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Short Communication

Genotype by Environment Interactions (G X E) and Stability Analyses of Malting Barley *(Hordeum Distichon* L.*)* Genotypes across Northwestern Ethiopia

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Abstract

Seven genotypes were evaluated under rainfed conditions at seven different locations across northwestern Ethiopia with the objectives of investigating phenotypic performance, determining the magnitude of effect of genotypes, environments, and their interactions on important traits and identifying stable malting barley genotype. The highest mean grain yield was recorded at Geregera followed by Debretabor but the lowest at Motta and Burie. Among the genotypes Miscale-21 gave the highest mean grain yield followed by HB-1533. Miscale-21 and Arna provided high kernel protein whereas HB-1533 the least. High thousand kernel weight and hectoliter weight was obtained at Laygaint,, whereas Adet was the least with regard to these traits. Miscale-21 and HB-1533 had high thousand kernel and hectoliter weight. All genotypes fulfill the requirements for germination capacity. Furthermore, G x E interaction was significant for grain yield. Partitioning of the G x E interaction using AMMI showed the first IPCA axis alone explained most of the sum of squares. Moreover, the biplot of AMMI revealed clear insight into the specific and general adaptation of genotype across locations. According to stability analysis measures genotype HB-1533 was the most stable for grain yield whereas Miscale-21 showed specific adaptation in low potential environments.

Introduction

Barley (*Hordeum distichon* L.) is an important grain crop in Ethiopia. It has diverse ecologies being grown from 1800 to 3400m altitude in different seasons and production systems. In the highest altitudes, barley is grown as a sole crop. The total area covered by the crop is about one million hectares with a total annual production of 1.3 million tons (CSA, 2005). Northwestern high and mid altitudes belong to the major barley producing areas all of the produce being for food purpose. On the other hand, breweries have been setup in the country, which required lots of malt annually. Majority of their requirement is obtained from import.

Since malting barley is a new crop to the northwestern Ethiopia, information is unavailable about cultivar performance across diverse environments. The

performance of malting barley grain yield and quality characteristics depends greatly on environmental conditions, which results in differential expression of grain quality from environment to environment. Verme and Nagaragam (1996) reported that there are environments where high quality malting barley can be produced. Soil and climate dominantly influence environment in determining the character of malting barley (Cook, 1962).

The genotype by environment interaction is other important aspect in affecting performance of genotypes across diverse environments. The G x E interaction arises when there is differential response of genotypes in environmental changes. It reduces the correlation between the genotype and phenotype, hindering the genetic potential of the cultivar (Kang and Gorman, 1989). Selection of stable genotype is described as one of the strategies to alleviate G x E interaction effect.

The objectives of this paper were to i) investigate phenotypic performance of malting barley genotypes under northwestern Ethiopia ii) determine the magnitude of effect of genotype, environment, and their interaction on grain yield, agronomic and malt quality traits and iii) identify stable genotype in grain yield.

Materials and Methods

Six improved (Beka, HB-120, HB-1533, HB-52, and Holker,) and two introduced malting barley genotypes (Arna and Miscale 21) were evaluated at seven locations. The locations represent the varying agro-ecologies of the major barley growing areas of northwestern Ethiopia (Table 1). They were grown under rainfed conditions in a randomized complete block design with four replications. Planting was done at the beginning of the rainy season, between May and June. Each experimental plot consisted of six rows spaced 20cm apart. The plot area used was $3m^2$ (1.2mX2.5m). A 1.5 meter distance was maintained between replications at all locations. The fertilizer rate used was 41/46 $kgha^{-1}$of $N\backslash P_2O_5$, respectively. A seed rate of 75 $kgha^{-1}$ was used. First weeding was carried out 35 days after emergence and second was done 30 days after the first weeding. Neither herbicides nor insecticides were applied during the course of the experiment.

