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Genotype X environment interaction of maize (*Zea mays* L.) across North Western Ethiopia

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A study was conducted at Northwestern Ethiopia, during 2010 main cropping season. Fifteen maize genotypes were evaluated at four locations that differ in soil type, altitude and mean annual rainfall. The experiment was laid out in a randomized complete block design with three replications. Stability parameters that are useful tools for identification of genotypes with specific and wide adaptations, and contrasting the role played by genotype, environment and G x E interaction in multilocational variety trials were considered and analyzed. The highly significant G x E interactions indicated that genotypes performance was inconsistent across testing locations and need to be tested in several locations in order to select stable genotypes. Jibat-851, Wonchi and BHQPY-545 exhibited high mean grain yield across environments and average responsiveness with high degree of stability indicating general adaptability and thus can be recommended for north western Amhara region and for areas with similar environments. The best genotype with respect to location Adet was Gibe-1 while Wonchi was the best genotype for Merawi area. Phb-3253 performed well at Motta, while Phb-30G19 and Jibat-851 performed well at Finoteselam. Therefore, these genotypes can be recommended according to their specific adaptation area.

Key words: Genotype by environment interactions, grain yield, maize, stability.

INTRODUCTION

Maize (*Zea mays* L.) belongs to the grass family Poaceae and tribe Maydeae. The maize plant has characteristics of wide adaptability in the different ranges of growing conditions. Thus, it has gained adaptation and productivity in all continents through introductions and breeding. The genetic diversity of maize, being an out crossing crop, is very broad for conservation and utilization in breeding programmes. Maize landraces exhibit significant morphological variation and genetic polymorphism and are grown from sea level to 3800 m. Maize is one of the world's three most important cereals along with wheat and rice. Maize is currently produced on nearly 100 million hectares in 125 developing countries and is among the three most widely grown crops in 75 of those countries and its global production is estimated to be over 800 million tons per year. Although much of the world's maize production (approximately 78%) is utilized for animal feed, human consumption in many developing and developed countries is steadily increasing. For example, maize is the most important cereal crop for food in sub-Saharan Africa and Latin America. The growing demand for food consumption in developing countries alone is predicted to increase by around 1.3% per annum until 2020. Between now and by 2050, the demand for

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Table 1. Description of testing locations.

Location	Altitude (m.a.s.l)	Annual rainfall (mm)	Soil type	Global position	
				Latitude	Longitude
Adet	2240	1331.8	Nitosol	11°16`N	37°29`E
Merawi	2000	1400	Alfisol	NA	NA
Motta	2470	1012.6	Nitosol	11°20`N	37°88`E
Finoteselam	1935	950	Nitosol	10°67'N	37°11'E

maize in the developing world will double.

In Ethiopia, cereals account for about 82.34% of the annual national crop production. Maize ranks first in total production and yield per unit area and second in area coverage among all the cereals. It is largely produced in western, central, southern and eastern regions (CSA, 2010). Maize research has advanced from landraces to varieties, to maize hybrids: double cross, three-way cross and single cross, and recently transgenic maize hybrids. The optimized use of adapted and exotic germplasm in various production environments is a key to the continued success in increasing grain yield and other trait-specific products: green ear, forage, oil, protein, starch, etc. *Ex situ* maize gene banks have a role in supporting the production of breeder gene pools with unique genetic diversity.

Maize improvement in Ethiopia started half a century ago (Benti, 1988). During the late 1960s and early 1970s, several promising genotypes of East African origin were introduced and evaluated at different locations. These resulted in the recommendation of several maize genotypes for the maize growing regions of the country. Through time, most of these genotypes have been replaced by locally developed and better adapted genotypes. But now a day increased private-sector participation in the maize seed industry has been accompanied by greater concentration (Rashid et al., 2001). However, the changing environmental conditions affect the performance of maize genotypes which requires a breeding programme that needs to take into account the consequences of environment and genotype interaction in the selection and release of improved genotypes. Therefore, crop breeders have been striving to develop genotypes with superior grain yield, quality and other desirable characteristics over a wide range of environmental conditions. Genotype x environment (G x E) interaction is one of the main complications in the selection of broadly adapted varieties in most breeding programmes. Numerous studies have shown that a proper understanding of the environmental and genetic factors causing the interaction as well as an assessment of their importance in the relevant G x E system could have a large impact on plant breeding (Magari and Kang, 1993).

Ethiopia is a country of great environmental variation (EMA, 1988). Where environmental differences are great, it may be expected that the interaction of genotypes with environment will also be great. As a result, one cultivar may have the highest yield in one environment, while a second cultivar may excel in others. This necessitated the study of genotype by environment interaction to know the magnitude of the interactions in the selection of genotypes across several environments besides calculating the average performance of the genotypes under evaluation. Under Ethiopian condition, various studies have been conducted to analyze the effect of G x E interaction on the Ethiopian maize genotypes (Wende, 2003; Gezahegn et al., 2008; Mosisa and Habtamu, 2008; Solomon et al., 2008; Muluken, 2009). However, the changing environmental conditions, the expansion of maize to new agro-ecologies coupled with inadequate maize genotypes available for the different agro-ecologies necessitate a rigorous and continuous G x E study. Moreover, information on the effect of genotype, environment and their interaction on yield of maize under diversified agro-ecologies of northwestern Ethiopia is limited. Therefore, the study was undertaken to evaluate the stability and adaptability of fifteen maize genotypes in the northwest Ethiopia by using different statistical models.

