced using specific cultivars for each environment or using cultivars with wide adaptability and good stability or by stratifying the region under study in mega-environments with similar environmental characteristics, within which the interaction becomes insignificant (TERASAWA JÚNIOR *et al.,* 2008). Mega-environments are generally identified through the analysis of multiple-environment trial data for a diverse set of genotypes. The purpose of mega-environment analysis is to understand the GEI patterns within a target region in order to explore the feasibility of dividing the target region into meaningful mega-environments that permits the GEI (which causes specific adaptation) to be exploited to maximize the response to selection within mega-

environments, and increase the productivity of the target region (YAN *et al.*, 2011). Furthermore, understanding and identification of mega-environment results in heritability increase within relatively well-defined and predictable environment. It improves the efficiency of the testing and breeding program by focusing on the most promising material (ABDALLA *et al.*, 1996).

The application of AMMI and site regression GGE models for explaining GEI and analyzing the performance of genotypes and test environments have been very frequent among plant breeders in recent years. In Ethiopia, because of diverse agro-ecologies for maize production, multi-location varietal evaluations of maize are carried out strategically by dividing the country into four target environments: humid highland; humid midland, dry lowland and humid lowland. Consequently, yielding potential of a variety over multi-location conditions is mostly affected by interaction of genotype with environment, which results into unstable performance. Various studies have been conducted in Ethiopia to analyze the effect of G x E interaction on maize genotypes (MOSISA AND HABTAMU, 2008; GEZAHEGN *et al.*,2008; WOKIE *et al.*, 2013), however none of these studies used GGE bi-plot analysis method. Also limited scientific evidences are available to suggest whether the genotype by environment interaction observed in maize varietal trials can be exploited for genotype discrimination or avoided by categorizing target environment to specific mega-environments. The objectives of this study were 1) to evaluate test locations in terms of discrimination ability, representativeness, and desirability using AMMI and GGE bi-plot, and 2) to investigate the presence of mega-environments and to suggest representative environments for breeding and variety testing purposes.

Materials and Methods

Study Material. Nineteen maize varieties (single, three ways, and top cross hybrids) recommended for the different maize agro-ecologies of Ethiopia (Table 1) were evaluated across eleven environments in 2013/2014. The experimental sites include locations that are found in the mid-altitude and highland sub-humid agro ecologies and moisture stress areas in Ethiopia. Three production practices namely, maize sole, maize haricot bean intercropping and low-N sites were considered altogether as separate environments in order to address different on-farm maize growing conditions.

Experimental design and field layout. The experimental trial consisting of 19 genotypes were laid out in a randomized complete block design replicated three times. The plot size was two rows of 5.1m long with inter and intra row spacing of 0.75 and 0.30 m, respectively. All management practices such as cultivation, fertilization and weeding were done based on the recommendations for each test

environments. Data for all relevant agronomic traits were collected, but only plot yield data converted to ton/ha was subjected to statistical analysis.

Table 1. Maize varieties evaluated across 11 environments in 2013

Genotype	Source	Recommendation domain	Year of release
30G19 (G1)	Dupont Pioneer	Mid-altitude	2006
BH140 (G2)	EIAR-Bako	Mid-altitude	1988
BH540 (G3)	EIAR-Bako	Mid-altitude	1995
BH543 (G4)	EIAR-Bako	Mid-altitude	2005
BH546 (G5)	EIAR-Bako	Mid-altitude	2013
BH547 (G6)	EIAR-Bako	Mid-altitude	2013
BH660 (G7)	EIAR-Bako	Mid altitude to transitional highland	1993
BH661 (G8)	EIAR-Bako	Mid altitude to transitional highland	2011
BH670 (G9)	EIAR-Bako	Mid altitude to transitional highland	2002
BH542 (G10)	EIAR-Bako	Mid-altitude	2002
BH545 (G11)	EIAR-Bako	Mid-altitude	20 2008
MH130 (G12)	EIAR-Melkessa	Moisture stress2012	2 2012
MH138 (G13)	EIAR-Melkessa	Moisture stress	2012
P3812W (G14)	Dupont Pioneer	Mid-altitude	2011
SC403 (DUMA) (G15)	Seed-co	Mid altitude	2012
SC627 (G16)	Seed-co	Mid-altitude	2006
AMH760Q (G17)	EIAR-Ambo	Transitional highland to true high highland	2012
Jibat (G18)	EIAR-Ambo	Transitional highland to true high highland	2009
Wenchi (G19)	EIAR-Ambo	Transitional highland to true high highland	2008

