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Trait Variability and Genotype by Environment Interaction of Malt Barley Genotypes in Tigray, Ethiopia

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Abstract: In an attempt to identify suitable malt barley genotypes for Tigray Region quantifying the magnitude of genotype by environment interaction and assessing the variability of the traits Is paramount importance for selecting and breeding of malt barley genotypes. Eight malt barley genotypes were evaluated in a randomized complete block design using three replications at six locations of Tigray during 2013/2014 cropping season. The combined analysis of variance revealed significant differences ($P \leq 0.01$) for genotype, location and genotype by location interaction for all response variables studied except the genotype were significant ($P \leq 0.05$) for the response variables harvest index, number of tillers per plant and thousand seed weight. The eleven traits studied showed wider range of variability except the response variables spike length, number of effective tillers and protein content. The principal component analysis showed that the four principal components with Eigen value greater than 1 cumulatively captured 9.27% of the variability in the data set. The cluster analysis revealed three major clusters by which the first and third cluster holding three genotypes and the second cluster only with two genotypes.

Key words: Genotype by Environment Interaction · Cluster analysis · Principal component analysis · Malt barley

INTRODUCTION

The ancestor of cultivated barley (*Hordeum vulgare* L.*)* is originated from its wild progenitor (*Hordeum spontaneum)*. It is identical in most respects to present day cultivate barley and this species is still found in abundance in many parts of Asia and North Africa [1]. The *H. vulgare* and *H. spontaneum* differ primarily in the attachment of the kernel to the spike. *H. spontaneum* having a brittle rachis that allows the kernels to shatter at maturity. The exact site where the barley was originated no conclusive agreement has been made, but according to Harlan [2]. Barley was first domesticated in the Fertile Crescent in the Near East, which is the present-day Israel, northern Syria, southern Turkey, eastern Iraq and western Iran.

Ethiopia has a long history of barley cultivation and diverse agro ecological and cultural practices dating back as early as 3000 B.C. The nation is renowned for its large number of landrace barleys and traditional agricultural practices. The diversity of barley types found in Ethiopia is probably not exceeded in any other region of comparable size [3].

Barley has been malted, or germinated, prior to consumption for thousands of years. It has been documented that any barley having a sound, viable kernel will produce malt, but quality factors would be sacrificed in most cases. In malting operations strict criteria are observed in the selection of barley for malting; among the major considerations paramount in the choice of barley for malting include genotypes, kernel size, soundness, color, brightness, a germinating capacity of greater than 96%, relatively low protein, less than 12.0 % [4].

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Genotype by environment interaction with purely environmental or genetic variation complicates genotype cause inconsistent performance of genotype across the different testing locations and complicates selection and recommendation of a genotype [5]. Hence, assessing the different traits across multi location and quantifying the magnitude of genotype by environment interaction and assessing the variability is important for selecting and lunching malt barely breeding program across barley growing environments of Tigray.

MATERIALS AND METHODS

Description Experimental Site: The experiment was conducted at different locations within altitude ranging from 2225 to 3000 meter above sea level and the detailed description of the site is given in Table 1.

Experimental Materials: All malt barley genotypes for this study were obtained from the Holetta Agricultural Research Center and the details of the genotypes are listed below (Table 2).

Experimental Design and Field Management: The experiment was conducted in the main cropping season 2013/2014 using randomized complete block design (RCBD) with three replications. Plots were 2.5 meter long and had six rows, with spacing of 0.2 meter between rows and 0.5 m between plots. Seed rate of 80 kg/ha and planting was made by drilling to the six rows. Fertilizer was applied at the rate 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 during the vegetative stage of the crop.

Data Collected: The traits such as plant height, productive tillers per plant, spike length and number of kernels per spike were recorded from five plants form the four mid rows and then the average is taken. The remaining traits were recorded on plot basis.

Days to heading (DH): number of days from planting to the date on which 50% of plants on the four middle rows of the plant set heads.

Days to maturity (DM): Number of days from planting to the stage when 75% of plants have reached maturity.

Thousand Kernel Weight (TKW): Weight of the 1000 sample seed in gram per plot taken at random.

Plant Height (PH): is a distance in centimeter from the ground surface to the tip of the spike excluding the awns of randomly taken plants in the plot by measuring.

Tillers per Plant (TPP): number of tillers per plant excluding the main plant was recorded at maturity.

Spike Lengths (SL): spike length of main tiller of each plant from base to tip excluding the awns was measured in centimeter.

