

Genotype by environment interaction and association among traits of barley genotypes evaluated in central and south eastern Ethiopia

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Abstract: Barley is one of the major cereal crop grown in highlands of Ethiopia. It is an important food, feed and industrial crop. In this trial a total 36 promising barley genotypes (mainly malt barley types) selected from advanced trails were evaluated using 6*6 simple lattice design at five locations. The objective of the study was to assess the performance of genotypes and genotype by environment interaction (GEI) of barley genotypes; stability of genotypes and association among important yield, yield related and malt quality traits of barley. The combined analysis of variance (ANOVA) showed the existence of significant difference among genotypes and high GEI effect. The mean separation analysis indicated the candidate genotype Entry # 26 (MBHIBYT-22) was the highest yielding genotypes with good malt quality (protein and extract). The association study among agronomic and malt quality traits showed that hectoliter weight has strong significant genetic association with extract in contrast extract has a strong negative association with grain protein content. This showed hectoliter weight can be used as indirect selection criteria in the selection program. The GGE biplot analysis based on the grain yield performance classified the test environments in to four mega environments. In addition, the mean vs stability pattern analysis revealed MBHIBYT-22 had good stability and performance that showed this variety can be recommended for production in similar environments with the testing locations.

Keywords: ANOVA, GGE biplot, grain yield, malt quality, stability

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1. INTRODUCTION

Barley is the fifth major cereal crop grown in Ethiopia, it covers 6.42% of land allotted for grain crop production, mainly found in highlands of Ethiopia (CSA, 2019). Beside its use as human food and industrial raw material (Malt barley), its straw serve as animal feed. In the country an organized barley research started in 1966 with the establishment of the Holetta Agricultural Research Centre (HARC). Since its inception more than sixty food and malt barley varieties were released/registered by both federal and regional research centers found in the country. These improvement efforts mainly consider yield, malt quality, pest resistance and other important agronomic traits.

Selecting good genotypes based on their performance in multi-environment trials (MET) is one of the major tasks of breeder that determines its success to release a variety (Basford, 2001). In MET Genotype by environment interaction (GEI) present when different genotypes perform differently to diverse environment. High magnitude of GEI decreases the reliability of the main effects, correspondingly make difficult to identify superior genotype across environments (Kang, 1998). GGE biplot the graphical tool was developed for analyzing MET data. Some of the applications includes, identifying best genotypes in each environment, evaluating genotypes based on average yield and stability and evaluating test environments based on their representativeness and discriminative ability (Yan, 2001). Many experiments evaluated the barley genotypes using GGE biplot (Abay and Bjornstad, 2009; Sinebo *et al.*, 2010; Zerihun, 2011; Mortazavian *et al.*, 2014; Mehari *et al.*, 2015; Mohtashami *et al.*, 2015; Solonechnyi *et al.*, 2015; Vaezi *et al.*, 2017).

The correlation coefficient analysis measures the association among different traits (agronomic and quality traits) and help to determines the component characters on which selection can be used for improvement of target traits in variety improvement program (Joshi and Okuno, 2010). The correlation analysis was employed by different authors in the barley research programs to identify traits for the indirect selection (Pržulj *et al.*, 2013; Mehripour *et al.*, 2014; Arpali and Yagmur, 2015; Singh *et al.*, 2015; Hailu *et al.*, 2016; Laidig *et al.*, 2017; Marzougui and Chargui *et al.*, 2018; Molla *et al.*, 2018; Ostos *et al.*, 2018; Ghimire and Mahat, 2019; Sayd *et al.*, 2019; Shiferaw *et al.*, 2020). Hence, this study was conducted to assess the association among important yield, yield related and malt quality traits of barley, to study the stability of the tested barley genotypes, to identify stable and high yielding barley genotypes with good malt quality traits for central and south eastern parts of Ethiopia.

2. MATERIALS AND METHODS

In the present study thirty-six materials were evaluated using 6x6 simple lattice design at five locations (Holetta, Bekoji, Debreberhane, Kofele, Adadi) (Table 1). The materials were comprised mainly from different malt barley advanced trials, released malt and food barley varieties (Table 2). The plot size was 5m², with 0.4m and 1.5 m between plot with in block and block spacing, respectively. All cultural management practices were done in accordance with the recommendations for each particular test locations.