MATERIALS AND METHODS

Description of locations

The study was conducted during the 2010 main cropping season at four locations: Adet, Merawi, Finoteselam and Motta. These locations represent the varying agro ecologies of the major maize growing areas in North West part of Ethiopia (Table 1).

Experimental materials

Fifteen maize genotypes obtained from Bako Agricultural Research Center; Pioneer Hibrid International, PLC office in Addis Ababa and Ambo Crop Protection Research Center – Highland Maize Research Project were included in the study. The experiment was laid out using randomized complete block design with three replications. Each plot consisted of four rows with row length of 3 m. The distance between rows was 75 cm and between plants within the rows was 30 cm. The spacing between replications was 1.5 m. Two seeds were planted per hill and then thinned to one plant per hill. To reduce border effects, data were recorded from the two central rows of each plot. Other management practices like fertilizer

Table 2. Description of fifteen maize genotypes with their agro-ecological adaptations and some agronomic traits.

Genotypes	Year of release	Altitude (m)	Rain fall (mm)	Plant height (cm)	Ear placement (cm)	Days to maturity	Yield (qt/h)	
							Research station	Farmers field
BH-660	1993	1600-2200	1000-1500	255-290	145-165	160	90-120	60-80
BH-540	1995	1000-2000	1000-1200	240-260	110-120	145	80-90	50-65
BH-543	2005	1000-2000	1000-1200	250-270	140-150	148	85-110	55-65
BHQPY-545	2008	1000-1800	1000-1200	250-260	120-140	144	80-95	55-65
BH-670	2001	1700-2400	1000-1500	260-295	150-165	165	90-120	60-80
BHQP-542	2001	1000-1800	1000-1200	220-250	100-120	145	80-90	50-60
Wonchi	2005	1800-2500	1000-1200	205-225	105-125	175	70-80	55-65
Argene	2007	1800-2600	1000-1200	220-235	120-130	183	80-120	60-80
AMH-851	2009	1800-2600	1000-1200	220-235	120-130	178	80-120	60-80
Horra	2005	1800-2400	1000-1200	200-215	100-120	170	60-70	40-45
Gibe-1	2000	1000-1700	1000-1200	240-260	130-140	145	60-70	40-45
30H83	2001	1500-1900	NA	NA	NA	NA	NA	NA
Phb30G19	2006	1000-2000	800-1200	274	134	162	70-110	65-80
Phb30D79	2008	1000-2000	800-1200	283	140	156	80-97	66-75
Phb-3253	1995	1000-2000	NA	NA	NA	NA	NA	NA

NA= not available.

application were done as recommended for each location (Table 2).

Statistical analysis

Single site analysis of variance for grain yield was done with the PROC ANOVA procedure in SAS software with genotypes being considered as fixed effects and replication within environment being as random effect. Least significant different (LSD) was used for mean separation. Grain yield was transformed using square root transformation as variances across locations had no homogeneity. Ratio and Bartlett's test were made for grain yield used to assess homogeneity of error variances prior to combine analysis over locations and then grain yield was transformed using square root transformation as variances across locations had no homogeneity. The combined analyses of the variance across locations was done using PROC GLM model of SAS program with genotypes being considered as fixed effects and replication with in environments being random mode in order to determine the effect of differences between genotypes, across locations, among locations and also to determine whether their interaction was significant. Genotype x environment interaction was quantified using the most common procedure; that is, pooled analysis of variance, which partitions the total variance into its component parts (genotype, environment, genotype x environment interaction and pooled error). Different stability models were performed using AGROBASE20 computer programm (Agrobase, 2000):

Shukla's stability variance (σ^2i)

Shukla (1972) defined the stability variance of genotype *i* as its variance across environments after the main effects of environmental means have been removed. Since the genotype main effect is constant, the stability variance is thus based on the residual (*GEij+ eij*) matrix in a two-way classification. The stability statistic is termed "stability variance" ($\sigma^2 i$) and is estimated as follows:

$$\sigma^2_i = \frac{1}{(G-1)(G-2)}[G \quad (G\text{-}1) \quad \sum_j (yij - yi - yj + y..)^2 - \sum_i \sum_j (yij - yi - yj + y..)^2$$

Where: Y_{ij} is the mean yield of the i^{th}genotype in the j^{th}environment, Y_j is the mean of the genotype *i* in all environments, Y_j is the mean of all genotypes in j^{th}environments and *Y*... is the mean of all genotypes in all environments. A genotype is called stable if its stability variance (σ^2_i) is equal to the environmental variance (σ^2_e) which means that σ^2_i =0. A relatively large value of (σ^2_i) will thus indicate greater instability of genotype (Shukla, 1972).

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Where: *Yij* is the mean yield of the i^{th} genotype in the j^{th} environment, *Yj* is the mean of the genotype *i* in all environments, *Yj* is the mean of all genotypes in j^{th} environments and *Y*... is the mean of all genotypes in all environments. A genotype is called stable if its stability variance ($\sigma^2 i$) is equal to the environmental variance (σ^2_e) which means that $\sigma^2 i$ =0. A relatively large value of ($\sigma^2 i$) will thus indicate greater instability of genotype *i.e.* as the stability variance is the difference between two sums of squares, it

can be negative, but negative estimates of variances are not uncommon in variance component problems. Negative estimates of $\sigma^2 i$ may be taken as equal to zero as usual (Shukla, 1972). Homogeneity of estimates can be tested using Shukla's (1972) approximate test (Lins and Binns, 1986). The stability variance is a linear combination of the ecovalence, and therefore both *Wi* and $\sigma^2 i$ are equivalent for ranking purposes.

