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Genotype X Environment Interaction and Yield Stability of Malt Barley Genotypes Evaluated in Tigray, Ethiopia Using the Ammi Analysis

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Abstract: Eight malt barley genotypes were evaluated in randomized complete block design using three replications at six locations in Tigray region during 2013/2014 main cropping season. The objective of this study was to quantify the magnitude of genotype by environment interaction and yield stability of malt barley genotypes. The additive main effect and multiplicative interaction effect model (AMMI) analysis revealed significant difference ($p<0.01$) for genotypes, locations and genotype by location interaction. The magnitude of the testing location was greater than the genotype by location interaction and the genotype. This indicates that the testing locations were diversified in discriminating the genotypes. The AMMI model clearly demonstrates the genotype by location interaction by partitioning into two significant interaction principal components that capture 83.84% of the genotype by location interaction. According to the stability analysis of the additive main effect and multiplicative interaction effect Stability Value (ASV) and the AMMI 1 biplot analysis the genotype Bekoji and Fire-Gebs were the most stable coupled with higher grain yield greater than the grand mean where as the genotypes Sabini and HB-1533 were unstable. Using the AMMI 1 biplot analysis, the testing locations, korem, Hashange, Mekhan and Emba-hasti were favorable testing locations whereas Hagara-Selam was unfavorable testing location.

Key words: AMMI, ASV, genotype by environment interaction

INTRODUCTION

Barley (*Hordeum vulgare* L.) is one of the oldest domesticated cereal crops and is expected to originate in the Fertile Crescent region of the Near East around 8000 BC (Harlan and Zohar, 1966). It has been used both as food and as a principal ingredient in fermented beverages since ancient times. Barley is one of the seven internationally grown cereal grains, currently ranking fourth in world production behind maize, wheat and rice and ahead of sorghum and rye (FAO, 2012) Barley has an extremely wide geographic range, wider than almost every other crop species and it is more productive and its yield is less variable than wheat and most other small grains. Therefore, it is widely used amongst farmers with limited and poor resources in less favorable climate and soil condition.

In Ethiopia the demand for malt barley is directly associated with the expansion of the brewery industry. The current malt barley supply is 36,000 mt but, the demand is 90,000 mt (USAID, 2012). Perhaps with the increased demand of barley for feed and malting purpose, the average production is very low in our country 17.49 Qt ha^{-1} and lowest in the Tigray region 16.18 Qt ha^{-1} (CSA, 2012). The lower yield generally in the country and particularly in the Tigray region is due to lower adoption and dissemination of the improved barley genotypes. Farmers mostly use local Landrace of barley and the nationally released genotypes do not fit the drought prone areas of the region (Abay and Bjornstad, 2009).

Great effort has been made to tackle the boosting demand and stunted supply of malt barley and different malt barley varieties released. But the dissemination and adaptation study of malt barley genotypes was very limited in the Tigray region. In Tigray rainfall is sparse and unpredictable, both over space and time. Mean annual rainfall has been estimated at 650 mm or less over the past few decades. The coefficient of variation for yield in Tigray is four times the national level (REST, 1995). Farms are characterized by highly variable micro-environments that differ in topography, soil type, rainfall and temperature and soil fertility. This heterogeneity varies over relatively small distances (Tadesse and Abay, 2011).

According to Banziger and Cooper (2001) the magnitude of genotype by environment interaction is

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higher where there is a wide variation between environments in incidence of the same stress, such as climatic, soil, biotic and management factors) Hence the magnitude of genotype by environment is believed to be higher in the Tigray region. Large magnitude of genotype by environment interaction reported in the region in barley (Abay and Bjornstad, 2009; Gebru and Abay, 2013).

Genotype by environment interaction is the variation, arising from the lack of correspondence between the genetic and non-genetic effects in multi location trials. The different response of genotypes across the testing environment is considered as a hindrance in selecting and recommending of crops and cause yield fluctuation (Kang, 1998). Genotype by environment interaction may offer opportunity for selection and adaptation of genotypes that showed positive interaction with the specific location which helps in the effective utilization of specifically adapted genotypes (Ceccarelli and Grando, 2007).