Table 1. Total annual rainfall, soil type and altitude of the locations

Location	Altitude (m.a.s.l)	Total annual rainfall (mm)	Soil type
Adet	2240	1331.8	Nitosol
Burie	2600	1622.6	Nitosol
Debretabor	2630	1378.6	Luvisol
Dabat	2620	963.4	Cambisol
Geregera	2370	1340.3	Nitosol
Laygaint	NA	950.4	NA
Motta	2470	1012.6	Nitosol

Sources: NMSA, BBO; Tsige 2002 and Yihenew 2004 NA: Not Available

Data were collected from the four central rows as follows. Stand percent after germination was taken at the time of emergence. Days to heading and maturity were taken from planting to when 50% of head emergence and 75% of the heads attained physiological maturity, respectively. Plant height (cm) was taken at full maturity from five randomly taken plants of the central four rows by measuring from the ground level to the tip of the plant. The mean value is recorded as plant height per plot. Yield data was recorded on clean, dried samples and plot yields were adjusted to 12.5 % moisture level and converted to tones per hectare. Thousand kernels were counted by using electronic seed counter and weighted (g). Hectoliter weight was measured using its standard equipment and then weighted. Germination energy in percent was determined from 100 seeds germinated in a petridish after 120 hours. Two hundred seeds were soaked in a flask with 0.3 H_2O_2 (hydrogen peroxide) and counting after 24 hours and converted to percentage to determine germination capacity. Seed size test was carried out using 2.2, 2.5, 2.8 mm size sieves and proportion of the seed trapped by each sieves were weighted and converted to percentage. Eight gram samples from each plot were milled and 5.0 g flour was placed in moisture dishes and was oven dried for one hour at 100^{o}C. Percent moisture was determined from the mass of water lost on drying to the original milled sample. Kernel protein content was determined using Kjeldahl method.

Bartlett`s test for homogeneity of variances was carried out to determine the validity of the individual and combined analyses of variance and different transformations were conducted. Data on percent of kernel trapped using 2.2, 2.5, 2.8+2.5, 2.8 mm size sieves were transformed using arcsine transformation. Logarithmic transformation was undertaken for grain yield as variances across locations have no homogeneity. Analyses of variance were performed on all traits of individual trials. Thereafter, combined analyses of variance were performed using mixed linear model where genotypes were fixed and environments were random. Mean separation was carried out using least significant (LSD) at 5 percent level of significant. The G x E interaction was further analyzed using different statistical methods. The Additive main effects and multiplicative interaction (AMMI) analysis were performed for grain yield. The AMMI analysis of variance summarizes most of the magnitude of genotype x environment interaction into one or few interaction principal component analysis (Zobel *et al*., 1988).

Results and Discussion

Grain yield

Mean grain yield of locations was between 16.4 ton ha^{-1} and 28.9 ton ha^{-1} at Motta and Geregera, respectively with overall mean of 21.6 ton ha^{-1} (Table 2). The highest grain yield was recorded from the genotype Miscale-21 (40.5 ton ha^{-1}) at Debre Tabor and the lowest from Arna at Lay Gaint (10.0 ton ha^{-1}). Moreover, performances of

Table 2. Mean grain yield (ton ha^{-1}) of malting barley genotypes evaluated at seven testing sites in the 2006 main rain cropping season.