Table 2. Environmental sites, designation, altitudes and rainfall

Environment	Environ. code	Latitu	Longit	Altitu. (m)	Ann. R.fall (mm)	Temperature ^{0}C Min.	Max.
Bako intercrop†	BKINT (E1)	9º 6´	37º 09´	1650	1200	13.1	28.4
Bako sole ‡	BKSL (E2)	9º 6´	37º 09´	1650	1200	13.1	28.4
Bako low nitrogen*	BKLN (E3)	9º 6´	37º 09´	1650	1200	13.1	28.4
Hawassa intercrop	AWINT (E4)	7º 04´	38º 31´	1700	1100	13.0	27.4
Hawassa sole	AWSL (E5)	7º 04´	38º 31´	1700	1100	13.0	27.4
Arsi-Negelle sole	ANSL (E6)	7º 09´	38º 35´	1900	850	12.0	27.0
Pawe intercrop	PWINT (E7)	11º 12´	36 º 20´	1550.	1250	16.36	38.5
Pawesole	PWSL (E8)	11º 12´	36 º 20´	1550.	1250	16.36	38.5
Melkessa sole	MKSL (E9)	8º 24''	39 º 20´	1600.	800	10.8	33.0
Haramaya sole	HRSL (E10)	9º 6´	48 º8'	2020	900	18.0	31.4
Tepi sole	TPSL(E11)	7º 3'	35º .0'	1250	1500	16.0	30.0

Intercropping =†; Low N =; Sole cropping =‡*

Statistical analysis

Following single site ANOVA for grain yield, the combined ANOVA and AMMI analysis of variance were done   with genotypes being considered as fixed effects and replication with in environments being random mode to determine the effect of differences between genotypes, across locations and to estimate G X E interaction through stability analysis using AMMI analysis model (ZOBEL *et al.,*

1988). The data were analyzed using CROPSTAT version7.2 software (IRRI, 2009) and AMMI bi-plot were constructed using the MATMODEL(GAUCH, 1997). The results of the AMMI model analysis were interpreted on the basis of tables and graphs that showed the main and first multiplicative axis term (PC1) of both genotypes and environments.

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 *et al.*, 2000; YAN, 2002).Using GGE bi-plot ranking of cultivars 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 locations and the average location, and the distance between the positions of a location and the "ideal" test locations were used as measures for the location discrimination ability, representativeness, and desirability indices for each test location. Graphs showing " which won where" pattern to reveal the presence or absence of different mega-environments were generated in GGE bi-plot (YAN AND RAJCAN, 2002).

Result and Discussion

AMMI Analysis

Combined ANOVA and AMMI analysis of variance for grain yield (Table 3) showed highly significant ($p < 0.01$) difference among environments (E), genotypes (G) and genotype by environment interaction (GE). Environments posed significant effect on grain yield, which explained 72.2 % of the total variation (G + E + GE) whereas the GE interaction contributed 15.7 % of the variation. Only 12.1% of the total variation was attributed to the genotypic effect. Large sum of squares for environments indicated that the contribution of environmental effect was much higher than the effect of genotype for the variation of grain yield observed. This is attributed to diverse environmental conditions in maize growing areas in Ethiopia.YAN (2002) indicated that typically, E explains most (up to 80% or higher) of the total yield variation, while G and GE are usually small. This is specifically true to traits like grain yield that has low heritability (BRAR *et al.*, 2010). The significant interactions of genotypes x environments suggest that grain yield of maize hybrids of the current study varied across test environments. The larger magnitude sum of squares of GXE compared to the effects of genotypes indicating larger differences in genotypic response across environments and previous researches had shown similar results of differences in grain yield of maize genotypes across locations (BUTRON *et.al.*, 2004; BABIC *et.al.*, 2011; BADU-APRAKU *et a*l., 2011; ADU *et al.*,2013; WORKIE *et al.*, 2013).

Also results from analysis of multiplicative effects (Table 3) indicated that the AMMI model with three IPCA axes captured 71.6 % of the sum of squares of the GE interaction and left the residual of 28.4. The first principal component axis (IPCA1) accounted for 37.3 % of the GE interaction sum of squares. The IPCA 2 and IPCA3 were also significant and accounted for 23.6% and 10.5% of the GE interaction sum of squares, respectively. This indicates that the maize varieties and the nine environments were significantly different from one another. Such result is in conformity with other studies that reported largest proportion of total variation in multi-environment trials due to location, whereas genotype and GXE source of variation are relatively small (BADU-APRAKU *et al.*,2011; ADU *et al.*, 2013).