Cultivar performance measure

Lin and Binns (1986) defined the superiority measure (*Pi*) of the i^{th}test cultivar as the MS of distance between the i^{th}test cultivar and the maximum response as:

$$P_i = [n (X_i - M)^2 + \sum_{j=1}^{n} (Xij - Xi - Mj + M)^2 / 2$$

Where X_{ij} is the average response of the i^{th}genotype in the j^{th}environment, X_i is the mean deviation of genotype *i*, M_j is the genotype with maximum response among all genotypes in the j^{th}location, and *n* is the number of locations. The first term of the equation represents the genotype sum of squares and the second part the GE sum of squares. The smaller the value of P_i, the less is the distance to the genotype with maximum yield and the better the genotype. A pair wise GEI mean square between the maximum and each genotype is also calculated (Crossa, 1990).

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$$P_i = [n (Xi - M)^2 + \sum_{j=1}^{n} (Xij - Xi - Mj + M)^2 / 2$$

Where *X ij* is the average response of the i^{th} genotype in the j^{th} environment, *X i* is the mean deviation of genotype *i*, *Mj* is the genotype with maximum response among all genotypes in the j^{th} location, and *n* is the number of locations. The first term of the equation represents the genotype sum of squares and the second part the GE sum of squares. The smaller the value of *Pi*, the less is the distance to the genotype with maximum yield and the better the genotype. A pair wise GEI mean square between the maximum and each genotype is also calculated. This method is similar to the one used by Plaisted and Peterson (1959), except that, (a) the stability statistics are based on both the average genotypic effects and GEI effects and (b) each genotype is compared only with the one maximum response at each environment (Crossa, 1990).

Wricke's ecovalence (*wi*)

Wricke (1962) defined the concept of ecovalencea, to describe the stability of a genotype, as the contribution of each genotype to the genotype x environment interaction sum of squares. The ecovalence (W_i) or the stability of the i^{th} genotype is its interaction with environments, squared and summed across environments. Genotypes with a low Wi value have smaller deviations from the mean across environments and are thus more stable.

Regression model (bi and S^2di)

Eberhart and Russell (1966) developed a regression model of stability. The model proposed that the regression of each variety on a given environmental condition and a function of the squared deviations from regression would provide more useful estimates of yield stability parameters. It was used to calculate the regression coefficient (bi), deviation from regression (S^2di). Based on the joint regression model, the most stable genotype is the lowest $S^2 di$ value and the highest bi value.

AMMI analysis and its stability value (ASV)

The AMMI analysis and the biplot were computed using crop stat computer software (IRRI, 2007). The AMMI model, which combines the standard analysis of variance with principal component analysis (Zobel et al., 1988), was used to investigate the nature of G x E interaction. The AMMI model first fits additive effects for the main effects of genotypes and environments, using the additive analysis of variance procedure. Subsequently the program fits multiplicative effects for G x E by principal component analysis (Zobel et al., 1988; Gauch and Zobel, 1996, Gauch and Zobel, 1997). In order to rank the genotypes used for this study in terms of stability, AMMI stability value (ASV) was calculated for each genotype following the procedure proposed by Purchase (1997) as follows:

$$\text{AMMI stability value (ASV)} = \sqrt{\left[\frac{\text{IPCA1 sum of squares}}{\text{IPCA1 sum of squares}}(\text{IPCA1score})\right]2} + [\text{IPCA2score}]^2$$

In effect the ASV is the distance from zero in a two dimensional scattergram of Interaction Principal Component axis 1 (IPCA 1) scores against IPCA 2 scores. Since the IPCA 1 score contributes more to G x E sum of squares, it has to be weighted by the proportional difference between IPCA 1 and IPCA 2 scores to compensate for the relative contribution of IPCA 1 and IPCA 2 to total G x E sum of squares.

RESULTS

Analysis of variance

A separate ANOVA was computed for each location and the mean grain yield of the varieties is presented in Table 3. The highest mean grain yield of 9.289 tonnes/ha was recorded from Gibe-1 at Adet and the least (3.00 tonnes/ha) from the same variety at Finoteselam. On average, the highest (8.3 tonnes/ha) and the lowest (4.05 tonnes/ha) environment mean grain yield were observed at Adet and Motta respectively. The mean grain yield of varieties across environments ranged from 4.39 tonnes/ha for phb-38H83to 6.16 tonnes/ha for Jibat-851 with the grand mean grain yield of 5.40 tonnes/ha (Table 3).

Partitioning of the sum of squares of the components indicated the contribution of locations to be 68.30% (Table 4) of the total variation which is in agreement with Yan and Kang (2003) as stated the environmental portionof the sum of squares in the multi-environmental trail has been usually known to be the largest among all sources of variation. The remaining 5.15, 10.65, 12.86 and 3.03% were contributed due to genotype, genotype x location, pooled error and replication within locations, respectively. The large sum of square of environment suggested that the big influence of environment on yield performance of maize genotypes in north western Ethiopia.

Table 3. Grain yield (tonnes/ha) mean performance across location.