Table 1: Description of the study site

Zone	District	Research site	Rainfall	Longitude	Latitude	Altitude (m.a.s.l.)	Soil type
Southern	Ofla	A/gara	1052.4 mm	39°33’	12°31’	2490	Sandy loam
Southern	Ofla	Hashange	820mm	39.52°E	12.58°N	2400	Sandy clay loam
Southern	Endamekoni	Mekhan	650 mm	39°32’	12°44’	2423	Loam
Southern	Endamekoni	Emba-Hazti	830mm	39.34°E	12.52°N	3000	Clay loam
Southern	Alaje	Astella	734.3mm	39°56’	12°91’	2465	Clay loam
South eastern	Hagra -selam	Hagra-selam	-	39°15’ E	13°61’ N	2225	Clay loam

Source BoARD, 2013

Table 2: Description of the malt barley genotypes

Entry NO	Genotype name	Year of release	Source	Characteristics
1	Bekoji	2010	Holetta ARC	Two row
2	Frie - Gebs	2011	Holetta ARC	Tow row
3	Sabini	-	Holetta ARC	Two row
4	IBONI174/03	-	Holetta ARC	Two row
5	Holker	1979	Holetta ARC	Two row
6	Bahati	2011	Holetta ARC	Two row
7	HB-1533	2004	Holetta ARC	Two row
8	EH-1847	2011	Holetta ARC	Two row

Kernel Numbers per Spike (KNPS): was recorded by counting the number of kernel produced on the main tiller of each plant.

Biological Yield (BY): was determined by weighting the four central rows of total air dried above ground biological yield.

Grain Yield (GY): was obtained by weighting the four middle rows adjusted at 12% moisture content.

$$\text{Harvest index (HI) was obtained} = \frac{\text{Grain Yield}}{\text{Biomass Yield}} \times 100$$

Protein Content (PC): was determined by using Kjeldahl method.

Statistical Analysis: Assumption of (ANOVA) normality test and test of equal variance was done using Minitab 16 for all response variables and no series ANOVA assumption violation for all response variables. The combined analysis was conducted using the SAS software edition 9.2. Mean comparison was done using LSD at 5% level of significance. The trait variability was done using the combined mean of the six locations and descriptive statistics, cluster analysis using ward method and principal component analysis were done using the XLSTAT software 2015.

RESULTS AND DISCUSSION

Combined Analysis Variance: The combined analysis of variance revealed significant differences ($P \leq 0.01$) for locations. This indicated that there was a large difference between locations in causing different genotypes performance. The variation of the location might be attributed due to the uneven rainfall distribution during the growing season. The result was in agreement with those reported by Abay [6] and Muluken [7] who found diversified environmental variation in barley growing areas of Ethiopia.

The genotypes were significant ($P \leq 0.01$ for the response variables grain yield, biomass yield, plant height, days to 50% heading, days to 75% maturity. Thousand-kernel weight, number of productive tillers and harvest index were significant ($P \leq 0.05$) (Table 3). The genotypes by location interaction was significant ($P \leq 0.01$) for all the traits studied (Table 3). This indicated that due to the presence of higher magnitude of genotypes by location interaction cause inconsistent performance of genotypes across the different testing locations and complicates selection and recommendation of genotypes [5].

The partition of the total sum square of variation captured by the environment was higher for the response variables thousand kernel weight, days to 75% maturity and kernel yield (95.8%, 82.47% and 74.36%, respectively). The environment had less influence for the response variable harvest index which was 12.32% and number of productive tillers 12.91% (Table 3). The contribution of genotypes to the total sum square was higher for the response variables days to 50% heading, number of kernels per spike, plant height and spike length (36.99 %, 19.79%, 17.38% and 15.1%, respectively). Thousand grains weight was less affected by the genotype which was 0.51% (Table 3). The sum of square explained by genotype by location interaction for the response variables harvest index, number of productive tillers and number of kernels per spike were higher 78.37%, 72.47% and 44.12%, respectively (Table 3). The magnitude of genotype by environment interaction were greater than the genotype 8.40, 7.15 and 4.71 for the response variable harvest index, number of productive tillers and grain yield respectively (Table 3).

Generally much of the variability was explained by the environment sum of square, thus had larger role for the G x E interaction in the yield and yield related response variables and the presence of higher environmental variance complicates the selection and recommendation of a genotype in targeted location [8]. The result of the study was in agreement with Farshadfar [9], Abay[6], Sadeghi[10] and Muluken[7] who obtained very large and significant environmental sum of square.

Descriptive Statistics

Trait Variation in Malt Barley Genotypes: The evaluated malt barley genotypes had a wide range of variation in all traits studied, except for spike length, number of effective tillers and protein content. Higher trait variability was observed in biomass yield (133.56±14.25), Plant height (82.61±4.64), days to heading 67.13 (±3.65), days to maturity 115.5±3.45) and yield (37.35±2.92), respectively (Table 4).