Different statistical models available for quantifying the genotype by environment study in multi location yield trial such as classical analysis of variance (ANVOA), stability analysis and multivariate. The additive, multiplicative interaction component (AMMI) model is a hybrid analysis that incorporates both the additive and multiplicative components of the two-way data structure. In AMMI, the additive portion is separated from interaction by analysis of variance (ANOVA) and the multiplicative component is further decomposed by interaction principal component (Zobel *et al*., 1988). Hence, this study was initiated to evaluate the performance and quantify the magnitude genotype by environment interaction stability of malt barley genotypes for grain yield.

MATERIALS AND METHODS

Experimental design and methods: The experiment was conducted during 2013/2014 main crop season. Comprised eight nationally released malt barley genotypes (Bekoji, Frie-Gebs, Sabini, IBONI174/03, Holker, Bahati and EH-1847) obtained from Holetta Agricultural Research Center the experiment was done at six different locations (Table 1). The genotypes were laid out in Randomized Complete Block Design (RCBD) with three replications. The experimental site contained a total of 6 rows with row spacing of 0.2 m and with a total plot size of 1.2 m by 2.5 m and spacing between plots was 0.5 m while spacing between block was maintained at 1 m. Seed rate was calibrated from the 80 kg ha^{-1} and planting was made by drilling to the six rows. Fertilizer was applied 41 kg N ha^{-1} and 46 kg P_2O_5 ha^{-1} at planting and the fertilizer urea was applied in split application in the vegetative stage of the crop and data for yield were collected from the four middle rows.

Statistical analysis: The assumption of analysis of variance (ANOVA) normality test and test of equal variance was done using Minitab 16 for each single location. Before combining the data Bartlett and Kendall (1946) test was done using the soft ware Minitab 16 response variables there were no series ANOVA assumption violation and the additive main effect and multiplicative interaction effect (AMMI) were done based on the model suggested by Crossa *et al*. (1991) and analysis were done using the Crop stat 7.2

$$y_{ij} = \mu + G_i + E_j + (\sum_{1}^{n} K_n U_{ni} S_{nj}) + Q_{ij} + e_{ij}$$

where, i = 1, 2……..8, j = 1……6; Y_{ij} is the performance of the i-th genotype in the j-th environment, μ is the grand mean, G_i is the additive effect of the i^{th} genotype (genotype mean minus the grand mean), K_n is the eigen value of the PCA axis n, E_j is the additive effect of the jth environment (environment mean deviation), U_{ni} and S_{nj} is the scorer of genotype i and environment j for the PCA axis n, Q_{ij} is the residual for the first n multiplicative components and e_{ij} is the error.

To see the yield Stability Analysis the equation suggested by Purchase (1997) was used:

$$ASV = \sqrt{\frac{SS_{IPCA1}}{SS_{IPCA2}}(IPCA1score)^2 + \lceil IPCA2score \rceil^2}$$

Where:

ASV = AMMI stability value
IPCA1 = Interaction principal component analysis 1
IPCA2 = Interaction principal component analysis 2
SSIPCA1 = Sum of square of the interaction principal component one
SSIPCA2 = Sum of square of the interaction principal component two

Table 1: Description of the study site where the eight malt barley genotypes tested

Zone	District	Research site	Rainfall (mm)	Longitude (°E)	Latitude (°N)	Altitude (m.a.s.l)	Soil type
Southern	Ofla	A/gara	750	39.33	12°31	2565	Sandy loam
Southern	Ofla	Hashange	820	39.52	12.58	2400	Sandy clay loam
Southern	Endamekoni	Mekhan	650	39.32	12.44	2423	Loam
Southern	Endamekoni	Emba-Hazti	830	39.34	12.52	3000	Clay loam
Southern	Alaje	Astella	655	39.56	12.91	2800	Clay loam
South eastern	Hagra-selam	Hagra–selam	400	39015	13061	2225	Clay loam