Grain Yield and Stability

Mean grain yield among the 19 maize varieties ranged from 4.47 t/ha for BHQY545 to 7.49 t/ha for BH546. According to AMMI analysis G19 (IPCA=-0.00095) and G4 (0.0104) showed the least GE interaction as measured by first IPCA which took 37.1% of the GE interaction sum of square and were the most stable in across all environments, however the yield performance of G19 was a little bit above average and of G4 was below average. On the other hand G6 (IPCA=-1.28409) followed by G5 (-1.1168) had the largest interaction and thus, the most variable hence indicating their specific adaptation to certain environments. Both these hybrids showed much better yield performances than the rest of the hybrids (Table 4).

Environment wise, both the highest and the lowest mean grain yields were recorded at BKSl (8.30 t/ha) and BKLN (2.54 t/ha). AMMI analysis also showed that the least first IPCA value of -0.06133 was recorded for MKSL while the highest IPCA value (I.6794) was observed for AWSL (Table 4). Despite its below average yield, low interaction of the climatic conditions in MKSL, may enable it to be more stable and desirable environment for evaluating the performance of the maize genotypes whereas AWSL was found to be most unstable environment. According to Yan et al.(2000) for environment to become desirable should have more discriminating ability of the genotypes in terms of genetic main effects and high stability index, which implies more representativeness of the overall environment.

Table 3. AMMI analysis of variance of grain yield of 19 maize varieties grown across 11 environments in 2013

Source	DF	SS	MS	% TSS	% treatments	%GXE
Total	626	3659.8	5.85			
Treatments	208	3056.7	14.70**	83.5		
Genotypes	18	369.4	20.52**		12.1	
Environment	10	2208.6	220.86**		72.2	
Block	22	103.3	4.69**			
GXE	180	478.7	2.66**		15.7	
IPCA 1	27	179.7	6.65**			37.5
IPCA 2	25	112.8	4.51**			23.6
IPCA 3	23	50.2	2.18**			10.5
GXE residual	105	136.1	1.30**			28.4
Error	396	499.96	1.26	16.5		

** indicates significance at 1% level of significance

In bi-plot analysis the relative magnitude and direction of genotypes along the abscissa and ordinate axis 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 (EBDON AND GAUCH, 2002). In Figure 1 of AMMI bi-plot, 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. G5 and G6, were the highest yielders, and G8 and G18 were relatively above average in yield but all of them were unstable indicating that they are responsive to environmental change. G14, G1 and G19 were the most stable and above average yielding genotypes indicating less interaction of these varieties with the environment to hinder the yield as shown in IPCA score of near zero (Table 4) suggesting these cultivars can be cultivated in any of the eleven environments. Also AMMI bi-plot graph revealed E2 and, E1 as the highest yielding but unstable environments. E8 and E10 were above average in yield and relatively more stable as compared to the rest of the environments except E9 which was the most stable but below average in yield.

Table 4. Mean grain yield of 19 released maize varieties in each of 11 environments and across environments and first IPCA score for genotypes and environment

Genotype	BKINT	BKSL	BKLN	AWSL	AWINT	ANSL	PWINT	PWSL	MKSL	HRSL	TPSL	Mean	First IPCA
30G19	8.14	9.77	3.19	7.75	6.52	7.05	7.35	9.17	6.77	8.76	3.42	7.03	-0.0142
BH140	7.41	8.01	2.87	5.34	3.85	4.62	6.27	7.13	4.92	6.20	2.32	5.51	0.9763
BH540	7.79	8.02	2.60	4.76	3.75	4.30	5.53	7.28	6.97	6.65	2.36	5.66	0.7207
BH543	7.89	8.07	1.83	6.28	6.38	5.86	5.07	7.47	7.77	7.17	2.23	5.90	0.0104
BH546	9.74	9.47	3.71	6.08	8.18	10.28	5.62	8.42	6.64	9.43	4.30	7.49	-1.1168
BH547	9.02	10.78	2.75	7.37	6.96	10.69	6.36	8.85	6.91	8.38	2.59	7.29	-1.2841
BH660	7.78	8.33	2.47	6.75	4.75	5.84	5.85	7.17	5.54	8.70	3.55	5.88	0.1943
BH661	10.69	8.76	3.05	7.69	5.32	8.97	5.50	7.99	5.43	8.78	3.35	6.75	-0.9063
BH670	8.40	9.27	2.18	6.85	4.86	6.76	5.89	7.16	4.54	8.73	2.06	6.18	0.1894
BHQP542	7.00	8.01	1.58	5.81	5.54	4.71	4.42	6.50	4.74	7.95	2.99	5.50	0.6004
BHQPY545	5.67	6.51	1.78	5.12	4.24	3.90	5.88	6.37	6.84	6.16	2.05	4.47	0.5747
MH130	4.76	4.38	1.80	5.52	4.63	6.74	5.07	5.87	5.76	7.01	1.12	4.94	0.2594
MH138	7.51	6.72	2.41	6.55	5.05	5.64	4.76	5.68	4.33	8.40	3.01	5.65	0.5010
P3812W	10.06	9.44	3.53	7.86	8.03	6.55	6.99	8.65	5.97	9.43	2.66	7.17	0.0279
SC403(DUMA)	7.17	7.34	2.34	5.65	5.21	5.89	6.07	6.73	5.51	6.49	2.11	5.82	0.6079
SC627	8.88	9.88	2.02	6.49	5.42	4.27	6.45	8.03	6.23	8.48	2.84	6.08	0.0887
AMH760Q	8.13	8.59	2.99	6.80	5.52	8.44	4.47	7.23	5.76	8.25	2.91	6.09	-0.8935
Jibat	8.47	8.56	2.91	7.17	6.65	7.41	4.46	6.09	7.77	9.02	3.09	6.42	-0.5372
Wenchi	7.55	7.87	2.27	6.69	6.24	6.85	5.48	6.84	6.25	9.89	2.79	6.34	0.0009
Mean	8.00	8.30	2.54	6.45	5.64	6.57	5.66	7.30	6.03	8.10	2.72	6.11	
CV	11.77	11.12	39.19	20.87	22.01	20.13	18.31	9.30	20.14	16.89	26.75		
First IPCA	-0.4437	-0.3977	0.379	1.6794	-0.3891	-1.8544	0.7945	0.1633	-0.0691	-0.2112	0.3487		