Principal Component Analysis: The four principal components analyses with Eigen value greater than 1 explained 92.7% off the variability in the data set. Principal component 1 with Eigen value 5.39 explained 48.98% of the variability and the traits heading date, maturity date, plant height, grains per spike and protein

Table 3: Mean squares of the combined analysis of variance for kernel yield and yield related traits of malt barley genotypes during 2013/2014.

		Mean squares of kernel yield and yield components										
Source	DF	Kernel yield Q/ha	Biomass yield Q/ha	Harvest index	Productive tillers	Kernels per spike	Spike length (cm)	1000 KWT (g)	Plant height (cm)	Days to 50% heading	Days to 75% maturity	Protein content
	5	3570.4**	43952 **	255.4**	0.4138**	50.05**	5.62**	4458.9**	1883.2**	393.64**	3022.3**	7.2**
R(L)	12	237.7	1532	28.5	0.1646	3.26	0.52	25.8	135	4.12	65.6	0.098
G	7	154 **	3656**	138.0*	0.3345*	19.6**	1.45**	16.9*	387.8**	240.62**	214.5**	5. 8**
GxL	35	145.1**	2276**	232.1**	0.3345**	8.74**	0.82**	24.2**	99.8**	25.7**	48.9**	2.45**
Error	84	26.5	543	62	0.1408	4.18	0.348	6.7	41.9	3.76	10.6	0.1
LSD		11.272	21.84	21.84	0.2904	1.52	0.4627	2.39	5.354	3.097	6.073	7.2
CV		18	18.6	26.7	15.8	10.6	9.4	7.4	9.8	8.734	10.24	
% ss of L		74.36	67.62	12.32	12.91	36.1	41.79	95.85	60.26	43.23	82.47	23.21
% ss of G		4.49	7.87	9.32	14.62	19.79	15.1	0.51	17.38	36.99	8.2	24.76
% ss of GxL		21.15	24.51	78.37	72.47	44.12	43.11	3.65	22.37	19.75	9.34	52.93

*, ** *significant at p= 0.05 and 0.01 respectively*

N.B. Abbreviations: r= réplications; L= location ; G=Genotypes

Table 4: Descriptive statistics of malt barley traits used in the study

Variable	Observations	Minimum	Maximum	Mean	Std. deviation
HD	8	62.167	71.778	67.139	3.65
MD	8	110.333	120.389	115.549	3.45
SL	8	7.220	7.969	7.481	0.284
PHT	8	75.082	90.952	82.610	4.64
grains/spike	8	20.211	23.025	21.791	1.04
TC	8	2.555	2.907	2.793	0.1
TKW	8	47.056	50.222	48.722	0.96
Yield	8	31.550	40.434	37.351	2.92
HI	8	25.674	32.493	28.750	2.76
Biomass	8	113.438	158.403	133.563	14.25
Protein	8	9.331	11.295	10.308	0.67

Table 5: principal component analysis of the eleven traits of malt barley.

	PCA 1	PCA2	PCA 3	PCA 4	PCA 5	PCA 6	PCA7	PCA 8	PCA 9	PCA10	PCA11
HD	0.38	-0.27	0.15	0.12	-0.09	0.22	0.12	-0.52	0.64	0.00	0.00
MD	0.41	-0.14	-0.04	0.10	-0.04	0.18	0.64	0.08	-0.43	0.41	-0.04
SL	0.23	0.38	-0.01	0.47	-0.51	-0.07	-0.21	-0.05	-0.11	-0.07	-0.50
PHT	0.36	0.00	-0.30	0.04	0.31	0.58	-0.42	0.39	0.09	0.04	-0.08
Grains/spike	0.34	-0.07	0.48	0.13	-0.29	-0.03	-0.16	0.33	-0.10	-0.21	0.60
TC	-0.05	0.50	-0.52	0.23	-0.11	0.04	0.17	-0.11	0.17	0.08	0.57
TKW	-0.11	0.45	0.36	-0.48	-0.27	0.28	0.01	0.13	0.23	0.45	-0.06
Yield	0.18	0.42	0.38	0.13	0.58	-0.03	-0.15	-0.42	-0.26	0.09	0.08
HI	-0.30	-0.04	0.26	0.60	0.26	-0.10	0.14	0.39	0.36	0.31	-0.06
Biomass	0.34	0.34	0.02	-0.21	0.23	-0.26	0.42	0.31	0.28	-0.47	-0.19
Protein	0.38	-0.09	-0.19	-0.17	0.03	-0.65	-0.29	0.06	0.14	0.50	0.03
Eigen value	5.39	2.26	1.30	1.02	0.63	0.31	0.09				
Variability (%)	48.98	20.54	11.81	9.27	5.75	2.81	0.84				
Cumulative %	48.98	69.52	81.33	90.60	96.35	99.16	100.00				