RESULTS AND DISCUSSION

Additive main effect and multiplicative interaction analysis (AMMI analysis): The AMMI analysis of variance for the (additive main effect) showed a significant difference ($p = 0.01$) for the testing locations, genotypes and genotype by location interaction. (Table 2). The result showed that the environment captured the maximum sum of square 74.36% followed by the genotype by testing location interaction sum of square which was (21.15%) and the genotype sum of square was the list (4.49%). The magnitude of genotype by testing location interaction was 4.7 times greater than the genotype indicating that substantial difference in genotypic response across environment. The large sum of square for environment indicated that the environment was diverse with large difference among environmental mean and caused variation in performance of the genotypes and this could be attributed due to the unequal distribution of rain fall in the growing season and large environmental sum of square was reported by (Farshadfar *et al*., 2012), Abay and Bjornstad (2009), Sadeghi *et al.* (2011) and Bantayehu (2009) had found a very large and significant environmental sum of square.

The AMMI analysis of variance (Multiplicative effect) was further exploited by decomposing into principal component analysis (Table 2). The first principal component (IPCA1) captured 64.29% of the total sum of square of the multiplicative interaction component and the second principal component further explained 18.55% of the multiplicative interaction component and cumulatively the two principal components explained 82.84%. The result of the study was in agreement with Gauch and Zobel (1988) the two interaction principal components can explained the genotype by location interaction in multi location trials where as the remaining interaction principal component does not help in the accurate prediction rather they may contribute to noise. The most accurate model for AMMI can be predicted using the first two IPCAs and (Yan and Kang, 2000) illustrated that most of the interaction occurs in the first few axes. Besides based on the postdiective evaluation using the (Gollob, 1968) F-test, the two multiplicative interaction principal components was significant ($p=0.01$) where as the remaining interaction principal component was non significant the result was not in agreement with Sivapalan *et al.* (2000) recommended an AMMI model with the first four IPCAs predicates the genotype by environment interaction.

AMMI 1 biplot analysis: The AMMI analysis provides a graphical representation (biplot) to summarize information on main effects and interactions effect of both genotypes and environments simultaneously. The closeness between pairs of locations or pairs of genotypes in the biplot is proportional to their similarity for genotype by location interaction effects (Crossa *et al*., 1990). The interaction principal component 1 (IPCA1) represented in the y-axis where as the genotype and environment mean represented on the x-axis (Fig. 1). Genotypes or Location placed in the right side of the midpoint of the perpendicular line have higher yields than genotypes or location placed to the left side of the perpendicular line (grand mean).

The genotype G6 (EH-1847), G1 (Bekoji), G5 (IBONI174/03), G3 (Fire-Gebs) and G4(Holker) was higher yielder genotypes located to the right of the perpendicular line (grand mean) with mean grain yield of (40.43, 39.92, 38.79, 38.71 and 37.08 Qt ha^{-1}, respectively). The genotypes G7 (HB-1533) and G8 (Sabini)) was genotypes with lower mean grain yield located to the left of the perpendicular line (grand mean). The genotypes G1 (Bekoji), G3 (Fire-Gebs) and G5 (IBONI 74/03) was nearly placed to the origin with lower contribution to the magnitude of genotype by environment interaction implying that the genotypes were stable. The genotypes G2 (Bahati), G4 (Holker) G6 (EH-1847) and G7 (HB-1533) were located distant from the origin which was interactive genotypes contributing much to the increasing magnitude of genotype by environment interaction and they were the most unstable (Fig. 1).