Furthermore, AMMI bi-plot grouped the test environment into three distinct groups: high yielding, average yielding and low yielding environments. Generally, E1, E2, E8 and E10 were high yielding environments despite their difference in stability. E1 and E2 were less stable than E8 and E10. For E2, the present results warrant it to be a site where genotypes express their maximum potential for selecting high performing genotype. E4, E5, E6, E7 and E9 can be categorized as average yielding environment but the stability varies in the group ranging from very stable like E9, with IPCA score of - 0.0691, to unstable like E4 and E6 with IPCA score of 1.6794 and -1.8544, respectively (Table 4). E3 and E11 appeared as stably and low yielding environments. Since E3 is managed low N environment created through depletion of N at Bako, the result and bi-plot mapping is acceptable. E8 and E10 were above average in yield and relatively more stable as compared to the rest of the environments except E9 which is the most stable but below average in yield.
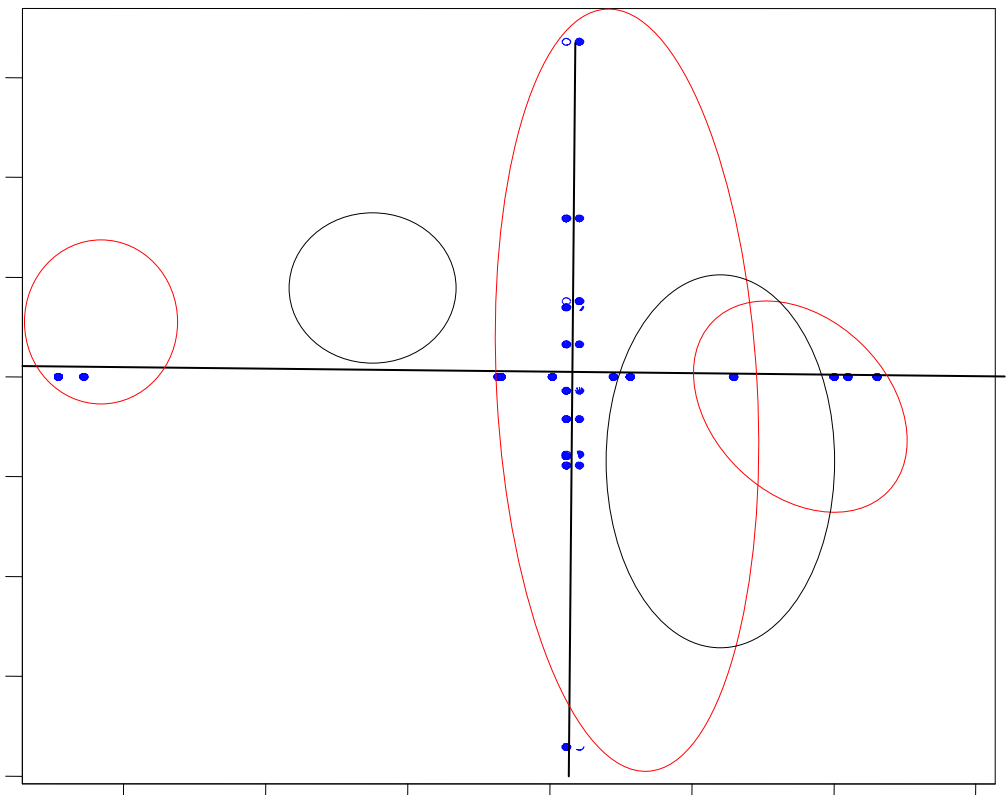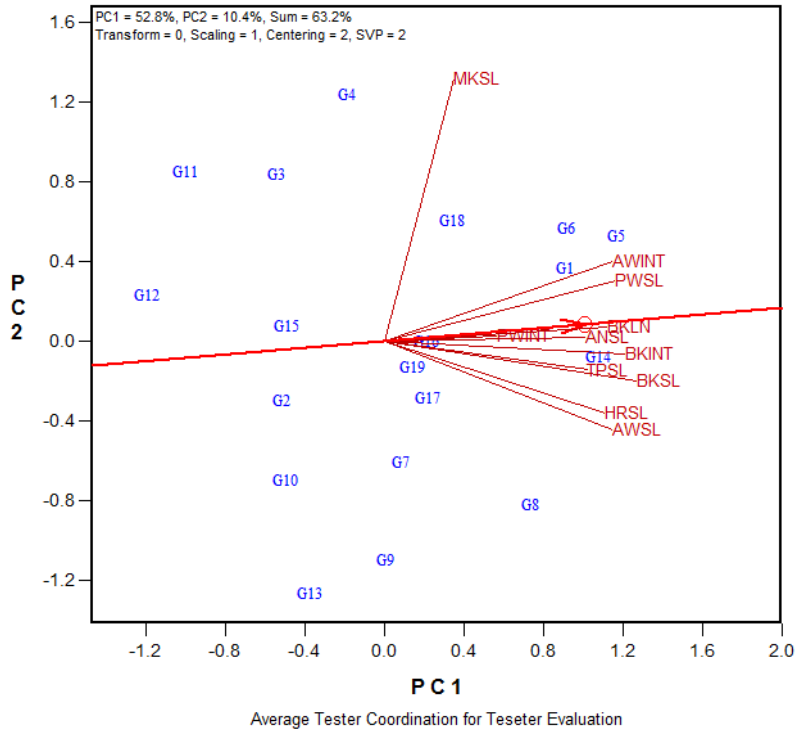