NO.	Genotypes	Adet	Burie	Debretabore	Dabat	Gereger a	Laygaint	Motta	Mean
1	BEKA	13.5 (3.1)	15.4 (3.2)	28.6 (3.5)	20.1 (3.3)	27.0 (3.4)	22.6 (3.4)	16.7 (3.2)	20.6 (3.3)
2	HB-52	18.2 (3.3)	17.6 (3.3)	30.5 (3.5)	30.4 (3.5)	29.6 (3.5)	21.9 (3.4)	14.4 (3.2)	23.2 (3.4)
3	HOLKER	16.5 (3.2)	18.6 (3.3)	22.0 (3.3)	13.5 (3.1)	28.8 (3.5)	18.0 (3.3)	15.1 (3.2)	18.9 (3.3)
4	HB-1533	16.8 (3.2)	20.0 (3.3)	32.8 (3.5)	20.9 (3.3)	34.5 (3.5)	22.9 (3.4)	21.1 (3.3)	24.1 (3.4)
5	MISCALE-21	32.4 (3.6)	21.4 (3.3)	40.5 (3.6)	25.8 (3.4)	34.8 (3.5)	21.5 (3.3)	21.4 (3.3)	28.2 (3.4)
6	ARNA	19.4 (3.3)	12.9 (3.1)	15.3 (3.2)	18.0 (3.3)	20.7 (3.3)	10.1 (3.0)	12.4 (3.1)	15.5 (3.2)
7	HB-120	18.3 (3.3)	19.5 (3.3)	30.0 (3.5)	17.0 (3.2)	27.2 (3.4)	19.6 (3.3)	13.8 (3.1)	20.8 (3.3)
MEAN ($\bar{X}$)		19.3 (3.3)	17.9 (3.2)	28.5 (3.4)	20.8 (3.3)	28.9 (3.451)	19.5 (3.3)	16.4 (3.2)	21.6 (3.3)
C.V (%)		2.3	2.2	1.6	2.2	2.1	2.3	1.3	2.5
SE ±		0.04	0.04	0.03	0.04	0.04	0.04	0.02	0.02
LSD (5%)		0.11	0.11	0.81	0.04	0.11	0.11	0.06	0.04

genotypes were not consistent across locations and Miscale-21 yielded highest except Dabat and Laygaint. At Dabat HB- 52 with grain yield 30.4 ton ha^{-1} and at Laygaint HB-1533 with 22.9 ton ha^{-1} were the top performing genotypes. Arna produced the least at Lay Gaint, Dabat, Burie, Motta and Geregera.

When locations were compared, the highest mean grain yield (28.9 ton ha^{-1}) was obtained at Geregera, while Motta (16.4 ton ha^{-1}) and Burie (17.9 ton ha^{-1}) were poor yielding locations. The low grain yield at these locations could be because of the stress after crop emergence. The high rainfall occurred at seedling stage of the crop development and water logging condition at Motta and cutworm damage at Burie when the crop reached at knee height resulted in poor stand and low grain yield.

Agronomic traits

Most genotypes were early to head at Adet (70.5 days) and late at Dabat (102.3 days) but matured early in 95.1 days at Geregera (Table 3). Most genotypes matured very late at Laygaint and Dabat (133.5 days). Four dominant types of barley production systems in northwestern Ethiopia have been identified of which, early and late maturing barley production system in the main seasons are the dominant systems (Alamnie *et al*., 2004). Early maturing barley varieties like Miscale-21 and Arna fit the early system while HB-1533 and HB-52 the late maturing barley production system.
Plant height and stand percentage after germination were found to show a highly significant ($P<0.01$) dissimilarity among genotypes across all locations. HB-1533 was the tallest genotype with mean plant height of 106.5 cm and Holker was found to be the shortest with mean height of 80.0 cm (Table 3). Highest plant height was recorded at Debretabor (103.8 cm) and the lowest at Burie (85.0 cm). As far as stand percentage after germination is concerned, Arna (77.3 %) was the least followed by Holker (82.2 %). At Geregera and Adet genotypes showed good average stand percentage after germination that were 90.3 % and 89.0 % respectively (Table 3). Genotypes were found to have low stand percentage after germination at Motta (72.3 %) and Laygaint (82.1 %) as compared to others.

Highest mean thousand kernel weight was recorded at Laygaint (45.8 g) and lowest mean at Adet (34.7 g). Genotypes HB-1533, Miscale-21 and Arna provided the highest thousand kernel weight but Genotype Beka, HB-52, HB-120 and Holker had low mean thousand kernel weight over locations with corresponding values of 65.6, 64.3, 64.8 and 64.0 $kghl^{-1}$ respectively. HB-1533 also produced highest hectoliter weight 65.7 kg hl^{-1} and Arna with 60.5 kg hl^{-1} gave the lowest. Laygaint, Geregera, Motta and Dabat with 66.3 kg hl^{-1}, 65.6 kg hl^{-1}, 65.8 kg hl^{-1} and 64.8 kg hl^{-1} gave high hectoliter weight correspondingly (Table 3). Among the genotypes HB-1533, Miscale-21, HB-120 and HB-52 offered highest average hectoliter weigh over all locations. Furthermore, these two attributes are important quality parameters in barley. The standards set for thousand kernel weight and hectoliter weight by National Standard Authority ranged from 35 to 45g and 60 to 65 Kg hl^{-1}, respectively. The mean thousand kernel weight and hectoliter weight of genotypes averaged over all locations except Adet met the standards.