Table 2: AMMI analysis of variance of yield of eight malt barley genotypes in six locations, in the production year 2013/2014 in Tigray

Source	df	Sum of squares	Mean square	Percentage sum of squares
Total	143	29084	203.4	
Treatments	47	24007	510.8**	82.54
Genotypes	7	1078	154**	4.49
Environments	5	17852	3570.4**	74.36
Block	12	2852	237.7**	11.88
Interactions	35	5077	145.1**	21.15
IPCA1	11	3264	296.7**	64.29
IPCA2	9	942	104.7**	18.55
IPCA3	7	485	69.2	9.55
IPCA4	5	280	56	5.52
IPCA5	3	106	35.5	2.09
Error	84	2225	26.5	

*,**Significant at $p \leq 0.05$ and 0.01, respectively

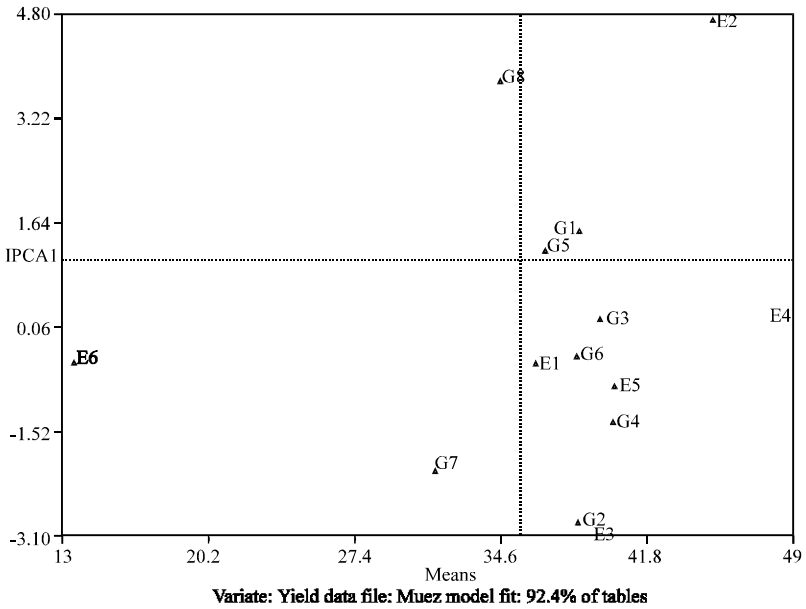

Fig. 1: AMMI biplot for grain yield of 8 malt barley genotypes tested in six testing locations of Tigray in the production season 2013/2014, Genotype plotted was as G1, G2, G3 and environments was plotted as E1, E2 and E3, N.B. abbreviations in the AMMI Biplot are as follows, A) Genotypes: G1: Bekoji, G2: Bahati, G3: Fire-Gebs, G4: Holker, G5: IBON174/03, G6: EH-1847, G7: HB-1533, G8: Sabini, Environments: E:1 Korem, E2: Hashange, E3: Mekan, E4 :Emba-hasti, E5: Astella, E6 : Hagara-selam

The testing locations E4 (Emba-hsti), E3 (Mekan), E5 (Astella), E2 (Hashange) and E1 (Korem) were favorable testing locations located to the right of the grand mean where as the only testing locations E6 (Hagara-selam) was un favorable testing location placed to the left side of the perpendicular line (grand mean). The testing locations E3 (Mekan), E1 (Korem), E5 (Astella) and E2 (Hashange) was located distant from the origin implying the testing locations had higher contribution to the magnitude of genotype by environment interaction and caused unstable genotype performance. The testing locations E4 (Emba-hsti) and E6 (Hagara-selam) was nearly placed to the origin with lower contribution to genotype by environment interaction and implying the testing locations had less contribution to the genotype by location interaction and contributes to the stable performance of the genotypes. The AMMI biplot analysis the first interaction principal component (IPCA1) had explained 13.6% of the genotype by environment interaction and the AMMI 1 had a model fitness of 92.4% of the treatment sum of square in the genotype by environment interaction of the malt barley genotypes and 7.6% was explained the noise .For the genotype by environment interaction of the malt barley genotypes the AMMI 1 model gives the best model fit. The result of the study was in agreement with (Abay and Bjornstad, 2009) in food barley but the result of the study was not in agreement with (Bantayehu, 2009) reported that the AMM2 had better fitness in malt barley and the deviation of the current study with the previous authors could be explained in the magnitude of the genotype by environment interaction.