Figure 1. Bi-plot of AMMI analysis based on phenotypic mean of 19 maize genotypes evaluated in 11 environments in 2013/ 2014 harvest year. The 19 genotypes are indicated in block letter G following number from 1 to19 and the 11 environments indicated by E following number from 1-11.

GGE bi-plot analysis

The GGE refers to the genotype main effect (G) plus the genotype-by-environment interaction (GE), which are the two sources of variation of the bi-plot model (YAN *et al.*, 2000, 2007). BALESTRE *et al.* (2009) found that the GGE bi-plot method to be superior to the AMMI1 graph due to more retention of GE and G + GE in the graph analysis. GGE bi-plot best fits for which-won-where pattern analysis, genotype, and test environment evaluation (YAN *et al.*, 2007). The bi-plot is also used for assessment of ideal genotype and test location in multi-environment data provided that a given data set has a high correlation between PC1 and G main effects (YAN *et al.*, 2000; CROSSA *et al.*, 2002).

Relationship among test environments: GGE bi-plot which depends on environment focused scaling was portrayed (Fig. 2) to estimate the pattern of environments and visualize the relationship between environments. Lines were drawn to connect the test environments to the bi-plot origin known as environment vector. The cosine of an angle between two environments is used to approximate the relation between them where an acute angle signifies positive correlation between any environments. An obtuse angle shows negative correlation and right angle indicates no correlation between any two environments (YAN, AND TINKER, 2006). As is shown in Figure 2, the test environments were grouped into two except MKSl. The other test environments vectors formed an acute angle of varying degree among each other. MKSL and AWSL, MKSL and HRSL were negatively correlated as the result of wide obtuse angle that indicates strong crossover GE, implying that the GE is moderately large. The result is consistent with the current agro-ecology classification of the test environments for maize research followed by the National Maize Research Program of Ethiopia. MKSL is the only site included from the low moisture maize agro-ecology in this study and thus it was singled out from other environments. According to YAN AND TINKER (2006) and YAN *et al.* (2007), the presence of close associations among test environments suggests that the same information about the genotypes could be obtained from fewer test environments, and hence the potential to reduce testing cost. Nevertheless, consistent positive correlation between years and locations should be recorded to respond to indirect selection between testing environments.