Measurements were recorded in the following traits; days to heading, days to maturity, plant height (cm), scald severity (%), net blotch severity (%), thousand kernel weight (g), hectoliter weight (Kg hl⁻¹), grain yield (Kg ha⁻¹), protein content (%) and extract (%). Malt quality traits, protein and extract were analyzed using Near infrared spectroscopy (NIRs) by Bruker Tango instrument. In addition scald and net blotch disease severity were recorded on 0-9 scale and changed to percentage data, where 0=0%, 1=3%, 2=12%, 3=25%, 4=42%, 5=58%, 6=75%, 7=88%, 8=97%, 9=100% before transformed using angular transformation for statistical analysis.

Analysis of variance and GGE biplot analysis

All analysis results presented in this study were performed using different packages of R -software (R Core Team, 2019). The analysis of variance for each and combined locations done using linear mixed effect model suggested Douglas *et al.*, (2015), were genotype as fixed and location as random effect. Mean separation was carried using emmean package (Russell, 2019). Genotypic correlation were done using biotools package (Da Silva *et al.*, 2017). In addition, GGE biplot analysis was carried out using GGEbiplotGUI (Frutos *et al.*, 2014) package of R- software.

Table 1: Description of experimental locations

No.	Testing sites	Altitude (m)	Rainfall (mm)	Longitude	Latitude
1	Holetta	2400	1100	38°38'E	9°00'N
2	Adadi	2383	1105	38°13'E	08°31'N
3	D/Berhane	2830	932	39°32'E	9°41'N
4	Bekoji	2810	1082	39°15'E	7°15'N
5	Kofole	2700	1232	38° 45' E	7° 00' N

Table 2: Lists of barley genotypes evaluated in this trial

Trt.#	Variety Name	Seed source	Trt.#	Variety Name	Seed source
1	Misccal-21 x Bahati	MBNVT 2015	19	Acc. 17148 (P# 42)	Accession
2	Misccal-21 x Karne	MBNVT 2015	20	IBON-HI 13/14 P# 128	MBPVT 2017
3	M 135	MBNVT 2016	21	IBON-HI 14/15 P# 144	MBPVT 2017
4	MN Brite	MBNVT 2016	22	IBON-HI 14/15 P# 129	MBPVT 2017
5	Burton	MBNVT 2016	23	ICARDA GP-75	MBPVT 2017
6	IBON 2013 P# 2	MBNVT 2017	24	IBON-HI 13/14 P# 41	MBPVT 2017
7	IBON 2013 P# 33	MBNVT 2017	25	IBON-HI 14/15 P# 153	MBPVT 2017
8	Bekoji-1 x Grace	MBNVT 2017	26	MBHIBYT-22	MBPVT 2017
9	HB 42	FB released	27	ICARDA GP-67	MBPVT 2017
10	Misccal-21	MB released	28	MBHIBYT-23	MBPVT 2017

11	HB 1307	FB released	29	IBON-HI 13/14 P# 49	MBPVT 2017
12	IBON 174/03	MB released	30	USDF5-11	MBPVT 2017
13	HB 1963	MB released	31	MB Belgium-5	MBPVT 2017
14	Planet	MB released	32	IBON-HI 14/15 P# 96	MBPVT 2017
15	G 13-64 Belgium	Int. Nursery 2017 MB Belgium P# 11	33	IBON 174/03	MB released
16	Irina	MB released	34	Traveller	MB released
17	Gobae	FB released	35	Holker	MB released
18	Acc. 3514A (P# 7)	Accession	36	HB 1964	MB released

MBNVT=malt barley national variety trial. MBPVT=malt barley preliminary variety trial. MB=malt barley, FB=food barley

3. RESULTS AND DISCUSSION

In the present study highly significant ($P < 0.05$) difference were observed among genotypes for all measured traits. On the other hand except for days to heading, net blotch and scald severity, significant genotype by location interaction variation recorded. This indicated the performance of tested genotypes were not consistent across all location for the specified traits. Location effect also significant for nine traits measured in the experiment, which illustrated the differences in test locations (Table 3 and 4).