Table 3. Mean values of agronomic traits of seven locations and genotypes in the 2006 main season.

Location	SAG (%)	DH (day)	DM (day)	PH (cm)	TKW (g)	HLW (kg hl^{-1})
Adet	89.0	70.5	100.5	93.8	34.7	56.2
Burie	87.6	84.9	120.5	85.0	37.3	62.8
Debretabor	86.6	73.6	116.3	103.8	41.2	62.9
Dabat	85.9	102.3	133.6	94.9	36.2	64.9
Geregera	90.3	73.4	95.1	88.7	41.8	65.6
Laygaint	82.1	99.0	133.5	93.2	45.8	66.3
Motta	72.3	84.3	124.9	90.3	40.2	65.8
Genotypes						
Arna	77.3	97.5	114.6	91.4	40.4	60.5
Beka	85.7	88.0	124.2	94.4	36.3	62.5
HB-120	84.7	85.7	124.4	98.2	37.8	64.9
HB-1533	87.3	92.1	127.1	106.5	45.2	65.7
HB-52	87.2	85.1	122.8	93.7	37.4	64.0
Holker	82.2	82.8	116.7	80.0	37.8	62.5
Miscale-21	89.5	74.8	113.0	85.3	42.3	64.3
Mean ($\bar{X}$)	84.9	84.0	120.4	92.8	63.5	39.6
C.V (%)	5.3	2.6	1.4	6.9	6.2	2.3
SE ±	0.8	0.4	0.3	1.21	0.5	0.3
LSD (5%)	2.4	1.2	0.9	3.4	1.3	0.8

SAG = stand percent after germination; DH = Days to heading; DM = Days to maturity; PH=Plant height; TKW=thousand kernel weight; HLW=Hectoliter weight

Malting quality traits

The mean kernel protein content of genotypes was between 9.5 % for HB-1533 and 10.8 % for Miscale 21 (Table 4). Protein content for Arna and Miscale 21 was high with 10.3 % and 10.8 %, respectively. Beka, HB-120, HB-1533, HB-52 and Holker gave acceptable mean kernel protein and met the standards (9-11.5) set by the National Standard Authority for malting barley. Kernel protein content that exceeds recommended levels is undesirable for malting because it increase steep times and cause uneven water uptake during steeping, uneven germination during malting, increased malt loss due to abnormal growth, excessive enzymatic activity, low extract yield, excessive nitrogenous compounds in the wort during brewing, and chill haze formation in beer (Burger *et al*., 1979). Adet (10.84), Debretabor (11.03) and Geregera (10.17) were the locations where high protein content was recorded while the mean kernel protein contents obtained from Dabat and Laygaint was 9.73 and 9.83 respectively (Table 4). Low protein content was recorded at Motta and Burie probably due to low and stunted plant population as a result of stress.

Table 4. Mean grain protein content and quality traits of malting barley genotypes grown at seven locations in the 2006 main cropping season