content were higher positive coefficient and selection based on the genotype EH-1847 and Bekoji is effective (Table 5). Principal component 2 with Eigen value 2.26 captured 20.54% of the variability and the variables spike length, number of effective tillers, thousand grains weight and yield were higher positive coefficient and selection based on genotype EH-1847, Bekoji, Fire-Gebs and IBONI174/03 is effective (Table 5).

Cluster Analysis: The eleven malt barley traits were categorized into three clusters. The first cluster was with three genotypes Bahati, Fire-Gebes and IBONI174/03. The second cluster were with only two genotypes Bekoji and EH-1847.The genotypes Sabini, HB-1533 and Holker were in the third cluster (Fig. 1). The clusters mean showed difference for the eleven characters of malt barley genotypes the first cluster was characterized as early

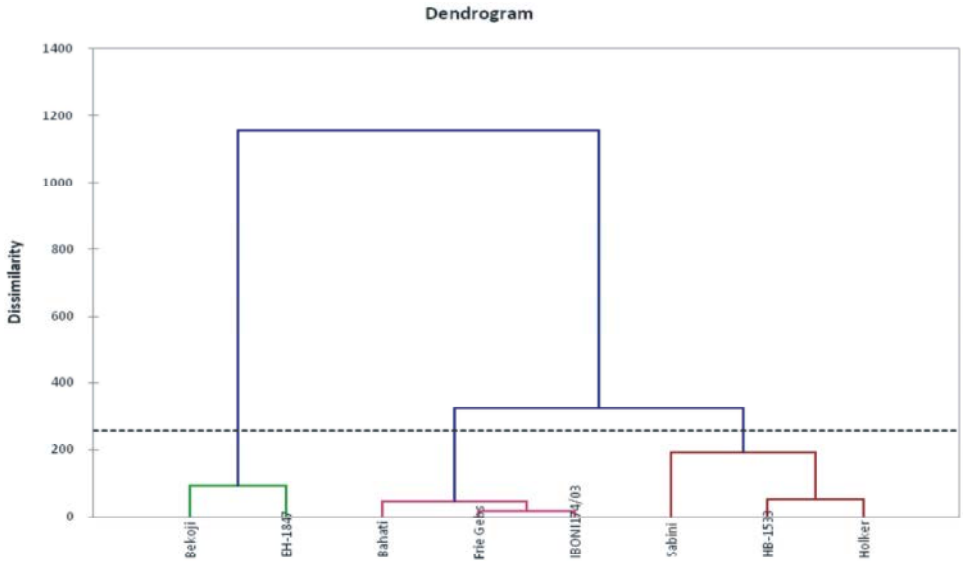

Fig 1: Cluster analysis of malt barley genotypes
Cluster 1=Bahati, Fire-Gebes, IBONI174/03 Cluster 2=Bekoji and EH-1847 Cluster 3=Sabini, HB-1533 and Holker

Table 6: Cluster mean value of the malt barley genotypes

Cluster	HD	MD	SL	PHT	Grain	TC	TKW	Yield	HI	Biomass	Protein
1	65.44	113.63	7.30	81.21	21.52	2.75	49.52	38.32	28.69	134.08	10.03
2	70.11	119.42	7.88	87.60	22.73	2.89	48.64	40.18	26.64	152.83	11.02
3	66.85	114.89	7.40	80.68	21.44	2.77	47.98	34.50	30.22	120.20	10.11

taking shorter days to heading and maturity and having average yield and thousand seed weight. The second cluster was categorized with higher yield, maturity date and thousand kernel weight and protein content. The third cluster was identified as low yield and thousand seed weight as well (Table 6).

CONCLUSION

The combined analysis of variance revealed significant difference for the response variables grain yield, biomass yield, harvest index, number productive tillers, number of kernels per spike, Spike length, thousand kernel weight, Plant height, days to 50% heading and Days to 75% maturity. The total sum square of variation captured by the environment was higher for the response variables thousand kernel weight, days to 75% maturity and yield (95.8%, 82.47% and 74.36%, respectively). Using the different multivariate analysis the eleven traits studied showed wider range variability and selection and incorporation of the genotypes in to breeding program could be effective.

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