PC1 = 52.8%, PC2 = 10.4%, Sum = 63.2%
Transform = 0, Scaling = 1, Centering = 2, SVP = 2

Average Tester Coordination for Teseter Evaluation

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Figure 1. Environment-vector view of the GGE-bi-plot showing relationship among 11 testing environments where MKSL= Melkasa sol, AWINT= Awasa intercrop, PWSL= Pawe sol, BKLN= Bako low-N, ANSL= Arsi-Negele sol, BKINT= Bako Intercrop, TPSL= Tape sol, BKSL= Bako sol, HRSL, Haramaya sol, AWSOL= Hwasa sol.

Discriminating and representativeness ability of environment: Discriminating power and representativeness view of the GGE bi-plot is an important measure of testing environments used to identify environments that effectively distinguish superior genotypes in a group of environments. Fig 3 shows ranking of testing environments based on GGE bi-plot analysis. The concentric circles on the bi-plot help to visualize the length of the environment vectors, which is proportional to the standard deviation within the respective environments, is a measure of the discriminating ability of the environments and also indicates the representativeness of the environment (YAN AND KANG, 2003; YAN AND TINKER, 2006).

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 (YAN *et al.,* 2001)

Accordingly, among the 11 environments MKSL, with the long vector was designated as the most discriminating while PWINT with the short vector was the least discriminating. With regard to representativeness, PWINT, BKLN and ANSL were more representative whereas, MKSL was the least representative. AWSL and HRSL were in between. The discriminating but non-representative test environments of MKSL, AWSL and HRSL are useful for selecting specifically adapted genotypes and serve for discarding unstable genotypes if the target environments can be divided into mega-environments They are useful for culling unstable genotypes if the target environment .is a single mega-environment (YAN *et al.,* 2007). Non-discriminating test environment, PWINT and TPSL , with very short vectors, are less useful testing environments as they are providing little discriminating information about the genotypes. According to YAN *et al.* (2007) test environment that are consistently non-discriminating (non-informative) provide little information on the genotype and, should not be considered as test environment. Test environments that are both discriminating and representative (BKSL PWSL, AWINP) are favorable environments for selecting generally adapted genotypes. According to Yan and Kang (2003) , location which has high discriminating ability and high representativeness tends to easily differentiate the performance among genotypes and suggested that the selected genotypes have the desired adaptation in that location, respectively. This findings agree with the work of SALEEM *et al.* (2016) who employed GGE bi-plot for identifying locations that optimized cultivar performance and for making better use of limited resource available for testing program.
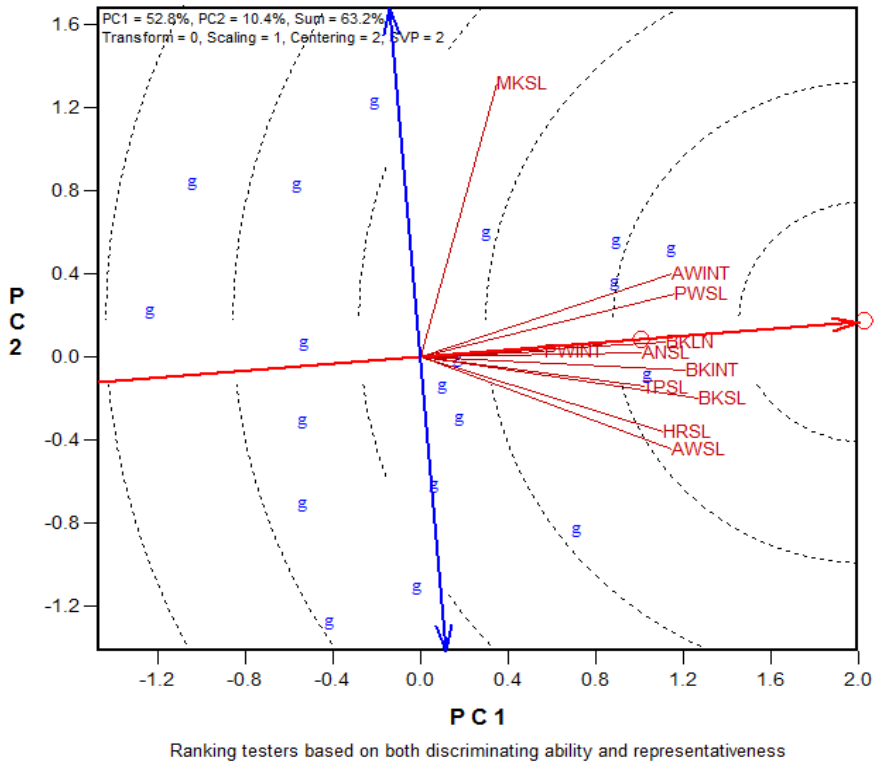
Figure 2. GGE bi-plot showing discriminating ability and representativeness of test environments