Table 3: Variances of random effects of 36 barley genotypes tested at five location during 2018 main cropping seasons

Groups	DHE	DMA	PH	SC	NB	TKW	HLW	GYLD	Protein	Extract
Loc	160.4**	447.6**	173.7**	399.8**	281.2**	33.6**	6.9**	599226	2.0**	0.7*
Gen:Loc	3.5	8.7**	29.1**	28.2	20.0	4.6**	2.5**	175693*	0.2**	0.5**
Loc:Rep	0.0	0.9	0.0	3.3	0.0	0.0	0.0	180803*	0.2**	0.1
Loc:Rep:Col	1.1	0.1	6.6	0.0	0.8	1.1	0.0	106208**	0.1**	0.0
Loc:Rep:Row	1.2	0.9	19.3**	41.3**	0.0	0.9	0.8*	233059**	0.1**	0.4**
Residual	29.0	11.1	75.6	198.3	124.6	13.7	6.8	595475	0.3	1.7

*,** significantly different at $Pr(Chisq) < 0.05$ and < 0.01 , respectively; DHE=days to heading (days); DMA= days to heading (days), PH=plant height (cm), SC=scald (%); NB=net blotch (%); TKW=thousand kernel weight (g); HLW=hectoliter weight(Kg hl⁻¹); GYLD=grain yield (Kg ha⁻¹)

Table 4: Fixed effects Type III Analysis of Variance of 36 barley genotypes tested at five locations with Satterthwaite's method

Groups	DHE	DMA	PH	SC	NB	TKW	HLW	GYLD	Protein	Extract
Gen	71.4**	34**	616**	375**	232**	77**	25**	915638*	2**	15**
NumDF	35	35	35	35	35	35	35	35	35	35
DenDF	137.2	137.2	137.2	101.3	105.1	136.4	139.5	125.4	127.8	131.3

*,** significantly different at $Pr(F) < 0.05$ and < 0.01 , respectively; DHE=days to heading (days); DMA= days to heading (days), PH=plant height (cm), SC=scald (%); NB=net blotch (%); TKW=thousand kernel weight (g); HLW=hectoliter weight(Kg hl⁻¹); GYLD=grain yield (Kg ha⁻¹)

The adjusted mean values of ten traits of 36 barley genotypes from the combined analysis of five location were presented in Table 5. Among the tested genotypes MBHIBYT-22, HB 1307 and MN Brite showed highest mean grain yield, through not significantly different from most of genotypes. On the other hand Entry # 3, #5, #6, #8, #1, #14, #15, #16, #20, #21, #22, #23, #24, #25, #26, #27, #28, #34 and #36 had good malt qualities (protein and extract values). Similarly, significant TKW and HLW variations were observed among the tested genotypes; IBON-HI 13/14 P# 128, HB 1963, IBON-HI 14/15 P# 144 and Bekoji-1 x Grace scored the highest mean HLW values (Table 5). Similarly, most registered European malt barley varieties were relatively susceptible to scald and net blotch diseases, whereas M135, MN Brite and

HB 42 had good resistance. Regarding plant height Gobae, had the higher mean plant height, while Irina, Traveller, Planet, G 13-64 Belgium had the lowest mean plant height. Additionally, HB 42 and the above mentioned registered malt barley genotypes had late maturing. However, most ICARDA materials included in the trials were relatively early maturing.

Table 5: Mean values of ten traits from combined analysis of 36 barley genotypes across five locations