Genotypes	Mo (%)	KPC (%)	Kernel size test (mm) using sieve sizes of					GE (%)	GC (%)
			2.8	2.5	2.5+2.8	2.2	<2.2		
Arna	10.59	10.28	28.23	41.22	67.41	19.77	11.50	66.00	98.82
Beka	10.66	9.68	8.59	29.04	38.84	37.55	23.31	63.39	99.21
HB-120	10.66	9.46	12.11	41.07	54.22	32.50	14.22	66.29	98.75
HB-1533	10.62	9.45	22.95	50.07	73.39	20.14	7.98	86.11	99.50
HB-52	10.75	9.49	13.69	40.44	55.08	31.81	14.28	67.36	99.39
Holker	10.74	9.49	10.83	34.79	46.22	34.05	20.71	88.11	98.89
Miscale-21	10.61	10.76	40.05	49.13	85.59	8.91	1.90	38.79	98.32
Locations									
Adet	10.66	10.84	10.59	26.42	37.36	33.05	30.77	89.82	97.04
Burie	10.39	8.51	10.58	46.20	56.79	29.20	14.04	75.32	99.50
Dabat	11.43	9.73	12.98	42.77	55.74	30.15	14.10	68.71	99.58
Debretabor	10.14	11.03	12.14	49.34	59.68	27.53	11.01	58.04	99.43
Geregera	10.48	10.17	15.51	45.78	61.28	28.09	10.61	56.85	99.86
Motta	10.51	8.51	9.54	47.89	57.40	31.45	11.14	64.82	98.11
Laygaint	11.04	9.83	65.13	27.38	92.50	5.27	2.22	62.46	99.39
Mean ($\bar{x}$)	10.66	9.80	19.49	40.82	60.11	26.39	13.41	68.01	98.98
C.V (%)	3.7	6.5	25.1	13.2	14.6	14.0	31.0	28.8	1.6
SE ±	0.07	0.12	0.93	1.02	1.66	0.70	0.79	3.70	0.30
LSD (5%)	0.21	0.34	2.59	2.85	4.64	1.95	2.19	10.4	0.83

Mo-Kernel moisture content; KPC-Kernel protein content; GE-germination Energy; GC- germination capacity

Miscale 21 and HB-1533 had the large mean percentage of kernels trapped by 2.8, 2.5 2.8+2.5 and 2.2 mm size sieves (Table 4). Among genotypes only Miscale-21 fulfills the standard with greater than 80 percent of the kernel that passed through 2.5+2.8 mm size sieve. Genotypes Holker and Beka had small kernel size much below the standard. HB-1533, HB-52, HB-120 and Arna provided kernel sizes in between these two ranges. Highest percentage of acceptable kernel size (92.5 %) was recorded at Laygaint, Geregera, Motta and Debretabor (Table 4). From the result it can be deduced that varieties grown at Laygaint meet the national standard of malt character. Relatively sparse plant population per plot and long duration for kernel setting at Laygaint compared to the other locations resulted in plump kernel size. On the other hand, high disease pressure during kernel filling period and shorter duration for kernel setting might have resulted in reduced kernel size of genotypes at Adet.

It can be seen from Table 4 that Holker obtained germination energy of 88.1 % followed by HB-1533 (86.1 %). The least germination energy was obtained from Miscale-21 (38.8%). All genotypes showed germination energy below the standard (< 95 % in 120 hours) indicating that they are dormant. This in turn indicated the need to know how long the seed should be stored before transferring to malting process. The highest germination energy (89.8 %) was observed from seeds harvested at Adet because of early harvesting. All genotypes had germination capacity (> 97%) which is well over set by National Standard Authority.

Genotype by Environment Interaction Components

The analysis of variance over locations revealed a highly significant ($p<0.01$) variation for the genotype and environment effects and genotype by environment interaction for grain yield, agronomic and quality traits of malting barley genotypes (Table 5). This indicated genotype, environment and their interaction are important in governing the expression of these traits. The significant G x E interaction indicated the differential genotypic performance across environments and reduces the association between phenotypic and genotypic values, and thus genotypes that perform well in one environment may perform poorly in another (Fox *et al*. 1996). Generally, larger interaction component cause difficulties in selection of widely adapted, high yielding genotypes under diverse environments. The presence of significant G x E interaction and environment effects on yield and agronomic traits were reported by (Finlay and Wilkinson, 1963; Tesfaye *et al*., 1998; Alaminie *et al*., 2004) in barley.