Ranking genotypes relative to the ideal genotype: An ideal genotype is defined as one that is the highest yielding across test environments and is absolutely stable in performance. An ideal genotype may not exist, however it can be used as a reference for genotype evaluation (YAN AND KANG, 2003). In Fig. 4, the hypothetical ideal genotype is shown as a small circle on the axis of average genotype yield. To use the ideal genotype as the measurement center, concentric circles were drawn in the bi-plot to graphically determine the distance between the test genotypes and the ideal one. According to GGE bi-plot a genotype that is located at the center of the circles or is the genotype closest to the hypothetical genotype is considered as superior genotype with high grain yield and good yield stability. G5 was the closest to the hypothetical ideal genotype and therefore identified as the best and G14, G6, G1 in the second order desirability category of maize hybrids. G11 and, G12 were positioned far away from it and thus not in the ideal hybrid category. The relative contributions of stability and mean grain yield for the identification of desirable genotype in this study following the GGE bi-plot procedure of ideal genotype was applied to identify best varieties by different researchers in crops like rice (SAMONTE *et al.*, 2005), barley (DEHGHANI *et al.*,2006) and, wheat (AHMADI *et al.*, 2012; NAROUI RAD *et al.*,2013).
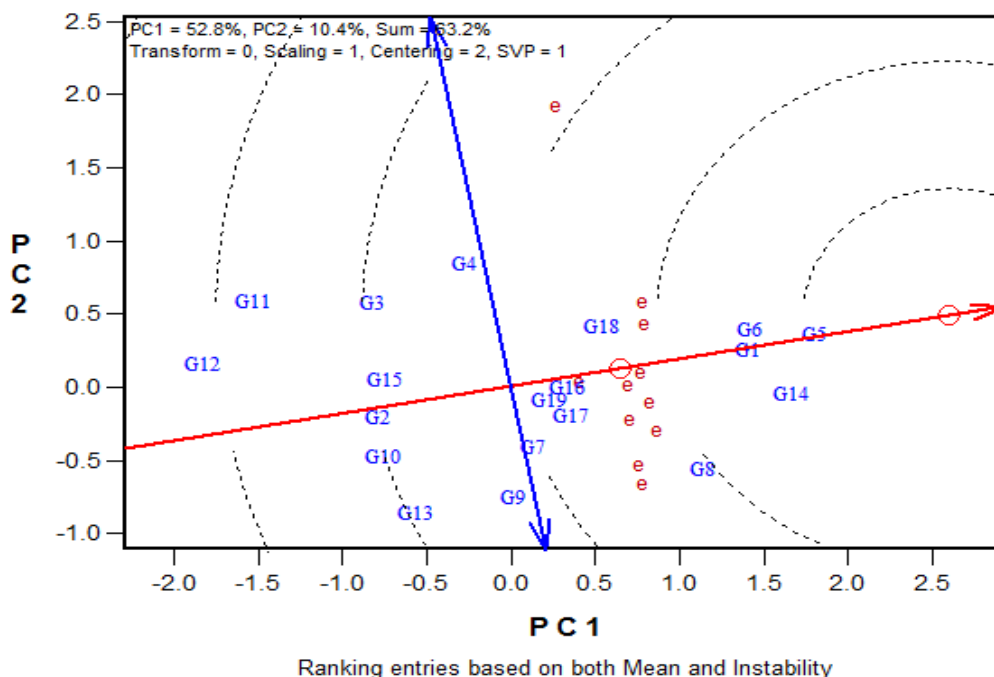
Ranking entries based on both Mean and Instability

Figure 3 GGE bi-plot indicating ranking of 19 tested genotypes based on mean and instability

Mega environment Identification: The visualization of "Which won where?" pattern is important for searching different mega-environments in a country or region. It is important because evaluation of test locations and genotypes is most useful when conducted within mega-environments (YAN *et al.*, 2007). The concept of mega-environment was proposed and defined as a portion of the growing region which is homogenous enough to lead genotypes to perform similarly (GAUCH AND ZOBEL, 1997), or as a group of geographical locations where the same or similar cultivars that performed the best across years (YAN AND RAJCAN, 2002).