Genotypes	Locations				Mean grain yield of varieties across environments
	Adet	Merawi	Motta	Finoteselam	
	Mean	Mean	Mean	Mean	
BHQP-542	8.05(2.84)	4.5 (2.12)	4.05 (2.00)	3.42 (1.84)	5.005
BH-543	8.13 (2.85)	5.21(2.27)	4.72 (2.17)	3.70 (1.92)	5.44
BHQPY-545	9.16 (3.00)	5.41 (2.27)	4.63 (2.14)	4.96 (2.22)	6.04
GIBE-1	9.289 (3.04)	4.91 (2.20)	3.32 (1.81)	3.00 (1.72)	5.13
BH- 660	9.281(3.037)	3.59 (1.88)	3.17 (1.78)	3.82 (1.91)	4.95
BH-670	8.85 (2.94)	5.16 (2.26)	4.00 (2.00)	3.36 (1.81)	5.34
BH-54 0	7.94 (2.81)	5.27 (2.29)	4.51 (2.11)	4.25 (2.06)	5.49
JIBAT-851	8.31 (2.880)	5.79 (2.41)	4.69 (2.16)	5.84 (2.42)	6.16
HORRA	8.33 (2.881)	4.33 (2.07)	3.92 (1.95)	4.45 (2.11)	5.26
WONCHI	9.24 (3.027)	6.32 (2.5)	4.31 (2.07)	4.45(2.12)	6.08
ARGENE	7.27 (2.69)	4.1 (2.00)	3.59 (1.89)	4.53 (2.11)	4.87
Phb-30D79	8.37 (2.89)	6.21 (2.47)	3.38 (1.83)	5.14 (2.26)	5.77
Phb-3253	6.96 (2.64)	4.5 (2.12)	5.6 (2.36)	4.92 (2.21)	5.49
Phb-30G19	7.96 (2.82)	3.97 (1.97)	3.51 (1.87)	4.91 (2.20)	5.08
Phb-30H83	7.45 (2.73)	3.56 (1.87)	3.47 (1.86)	3.08 (1.75)	4.39
MEANS	8.3(2.87)	4.98 (2.18)	4.05 (1.99)	4.25 (2.04)	5.40
LSD (5%)	Ns	0.51	0.39	0.35	
CV (%)	8.01	14.22	11.35	13.42	
SE(d)	Ns	0.25	0.19	0.45	

SE (d) = standard error of difference, CV= coefficient variation, LSD= least significant difference, ns= not significantly different, Figures in parenthesis are square root transformed value.

Table 4. ANOVA for the additive model for grain yield and the percentage sum of square.

Sources of variation	Degree of freedom	Sums of squares(ss)	Means of squares	SS %
Environments (E)	3	141.66	47.22**	68.3
Genotypes	14	10.69	0.76**	5.15
G x E	42	22.09	0.526**	10.65
Rep. with Env.	8	6.28	0.78	3.03
Pooled error	112	26.67	0.24	12.86
Total	179	207.39		

*;** = Significant at 5% and 1% probability level respectively, Grand mean = 2.27 LSD= 0.4 CV= 21.58 SE (d) =0.2.

The relatively large proportion of genotype environment variance, more than double, when compared to that of genotypes as main effect is very important consequence. The presence of significant G x E interaction indicated the inconsistency in performance of maize genotypes across environments.

According to Ghaderi et al. (1980) standard analysis of variance procedure is useful for estimating the magnitude of genotype x environment interaction but fails to provide more information on the contribution of individual genotypes to genotype x environment interaction. To tackle the problem, different statistical procedures have been developed. Therefore, the different stability parametric procedures were used to evaluate and describe maize genotype performance and their result presented in Table 5.

Lin and Binns cultivar superiority measure (Pi) the most stable genotypes ranked first for Pi and for mean yield were Jibat-851 followed by Wonchi and BHQPY-545 ranked second and third. The most stable genotypes according to the ecovalence method of Wricke (1962) were BH-540, Horra, BHQP- 542, Phb- 30H83 and Wonchi. According to Shukla's stability variance (σ^2i) stability parameter, the most stable genotypes were BH-540, Horra and BHQP- 542. Based on the joint regression model, the most stable genotypes with the

Table 5. Shukla's stability variance (σ^2i), Cultivar performance measure (Pi), Wricke's ecovalence (*w*i), Regression coefficient (β) and deviation mean square (S^2di) for of fifteen maize genotypes tested in four environments.

Genotype	$\sigma^2 i$	Pi	*Wi*	β	S^2di
BHQP-542	-0.0049	0.6944	0.0336	0.529	0.000096
BH- 543	0.3028	0.3750	0.3002	-2.696	0.00115
BHQPY-545	0.6896	0.0972	0.6355	7.438	0.00099
GIBE-1	1.4588	0.9306	1.3021	1.133	0.00120
BH- 660	1.1168	0.9583	1.0057	-1.004	0.00018
BH-670	0.6554	0.4167	0.6058	-0.462	0.000058
BH-540	-0.0284	0.1389	0.0132	5.770	0.000078
JIBAT-851	0.3305	0.0278	0.3243	-1.702	0.00031
HORRA	-0.0280	0.375	0.0133	1.587	0.00070
WONCHI	0.0550	0.0694	0.0860	-0.462	0.000059
ARGENE	0.2772	0.7083	0.278	-1.960	0.00059
Phb-30D79	0.7066	0.250	0.6502	-0.278	0.00122
Phb-3253	2.4396	0.3611	2.1521	2.247	0.00032
Phb-30G19	0.4822	0.5278	0.4557	1.080	0.00017
Phb-30H83	0.0549	1.1528	0.0854	-1.470	0.0014

Table 6. Analysis of variance for stability analysis according to the joint regression model.