AMMI 2 biplot analysis: The interaction principal component 1 (IPCA1) was plotted in the x-axis where as the interaction principal component two (IPCA2) plotted in the y-axis (Fig. 2). The AMMI analysis for the first Interaction Principal Component (IPC1) captured 64.29% and the second interaction principal component explained 18.55% the two interaction principal components cumulatively captured 83.04% of the sum of square the genotype by environment interaction of malt barley genotypes, when the interaction principal component (IPCA1 was plotted against IPCA2, Purchase (1997) pointed out that the closer the genotypes score to the center of the biplot the more stable is the genotype and the reverse is true.

The G3 (Fire-Gebs) was located near to the origin implying that it was stable malt barley genotypes. The rest of the malt barley genotypes were unstable located distant from the origin. Genotypes with interaction principal component one (IPCA1 values higher than zero

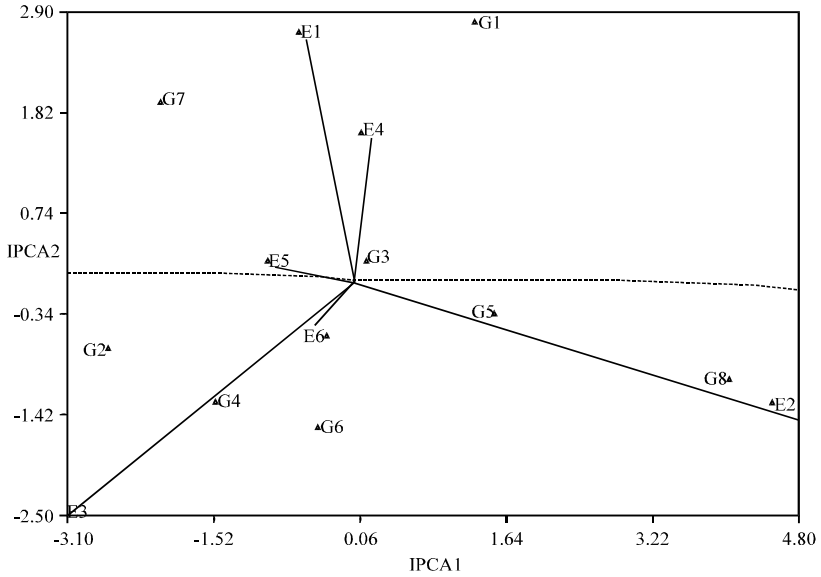

Fig. 2: AMMI biplot for grain yield of 8 malt barley genotypes tested in six testing locations of Tigray in the production season 2013/2014, Genotype plotted was as G1, G2, G3 and environments was plotted as E1, E2 and E3, N.B. abbreviations in the AMMI biplot are as follows: a) Genotypes: G1:Bekoji, G2: Bahati, G3 : Fire-Gebs, G4:Holker, G5: IBON174/03, G6: EH-1847, G7: HB-1533, G8:Sabini, Environments: E1: Korem, E2: Hashang, E3: Mekan, E4: Emba-hasti, E5: Astella, E6: Hagara-selam

Table 3: AMMI stability value for eight malt barley genotypes in six locations, in the production year 2013/2014 in Tigray

	Grain yield				
Genotype	Mean	IPCA1	IPCA2	ASV	Rank
Bahati	37.45	-1.40	-2.80	5.59	5
Bekoji	39.92	-0.18	-0.26	0.68	1
EH-1847	40.43	1.42	1.29	5.09	4
Frie - Gebs	38.71	0.36	1.57	2.01	2
HB-1533	31.55	2.03	-1.97	7.31	6
Holker	37.08	-1.29	0.39	4.50	3
IBONI174/03	38.79	2.89	0.74	10.04	7
Sabini	34.88	-3.83	1.04	13.33	8