Trt.	Genotype	DHE	DMA	PH	SC	NB	TKW	HLW	GYLD	Protein	Extract
1	Miscal-21 x Bahati	79 ^{a-e}	130 ^{c-h}	110 ^{ab}	34.0 ^{b-c}	26.3 ^{efg}	50.9 ^{a-f}	66.6 ^{a-i}	3690 ^{gh}	11.7 ^{b-e}	79.2 ^{g-m}
2	Miscal-21 x Karne	76 ^{b-j}	131 ^{b-f}	104 ^{a-f}	35.8 ^{b-e}	28.7 ^{c-g}	51.5 ^{a-d}	65.9 ^{b-j}	4123 ^{c-h}	11.3 ^{c-g}	79.4 ^{f-m}
3	M 135	75 ^{c-j}	129 ^{e-j}	97 ^{e-j}	24.1 ^e	20.0 ^g	46.9 ^{f-n}	65.5 ^{c-k}	4907 ^{a-d}	11.4 ^{c-g}	80.2 ^{c-j}
4	MN Brite	72 ^{ijk}	129 ^{e-i}	94 ^{f-k}	22.1 ^e	20.2 ^g	49.8 ^{a-i}	67.1 ^{a-g}	5016 ^{abc}	11.4 ^{c-f}	79.6 ^{e-l}
5	Burton	74 ^{c-k}	128 ^{e-j}	87 ^{jk}	58.7 ^a	21.3 ^{fg}	42.2 ^{o-r}	68.8 ^{ab}	4574 ^{a-g}	10.5 ^{ij}	81.9 ^{ab}
6	IBON 2013 P# 2	72 ^{ijk}	127 ^{f-j}	107 ^{a-e}	33.6 ^{b-c}	30.1 ^{b-g}	52.1 ^{ab}	68.3 ^{a-d}	4470 ^{a-g}	11.3 ^{c-g}	80.5 ^{b-i}
7	IBON 2013 P# 33	74 ^{e-k}	127 ^{f-j}	108 ^{a-d}	23.3 ^e	26.5 ^{efg}	49.6 ^{a-i}	67.2 ^{a-g}	4381 ^{a-h}	11.6 ^{b-e}	80.7 ^{b-g}
8	Bekoji-1 x Grace	77 ^{a-i}	127 ^{f-j}	112 ^a	47.5 ^{ab}	31.2 ^{b-g}	48.9 ^{a-k}	69.1 ^a	3915 ^{e-h}	11.2 ^{d-i}	80.7 ^{b-g}
9	HB 42	78 ^{a-g}	138 ^a	103 ^{a-g}	22.0 ^e	21.4 ^{fg}	52.8 ^a	62.2 ^l	4000 ^{d-h}	11.4 ^{c-f}	75.4 ^o
10	Miscal-21	73 ^{g-k}	126 ^{g-j}	98 ^{e-i}	42.6 ^{a-d}	27.4 ^{c-g}	47.7 ^{c-m}	68.3 ^{a-d}	4265 ^{b-h}	12.6 ^a	78.1 ^{lmn}
11	HB 1307	78 ^{a-h}	131 ^{b-g}	109 ^{abc}	38.6 ^{b-c}	28.7 ^{c-g}	48.0 ^{b-l}	65.1 ^{e-l}	5099 ^{ab}	11.0 ^{d-i}	78.7 ^{klm}
12	IBON 174/03	73 ^{f-k}	127 ^{f-j}	92 ^{g-k}	34.7 ^{b-c}	29.9 ^{b-g}	49.4 ^{a-i}	65.3 ^{d-l}	4319 ^{a-h}	11.1 ^{d-i}	79.5 ^{f-m}
13	HB 1963	78 ^{a-g}	130 ^{c-h}	102 ^{a-g}	33.8 ^{b-c}	32.5 ^{b-g}	50.3 ^{a-h}	69.3 ^a	4646 ^{a-f}	10.7 ^{f-j}	80.9 ^{b-f}
14	Planet	81 ^a	132 ^{b-f}	76 ^{lm}	43.8 ^{a-d}	42.7 ^{ab}	41.5 ^{qrs}	63.6 ^{i-l}	4109 ^{c-h}	9.1 ^l	82.6 ^a
15	G 13-64 Belgium	79 ^{a-c}	134 ^{a-d}	76 ^{lm}	42.9 ^{a-d}	26.4 ^{efg}	43.3 ^{m-r}	63.9 ^{b-l}	4091 ^{c-h}	9.5 ^{kl}	81.5 ^{a-d}
16	Irina	80 ^{a-d}	134 ^{abc}	71 ^m	45.1 ^{abc}	46.1 ^a	37.7 ^s	63.8 ^{i-l}	3535 ^h	10.1 ^{jk}	81.9 ^{ab}
17	Gobae	80 ^{a-d}	130 ^{c-h}	113 ^a	34.5 ^{b-c}	26.3 ^{efg}	41.8 ^{p-s}	62.4 ^{kl}	4419 ^{a-h}	11.7 ^{a-d}	76.9 ⁿ
18	Acc. 3514A (P# 7)	78 ^{a-h}	130 ^{c-h}	104 ^{a-f}	34.3 ^{b-c}	41.3 ^{abc}	44.6 ^{k-q}	63.1 ^{ijkl}	4430 ^{a-h}	10.8 ^{e-j}	78.0 ^{mn}
19	Acc. 17148 (P# 42)	78 ^{a-g}	131 ^{b-g}	106 ^{a-e}	34.1 ^{b-c}	33.9 ^{a-f}	45.8 ^{i-q}	64.1 ^{g-l}	4959 ^{abc}	11.0 ^{d-i}	77.9 ^{mn}