Sources	Df	SS	MS
Total	179	62.87	
Genotypes	14	3.4	0.24**
Env. + in gen.x Env.	45	59.93	1.33
Env. In linear	1	51.83	
Gen.x Env. (linear)	14	6.18	0.44**
Pooled deviation	30	1.92	0.06
Residual	120	13.42	0.11

** = Significant at 1% probability level, Df- Degree of freedom; SS-Sum of squares; MS-Mean of squares, Grand mean = 2.27, R-squared = 0.96, C.V. = 14.61%.

lowest S^2di values were BH-670, Wonchi, BH-540 and BHQP-542 which ranked first, second, third and fourth respectively (Table 6). The most unpredictable genotypes were Phb- 30H83, Phb- 30D79, Gibe-1 and BH-543 with the highest S^2di. But when β value is considered, 30D79 and Gibe-1 could be regarded as the most stable genotype. If the mean yield, regression coefficient value (β) and the deviation from the regression S^2di are considered together, then the most stable genotype was Wonchi. Relatively better stability was shown by Jibat-851 (mean= 6.16, β= -1.702, S^2di=0.00031), Phb-3253(mean=5.49, β= -2.78, S^2di= 0.00032) and BH-670 (mean=5.343, β= -0.462, S^2di= 0.00122).

According to Alberts (2004) and Solomon et al. (2008), the regression coefficient should be better considered as an indicator for genotypic responses to varying environments. And hence, Wonchi which had a regression coefficient close to unity, minimum deviation from regression and the highest yield can be considered as the most desirable genotype.

Additive main effects and multiplicative interaction (AMMI) model

Combined analysis of variance (ANOVA) of 15 maize genotypes evaluated across four locations according to the AMMI model showed that environments, genotypes and G x E interaction were highly significant (Table 7). Genotype by environment interaction effects were further partitioned into interaction principal component axes (IPCA) using the AMMI model. The first three IPCA axes explained the total G x E interactions. By plotting both the genotypes and the environments on the same graph, the

Table 7. AMMI analysis of variance for grain yield (tonnes/ ha) of the genotypes across environments.

Sources of variation	Degree of freedom	Sum of squares	Means of squares	Total variations explained (%)	GxE explained (%)	GxE cumulative (%)
Environments (E)	3	141.66	47.22**	68.30		
Genotypes	14	10.69	0.76**	5..15		
Rep. with Env.	8	6.28	0.78	3.03		
Genotypes x E	42	22.09	0.53**	10.65		
IPCA1	16	15.31	0.96**		69.33	69.33
IPCA2	14	6.15	0.44*		27.88	97.12
IPCA3	12	0.63	0.05ns		2.79	100
Pooled error	112	26.67	0.24			
Total	179	207.39				

*;** = Significant at 5% and 1% probability level respectively, ns= non significant, IPCA- interaction principal component axis.

associations between the genotypes and the environments can be seen clearly. The greater the IPCA scores, either positive or negative, as it is a relative value, the more specifically adapted a genotype is to certain environments. The more IPCA scores approximate to zero, the more stable the genotype to over all environments sampled (Purchase, 1997; Adugna and Labuschagne, 2002). Adet is the most favorable environment for all genotypes with nearly similar yield response. The rest of the environments (Finoteselam, Motta and Merawi) were the least favorable environments for all genotypes with different yield response. Motta is generally categorized under low yielding maize environment as compared to the two low yielding environments (Merawi and Finoteselam).

Genotypes that are close to each other tend to have similar performance and those that are close to environment indicates their better adaptation to that particular environment. Here, Argene and Phb-30G19, BH-543 and Phb-30D79 showed similar performance as they are close to each other (Figure 1).

Estimation of environmental indexes (Ii) were used to classify environments into three classes Viz. positive significant as good (favorable environments), positive or negative non-significant as average environments and negatively significant as poor (unfavorable) environments (Solomon et al., 2008). The results of this work indicated that Adet was favorable environments with environmental index positive significant. Motta, Finoteselam and Merawi were poor (unfavorable) environments with negatively significant environmental index (Table 8).

Jibat-851, Wonchi and BHQPY-545 are specifically adapted genotypes to favorable environments. When considering only the IPCA1 scores, Gibe-1 and Phb-3253 were unstable genotypes, Phb-3253 relatively adapted to the high yielding or favorable environments (Table 9). Genotypes adapted to lower yielding environments and stable by considering IPCA1 scores were 30H83, Horra, BH-543 and BHQP-452. BH-660, BH-670 and Gibe-1 were adapted to low yielding environments but they were not stable. The most stable genotype based on IPCA1 scores and high yielding genotype was BHQPY-545.