classified as high yield while those with PC1 values lower than zero are classified as low yield and low adaptability (Kaya *et al*., 2006) Hence G1 (Bekoji), G5 (IBONI174/03), G8 (Sabini) and G3 (Fire-Gebs) was genotypes with IPCA1 greater than zero implying that had higher grain yield. The genotype G6 (EH-1847), G4 (Holker), G2 (Bahati) and G7 (HB-1533) was with the interaction principal component less than zero implying that the genotypes was with low yield and adaptability (Fig. 2). The best malt barley genotype with respect to the testing locations E2 (Hashange) were G8 (sabini). The best genotype with respect the testing location E3 (Mekan) was the G4 (Holker), G2 (Bahati) and G6 (EH-1847). The genotype G3 (Fire-Gebs) were best suitable to the testing locations of E4 (Emba-Hasti) and E5 (Astella) (Fig. 2).

AMMI Stability Value (ASV) analysis: The malt barley genotypes showed significant genotype by testing location interaction effect and the additive main effect and multiplicative interaction effect Stability Analysis (ASV) were used decompose the interaction effect. Considering mean grain yield as a first criteria for evaluating the malt barley genotypes EH-1847 was with a higher mean grain yield 40.43 Qt ha^{-1} followed by the genotype Bekoji with the mean grain yield of 39.9 (qt ha^{-1}) while the genotype Sabini and HB-1533 were with low mean grain yields across the testing locations (Table 3). The interaction principal component one (IPCA1) scores and the interaction principal component two in the AMMI model are indicators of stability (Purchase, 1997). Considering the first interaction principal component (IPCA1) the genotype Bekoji were the most stable genotype with IPCA1 value (-0.18) followed by Frie-Gebs with IPCA1 value (0.36). When the second interaction principal component (IPCA2) was considered Bekoji was the most stable genotype with interaction principal component value (0.26) followed by the genotype Holker with the IPCA2 value (0.39).

The two principal components have their own extremis but calculating the AMMI Stability Value (ASV) is a balanced measure of stability (Purchase, 1997). The Genotype with lower ASV values is considered more stable and genotype with higher ASV is unstable. According to the ASV ranking in the (Table 3) the genotype Bekoji was the most stable with an ASV value of (0.68) followed by the genotype Frie-Gebs with ASV value (2.01) .The genotype Sabini was the most unstable with ASV value (13.33). The stable genotypes was followed with mean grain yield above the Grand mean and this result was in agreement with (Gebru and Abay, 2013) who has used ASV as one method of evaluating grain yield stability of bread wheat varieties in Tigray and similar reports been made by Abay and Bjornstad (2009) in barley in Tigray and (Tadesse and Abay, 2011) had also reported the yield stability of the Sesame genotypes in Tigray using the AMMI stability value.

CONCLUSION

Yield and Stability are very important in malt barley production. In Tigray where the yield fluctuation and yielding pattern of genotypes were highly varied with small geographic location. Selecting genotypes in diversified testing locations and assessing yield stability of malt barley genotypes is vital.

The AMMI analysis for the additive main effect and multiplicative interaction effect reveled significant difference for Genotype, testing location and genotype by testing location interaction The first interaction principal component (IPCA 1) captured most of the interaction 64.29 and the second interaction principal component explained additional 18.55 cumulatively the two interaction principal component explained 83.04% of the genotype by environment. The AMMI 1 model provided 92.4% model fitness and the malt barley genotype by environment interaction were well predicted by the AMMI 1 model In multi location adaption trial considering both the stability and mean grain yield is important. According to the ASV and AMM1 biplot the malt barley genotypes Bekoji, Frie-Gebs and Holker were stable genotypes coupled with higher mean grain yield greater than the grand mean. The genotype Sabini and HB-1533 were unstable with lower mean grain yield less than the grand mean. Using the AMMI 1 biplot analysis Korem, Hashange, Mekhan, Emba-Hasti and Astella were favorable testing location while the testing location Hagara-selam was unfavorable.

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