20	IBON-HI 13/14 P# 128	74 ^{c-k}	128 ^{f-j}	91 ^{b-k}	43.3 ^{a-d}	19.9 ^g	44.5 ^{l-r}	69.7 ^a	4822 ^{a-c}	10.4 ^{ij}	81.7 ^{abc}
21	IBON-HI 14/15 P# 144	75 ^{d-k}	127 ^{g-j}	95 ^{f-k}	47.7 ^{ab}	31.4 ^{b-g}	47.0 ^{e-n}	69.2 ^a	4561 ^{a-g}	10.4 ^{ij}	81.4 ^{a-d}
22	IBON-HI 14/15 P# 129	70 ^k	124 ^j	87 ^{jk}	46.7 ^{ab}	28.8 ^{c-g}	41.2 ^{rs}	68.3 ^{a-d}	4657 ^{a-f}	10.7 ^{f-j}	80.4 ^{b-j}
23	ICARDA GP-75	76 ^{b-j}	130 ^{c-h}	92 ^{g-k}	31.7 ^{b-c}	37.5 ^{a-e}	49.0 ^{a-k}	67.0 ^{a-h}	4123 ^{c-h}	11.2 ^{d-i}	81.0 ^{b-e}
24	IBON-HI 13/14 P# 41	71 ^{jk}	124 ^{ij}	84 ^{kl}	41.1 ^{bcd}	32.5 ^{b-g}	47.0 ^{f-n}	67.9 ^{a-e}	4473 ^{a-g}	11.3 ^{c-h}	81.7 ^{abc}
25	IBON-HI 14/15 P# 153	71 ^{jk}	126 ^{hij}	94 ^{f-k}	31.9 ^{b-e}	28.9 ^{c-g}	41.4 ^{rs}	65.7 ^{b-j}	4678 ^{a-f}	11.0 ^{d-j}	80.5 ^{b-h}
26	MBHIBYT-22	73 ^{h-k}	127 ^{f-j}	88 ^{ijk}	36.0 ^{b-e}	27.5 ^{d-g}	44.8 ^{k-r}	68.8 ^{ab}	5219 ^a	10.7 ^{f-j}	80.9 ^{b-f}
27	ICARDA GP-67	76 ^{b-j}	131 ^{b-g}	95 ^{f-k}	29.6 ^{cde}	26.4 ^{efg}	46.0 ^{h-p}	68.4 ^{abc}	4599 ^{a-g}	10.5 ^{g-j}	81.8 ^{abc}
28	MBHIBYT-23	74 ^{e-k}	129 ^{e-j}	103 ^{a-f}	33.6 ^{b-c}	25.1 ^{efg}	48.7 ^{a-l}	67.7 ^{a-e}	3986 ^{d-h}	11.1 ^{d-i}	80.5 ^{b-i}
29	IBON-HI 13/14 P# 49	74 ^{e-k}	129 ^{e-i}	103 ^{a-f}	27.9 ^{de}	26.2 ^{efg}	50.7 ^{a-g}	65.8 ^{b-j}	4811 ^{a-e}	11.6 ^{b-e}	78.9 ^{j-m}
30	USDF5-11	80 ^{abc}	134 ^{abc}	94 ^{f-k}	32.1 ^{b-c}	27.6 ^{d-g}	43.2 ^{n-r}	64.5 ^{f-l}	3982 ^{d-h}	11.6 ^{b-e}	78.4 ^{lmn}
31	MB Belgium-5	78 ^{a-f}	133 ^{b-e}	95 ^{f-j}	35.7 ^{b-e}	35.1 ^{a-e}	51.4 ^{a-e}	67.0 ^{a-h}	4105 ^{c-h}	12.3 ^{ab}	79.0 ^{i-m}
32	IBON-HI 14/15 P# 96	74 ^{e-k}	129 ^{e-i}	97 ^{d-j}	27.8 ^{de}	31.3 ^{b-g}	47.5 ^{d-n}	67.7 ^{a-e}	3916 ^{e-h}	11.7 ^{bcd}	78.9 ^{j-m}
33	Bekoji 1	78 ^{a-h}	130 ^{b-h}	111 ^{ab}	32.3 ^{b-c}	28.7 ^{c-g}	49.3 ^{a-j}	67.5 ^{a-f}	4342 ^{a-h}	12.1 ^{abc}	79.1 ^{h-m}
34	Traveller	81 ^{ab}	135 ^{ab}	74 ^{lm}	45.5 ^{abc}	40.1 ^{a-d}	44.9 ^{j-r}	65.0 ^{e-l}	3776 ^{fgh}	10.5 ^{hij}	82.6 ^a
35	Holker	75 ^{d-j}	129 ^{d-h}	10 ^{b-h}	36.5 ^{b-c}	28.8 ^{c-g}	46.4 ^{g-o}	67.5 ^{a-f}	4415 ^{a-h}	12.1 ^{abc}	79.5 ^{e-l}
36	HB 1964	76 ^{b-j}	129 ^{e-i}	103 ^{a-f}	32.7 ^{b-e}	27.8 ^{d-g}	51.9 ^{abc}	64.5 ^{f-l}	4533 ^{a-g}	12.1 ^{abc}	80.0 ^{d-k}
	CV %	3.11	1.89	10.42	12.41	14.19	7.19	2.65	3.60	6.15	1.92
	Mean	75.7	129.6	96.6	36.0	29.6	46.9	66.4	4387	11.1	80.0