Table 5. Combined analysis of variance for seven genotypes for seventeen traits grown in 2006 main cropping season

Traits	Mean Squares (MS)			
	Environments (E)	Genotypes (G)	G x E	error
d.f	6	6	36	144
SAG	1047.01**	455.97**	42.29**	19.90
DH	3891.98**	898.24**	48.16**	4.67
DM	6159.60**	860.95**	43.97**	2.62
PH	983.54**	2077.44**	94.55**	40.79
TKW	407.39**	284.91**	22.86**	6.11
HLW	342.01**	85.70**	13.1**	2.14
GY	0.262**	0.199**	0.024**	0.007
MO	5.32**	0.11^{ns}	0.09^{ns}	0.15
KPC	28.30**	7.44**	1.06**	0.41
SF	1.44**	0.42**	0.03**	0.003
SS	0.32**	0.20**	0.04**	0.004
ST	1.60**	1.37**	0.58**	0.01
SY	0.27**	0.32**	0.02**	0.002
SL	0.22**	0.15**	0.01**	0.002
GE	0.82**	1.84 **	0.16 *	0.10
GC	0.13**	0.02^{ns}	0.01^{ns}	0.008

ns = non significant, * = significant (P<0.05) and ** = highly significant (P<0.01)

Additive Main Effects and Multiplicative Interaction Analysis for Grain Yield

Additive main effects and multiplicative interaction (AMMI) analysis proved significant ($P<0.05$) main effects and interaction effects for grain yield (Table 6). It showed that 33.9 % of the total sum of squares was attributable to environmental effects, 25.9 % of genotypic effects, and 18.5% to G x E effects (Table 6). A large sum of squares for environments indicated that the environments were diverse; with large differences among environmental means causing most of the variation in grain yield. The magnitude of the G x E sum of squares was highly significant ($p<0.01$) indicating that there were large differences in genotypic response across locations.

Table 6. Additive main effects and multiplicative interactions analyses of variance for grain yield of the genotypes tested across locations in 2006 main cropping season

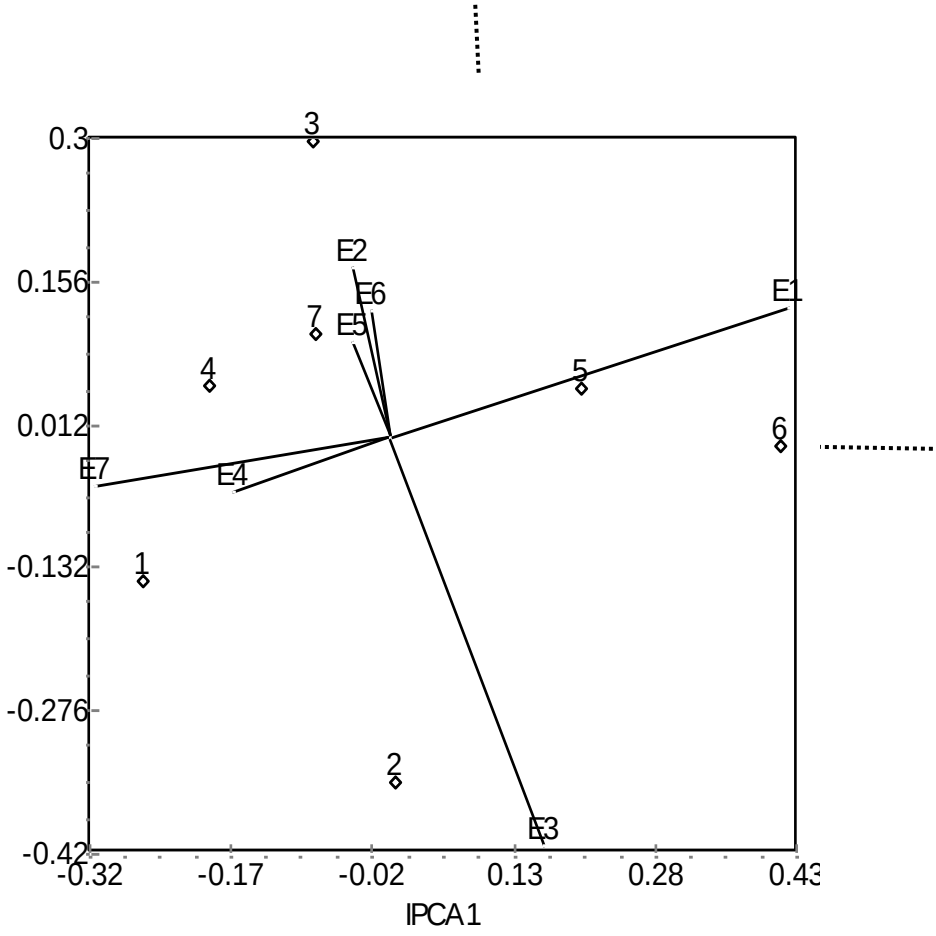
Source	df	Sum of squares	Mean Squares	Explained (%)
Total	195	4.64		
Env.	6	1.57	0.26**	33.90
Rep. with Env.	21	0.38	0.18	
Genotypes	6	1.20	0.20**	25.90
Gen.X Env.	36	0.86	0.02**	18.48
IPCA 1	11	0.45	0.04**	52.01
IPCA 2	9	0.24	0.03**	28.44
IPCA 3	7	0.10	0.02**	12.06
IPCA 4	5	0.06	0.01	6.94
IPCA 5	3	0.05	0.02	0.56
IPCA 6	1	0.03	0.005	
Residual	126			
Grand Mean ($\bar{x}$) = 3.31		C.V = 2.14		