AMMI2 analysis positioned the genotypes in different locations, indicating the adaptation pattern of the genotypes. Since IPCA2 scores also play a significant role (27.88 %) in explaining the G X E, the first two IPCA axes were plotted against one another to investigate the G x interactions pattern of each genotype. When looking at the environments it is clear that there is a good variation in the different environments. Finoteselam and Motta were the most discriminating environments as indicated by the longest distance between its marker and the origin (Figure 2). However, due to their large IPCA2 score, genotypic differences observed at these environments may not exactly show the genotypes in average yield overall locations. For the environments closer relationships were observed between Merawi and Adet. Genotypes with a smaller vector angle in between and have similar projection, designate their proximity in the grain yield performance. Those genotypes that are clustered closer to the centre tend to be stable, and those plotted far apart are unstable in performance. According, genotype Phb-30D79 (12), Phb-3253 (13) and Gibe-1(4) were unstable as they are located far apart from the other genotypes in the biplot when plotted on the IPCA1 and IPCA2 scores. BHQPY-545 (3), Wonchi (10), BH-540 (7) and Phb-30H83 (15) were genotypes positioned closer to the origin of the biplot which indicates their stability in performance across environments. The closer association between Argene (11) and Jibat-851(8) indicate similar response of the genotypes to the environment. Projection of genotypes point to environmental vectors indicated specific interactions between genotype and an environment. The best genotype with respect to location Adet was Gibe-1 (4), while Wonchi (10) was the best genotype for Merawi

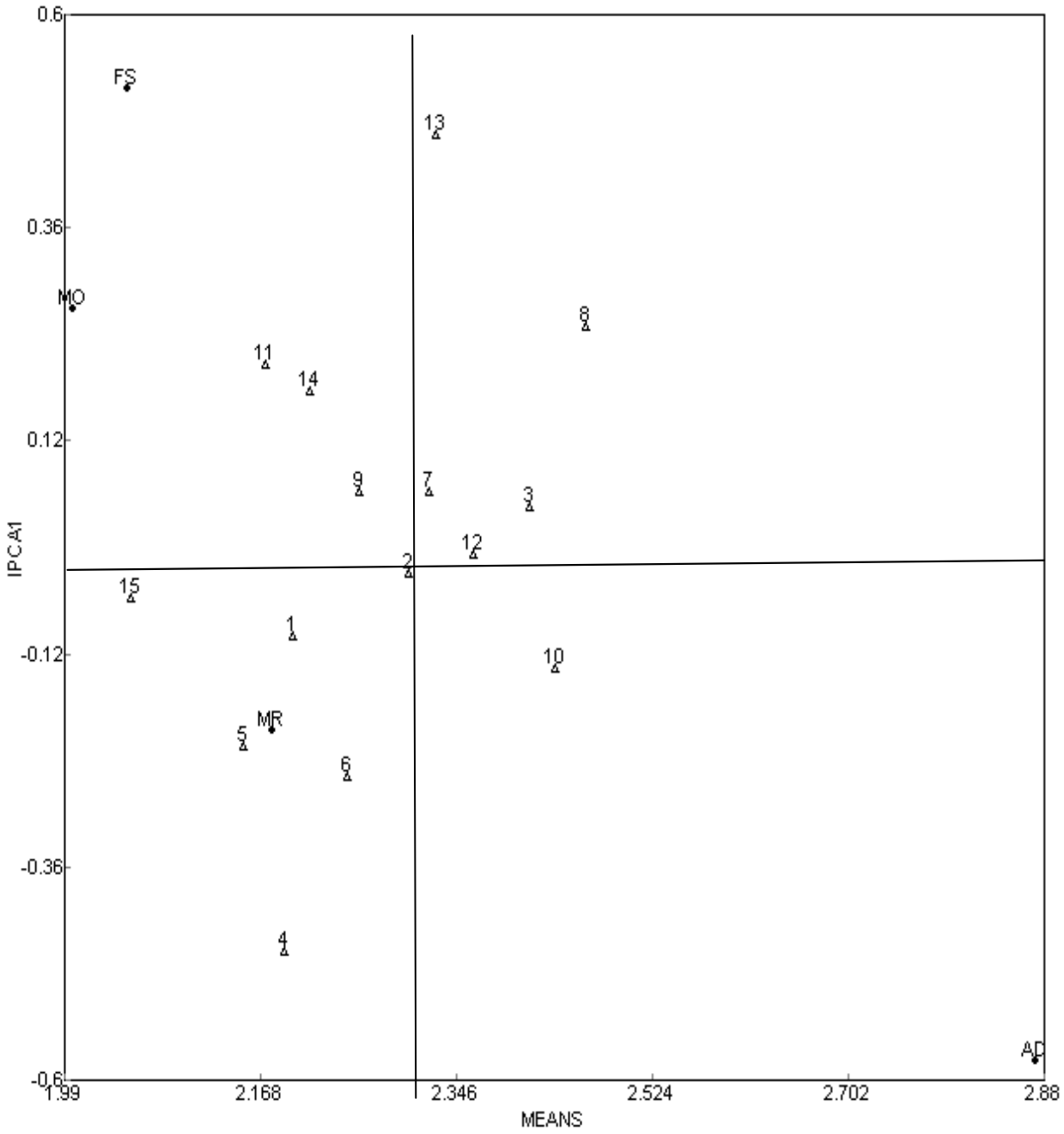

Figure 1. AMMI 1 biplot for grain yield of maize genotypes showing means of genotypes (numbers) and environments (upper case letters) plotted against their IPCA1 scores.

Table 8. The IPCA1, IPCA2 scores and the graph ID for the four environments, sorted on environmental mean yield.