The existence of mega-environment is justified by different genotypes performing best in different test locations, clear crossover GEI, and joint analysis of multiple-environment trial data (GAUCH AND ZOBEL, 1997; YAN AND KANG, 2003).The polygon view of the GGE bi-plot (shown in figure 5) indicates the best genotype(s) in each environment and groups of environments (YAN AND HUNT, 2002). Also, the polygon view of a GGE-bi-plot(in figure 5) explicitly displays the which-won-where pattern and is helpful to visualize and interpret the pattern of GEI recorded in this study. The polygon is divided into seven sectors, but the 11 environments fall into three of them. Therefore, the analysis indicates the existence of three mega-environments namely the G4-winning niche

(MKSL- low moisture stress regions following the current maize agro-ecology classification) , and G5 and G14-winning niche (AWINT, PWSL, BKSL, ANSL, PWINT, BKINT, and TPSL-Mid-altitude sub-humid region following the current classification). The third group included AWSOL and HRSl, (mid-altitude and-transition highland) with no winning genotypes. The three other corner genotypes, G11, G12 and G13, were the poorest-yielding. These genotypes were located far away from all the test locations, reflecting the fact that they yielded poorly at each location. Also, those genotypes within the polygon were less responsive to location than the corner genotypes. This result is in para with the findings of several authors who reported access to delineate mega-environments using AMMI and GGE bi-plot models(YAN *et.al.*, 2007; OLIVEIRA *et al.*,2010; CHOUKAN, 2011,).
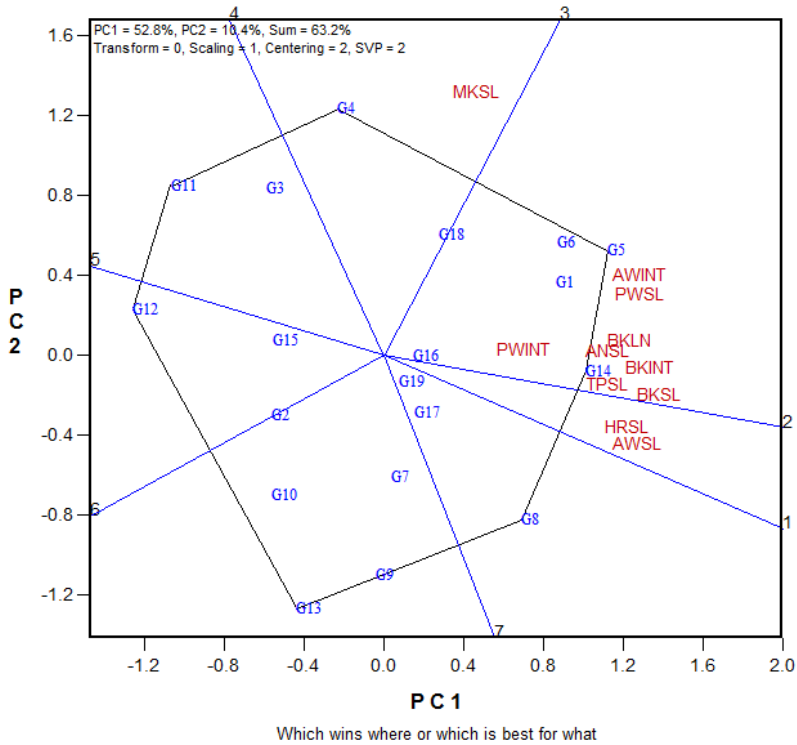

Figure 4. Polygon views of the GGE bi-plot based on symmetrical scaling for which won where pattern for 19 maize genotypes and 11 locations.

Conclusion

The result of the current study indicated very high variation in grain yield across test locations. Among the 11 test locations, three distinct mega-environments were identified. Melkassa, Hawassa, and Haramaya were discriminating but non-representative test environments useful for selecting specifically adapted genotypes Pawe-intercrop and Tepi, were non-discriminating less useful environments. Bako sol, Pawe sol and Hawassa-intercrop were both discriminating and representative favorable environments for selecting generally adapted genotypes. G5 was closest to the ideal genotype may be considered as best hybrid, whereas G1, G6 and G14 were desirable and stable genotypes as revealed by GGE bi-plot analysis. On the other hand AMMI bi-plot depicted G14, G1 as the higher and G19 above average yielding stable genotypes. In general analyzing the two components of the bi-plot graphs, the conclusion was drawn that the best genotypes, considering adaptability and stability, were hybrids , G14 and G1 , for being among the most stable and high yielding hybrids. GGE-bi-plot have better defined mega-environments and varieties that optimize performance in the mega- environments.

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