** = Highly significant at 0.01 probability level, * = Significant at 0.05 probability level
D.F = Degree o freedom IPCA = Principal Component axis for interaction

Results from AMMI analysis also showed that the first principal component axis (IPCA1) of the interaction captured 52.0 % of the interaction sum of squares at 11 degrees of freedom. Similarly Purchase *et al*. (2001) and Romagosa *et al*. (1996) reported 41% and 72 % of the G x E interaction explained by the first IPCA in wheat and barley, respectively. The second interaction principal component axis explained a further 28.4 % of the G x E sum of squares and only 12.1 % by the third IPCA axis. The mean squares for the IPCA1 and IPCA2 were significant at P=0.01 and cumulatively contributed to 80.4 % of the total G x E. Regardless of the positive or negative signs, genotypes with large scores have high interactions (Unstable), whereas genotypes with small IPCA scores close to zero have small interactions and are stable (Zobel *et al.,* 1988). In AMMI biplot (Figure 1), the genotypes showed more variation for main effects than interaction. This was manifested by relatively wider distribution of genotypes in the horizontal than in the vertical direction. The genotypes Holker, HB-52, and HB-120 showed relatively smaller absolute IPCA1 scores. Higher IPCA1 scores for grain yield were recorded for Beka, Arna and Miscale-21 (Figure 1). Environments with higher IPCA scores discriminate among genotypes more than environments with lesser scores (Zobel *et al*., 1988; Kempton, 1984). Motta , Burie and Geregera locations discriminate less among genotypes as their IPCA1 score were less whereas Adet and Laygaint discriminate more among genotypes.

F-test at P=0.01 revealed that the first three principal component axes of the interaction were significant for the model. However, the prediction assessment indicated that AMMI 2 with only two interaction principal component axes was the best predictive model (Zobel *et al*., 1988). Further interaction principal component axes captured mostly noise and therefore did not help to predict validation observations. Thus, the interaction of the seven genotypes with seven environments was best predicted by the first two principal components of genotypes and environments; and genotypes and environments with similar signs of their IPCA scores interact

positively for that trait. AMMI 2 biplot as shown in figure 1 has four sections. The locations fall into four sections; genotype HB-120 and Holker were good for locations Burie, Motta and Geregera; genotype Beka was good for locations Debretabor and Laygaint; and Arna and Miscale 21 were good for Adet; and genotypes HB-1533 and HB-52 for Dabat. Genotypes HB-1533 and HB-120 located near the plot origin have low GxE interaction than the vertex genotypes and thus stable. Genotypes Holker, HB-52 and Arna located far from the vertex were unstable over locations.



1 = Beka; 2 = HB-52; 3 = Holker; 4 = HB-1533; 5 = Miscale-21; 6 = Arna; 7 = HB-120
E1 = Adet; E2 = Burie; E3 = Dabat; E4 = Debretabore; E5 = Geregera; E6 = Motta;
E7 = Laygaint

Figure 1. Biplot of principal component analysis axis (PCA) 1 against principal component analysis axis (PCA) 2 of seven genotypes grown at seven environments.

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