Number	Environment	Graph ID	Environment mean	Environment index	IPCA1	IPCA2
1	Adet	AD	2.87	0.60	-0.578	0.123
2	Merawi	MR	2.18	-0.09	-0.206	0.101
3	Motta	MO	1.9a9	-0.28	0.267	-0.573
4	Finoteselam	FS	2.04	-0.23	0.517	0.439

IPCA- interaction principal component axis.

Table 9. The IPCA 1 and IPCA 2 scores for each genotype and the ASV with its ranking for the 15 genotypes.

No.	Genotypes	Means	Rank	IPCA1	IPCA2	ASV	Rank
1	BHQP-542	5.00	12	-0.100	-0.175	0.279	7
2	BH-543	5.44	7	-0.029	-0.285	0.153	2
3	BHQPY-545	6.04	3	0.045	0.022	0.112	1
4	GIBE-1	5.13	10	-0.454	-0.026	1.131	14
5	BH-660	4.96	13	-0.224	0.155	0.582	11
6	BH-670	5.34	8	-0.257	-0.157	0.664	13
7	BH-540	5.99	6	0.062	-0.119	0.168	5
8	JIBAT-851	6.16	1	0.249	0.139	0.639	12
9	HORRA	5.26	9	0.062	0.122	0.169	6
10	WONCHI	6.08	2	-0.135	0.044	0.338	8
11	ARGENE	4.87	14	0.205	0.124	0.526	10
12	Phb-30D79	5.78	4	-0.008	0.366	0.154	3
13	Phb-3253	5.49	5	0.465	-0.313	1.255	15
14	Phb-30G19	5.08	11	0.175	0.239	0.493	9
15	Phb-30H83	4.39	15	-0.057	-0.135	0.160	4

area. PHB-3253 (13) Showed smaller projection on the vector of Motta, while Phb-30G19 (14) and Jibat-851(8) performed well at Finoteselam.

The AMMI stability value (ASV)

The ASV as described by Purchase (1997) was calculated for each 15 genotypes. Genotypes with lower ASV values are considered more stable than genotypes with higher ASV. The ASV as described by Purchase (1997) on Wheat and Alberts (2004) on maize is comparable with Shukla (1972), Wricke ecovariance (1962) and Eberhart and Russell (1966). This study is also in agreement with their finding between ASV, Shukla (1972), Wrick ecovariance (1962) and S^2di. According to the ASV ranking the most stable genotypes were BHQPY-545, BH-543, Phb-30D79, Phb-30H83, BH-540 and Horra. The most unstable genotypes were Phb-3253 and Gibe-1 (Table 9).

DISCUSSION

The results of this research confirmed the presence of significant statistical difference among genotypes, environments and G x E interactions, suggesting the need to assess the stability of genotypes across environments. The analysis of variance (ANOVA) and the partitioning of the sum of squares to the components showed the contribution of locations to be 68.30% of the total variation, 5.15% due to genotypes and 10.65% due to genotype x location. This indicated the significant influence of environment on yield performance of maize genotypes in north western Ethiopia. The presence of significant G x E interaction indicated the inconsistency in performance of maize genotypes across environments. Therefore, developing genotypes that would have low G x E interaction could result in improving maize productivity for the target area. The relatively large proportion of genotype x environment variance, more than double, when compared to that of genotypes as main effect is very important consequence. Similar results were found by Kaya et al. (2002); Alberts (2004) and Solomon et al. (2008).

The significant effects of environments indicated that the testing environments were statistically different in yield potential, that is, the genotypes performed differently across locations. In other words, the mean yield of genotypes differed from location to location. The significant difference among the genotypes showed vitiations in their response (yield potential) to different locations. The statistical difference among genotypes indicates only the mean yield difference of genotypes not their yield fluctuation across testing sites. It is the significant of G X E which indicates the presence of fluctuation of genotypes performance across environments or testing sites. The presence of significant G x E interaction indicated the inconsistency in performance of maize genotypes across environments. Similar results recorded by other authors (Akcura et al., 2005; Acura and Kaya, 2008; Asfaw, 2008; Dagne, 2008; Solomon et al., 2008; Abdurhaman, 2009 and Muluken, 2009).

Genotypes exhibited significant differences at all locations for grain yield except at Adet. The highest garin yield (9.289 tonnes ha^{-1}) was obtained from Gibe-1 at Adet and the lowest grain yield was also obtained from this genotype (3.0 tonnes ha^{-1}) at Finoteselam. Taking the mean yield for the assessment of the environments,

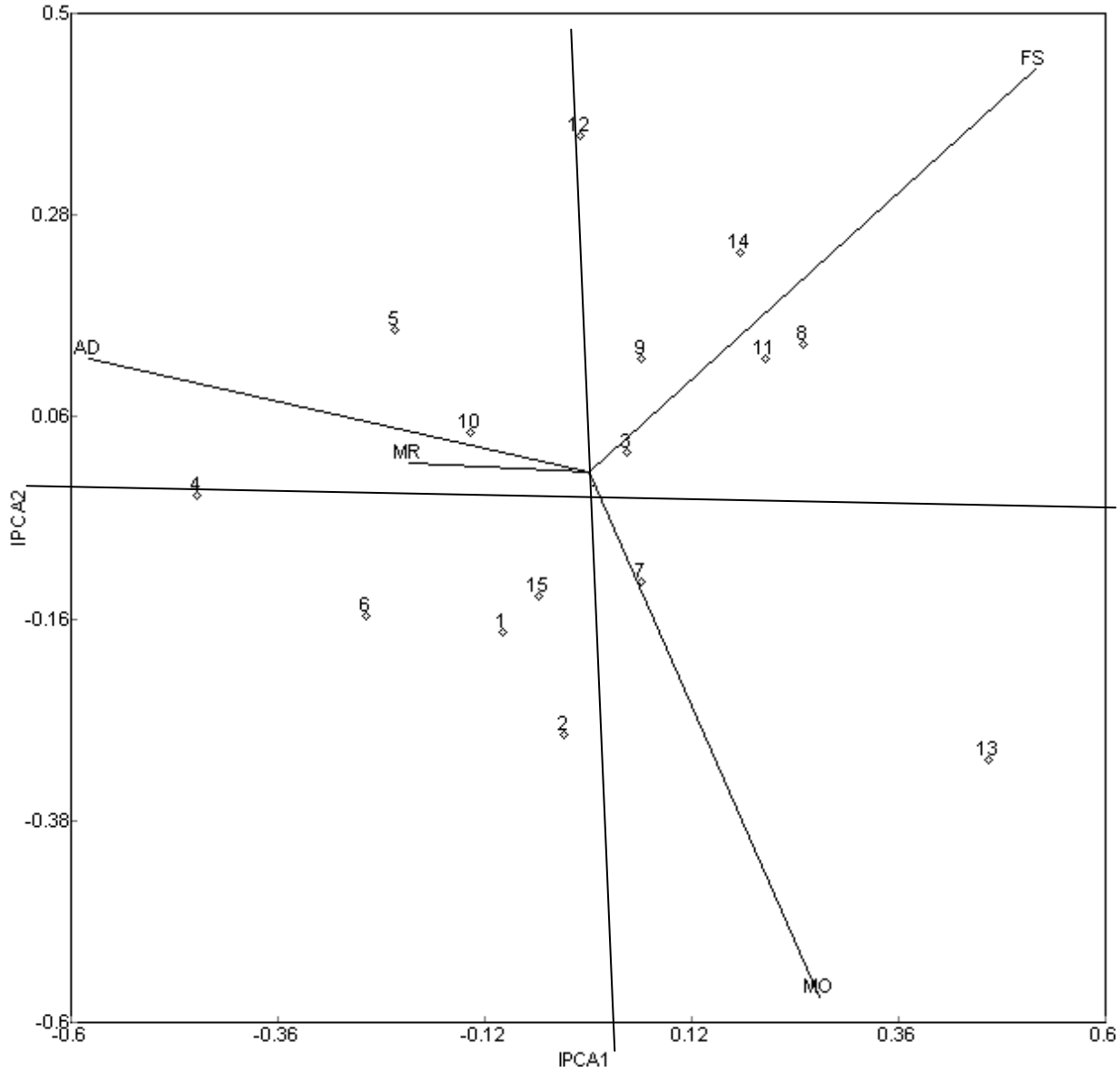

Figure 2. AMMI 2 biplot for grain yield of maize genotypes showing the plotting of IPCA1 and IPCA2 of genotypes. 1= BHQP-542, 2= BH-543, 3= BHQPY-545, 4= GIBE-1, 5= BH-660, 6= BH-670, 7= BH-540, 8= JIBAT-851, 9= HORRA, 10= WONCHI, 11= ARGENE, 12= Phb-30D79, 13= Phb-3253, 14= Phb-30G19, 15= Phb-30H83.

Adet gave the best yield (8.3 tonnes ha^{-1}), while Motta gave the lowest yield (4.05 tonnes ha^{-1}). This may be due to shortage of rain fall during grain filling stage. Spearman's coefficient of rank correlation was computed among all the stability parameters together with grain yield. From the highly significant (P<0.01) rank correlation between *Wi* and σ^2i (r=1.00) was observed. Similar results were reported by Annicchiarico (2002); Alberts (2004); Solomon et al. (2008) and Abdurhaman (2009). The same held true between Pi and mean yield (r=0.95). Similarly, Alberts (2004) and Abdurahman (2009) reported high rank correlations between Pi and mean yield. This indicates that selection for yield would change yield stability by increasing Pi leading to development of genotypes that are specially adapted to environments with optimal growing conditions. Dissimilar results were observed by Solomon et al. (2008). Conversely, mean grain yield was weakly correlated with the other stability parameters of *Wi*, σ^2i andβ. Similarly, negative rank correlation was found between these parameters and Pi. Negative rank correlation was found between mean yield and regression coefficient (β) which disagrees with the previous results (Acura et al., 2006). But this finding is consistence with the result of Muluken (2010) on wheat.

A rank correlation coefficient of 1.0 was found among Wricke's ecovalence (*Wi*) and Shukla's (σ^2i). This indicated that these two procedures were equivalent for ranking purposes. The study has clearly proved that the AMMI model can summarize patterns and relationships of genotypes and environments successfully. And therefore, the information from the AMMI model could be important to release genotypes to target environments based on their responsiveness.

Jibat-851, Wonchi and BHQPY-545 exhibited high mean grain yield across environments and average responsiveness with high degree of stability indicating general adaptability and thus can be recommended for north western Amhara region and for areas with similar environments. The best genotype with respect to location Adet was Gibe-1 while Wonchi was the best genotype for Merawi area. Phb-3253 performed well at Motta, while Phb-30G19 and Jibat-851(8) performed well at Finoteselam. Therefore, it is reasonable to recommend these varieties according to their specific adaptation.

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