DHE=days to heading (days); DMA= days to heading (days), PH=plant height (cm), SC=scald (%); NB=net blotch (%); TKW=thousand kernel weight (g); HLW=hectoliter weight (Kg hl⁻¹); GYLD= grain yield (Kg ha⁻¹)

Correlation of barley traits

Correlation explained the degree of association between two traits. The interrelationship of characters determines the response to selection in breeding programs. It also helps to apply indirect selection to improve the target traits of interest (Dewey and Lu, 1959; Asuero *et al.*, 2006; Joshi and Okuno, 2010). The barley improvement programs considered different phenological, morphological, agronomic and malt quality traits. Among these grain yield, disease severity and malt quality traits have prominent values. In this experiment grain yield showed negative and highly significant genotypic correlation with days to maturity and days to heading (Table 6). This is may be due to the effect of terminal drought after flowering, which affects the grain felling capacity of long maturing genotypes. Likewise, grain yield had negative correlation with net blotch disease severity. Marzougui and Chargui (2018) also found significantly negative association between grain yield and days to heading on 24 barley accessions evaluated under semi-arid climate condition. However, in field experiment on 320 barley genotypes (293 landraces and 27 released varieties), Shiferaw *et al.*, 2020 reported significantly positive correlation between grain yield and phenological traits like days to heading and maturity. Regarding malt quality traits, plant height and thousand kernel weight showed significant positive correlation with protein content. Whereas, genotypic correlation of protein content with scald was significantly negative. The other malt quality trait, extract was positively associated with scald and hectoliter weight but it had negative significant correlation with protein content. Significantly negative phenotypic correlations of extract with protein content were reported by Pržulj *et al.*, 2013 and Laidig *et al.* 2017. These correlation between scald and malt quality traits may be due to the inherent nature of most foreign malt barley genotypes included in the trial, which had high extract, low protein and high scald susceptibility in Ethiopian environment. In addition the disease pressure on barley may not produced a significant effect unless it affect the grain quality. Besides hectoliter weight may serve as indirect selection traits for important malt quality traits, extract. The strong negative association of protein with extract ($r=-0.62$) helps to select good malt barley genotypes by considering one of the two traits in malt barley improvement program, since high extract (> 80%) and low protein content (9-11.5%) is recommended by most malt companies and breweries. On the other hand scald and net blotch were negatively correlated with plant height. This showed that these locally released barley genotypes which have long plant height had better disease resistant than imported barley genotypes (shorter plants) included in this experiment. In addition a significant positive correlation was observed between plant height and thousand kernel weight, similar result also reported by Shiferaw *et al.*, (2020) and Singh *et al.* (2015). Moreover, significantly higher association were observed between days to heading and maturity and many studies (Mehripour *et al.*, 2014; Molla *et al.*, 2018; Ghimire and Mahat, 2019; Singh *et al.*, 2015; Shiferaw *et al.*, 2020) had similar findings with this result. This in turn helps to indirectly and efficiently select for early/medium maturing genotypes using heading dates, since researcher face difficulties in recording maturity date when the plants were forced to mature due adverse environmental condition.

Table 6: Genotypic correlations among 10 traits for 36 barley genotypes

	DHE	DMA	PH	SC	NB	TKW	HLW	GYLD	Protein	Extract
DHE	1.00									
DMA	0.84**	1.00								
PH	-0.01	-0.15	1.00							
SC	0.07	0.07	-0.53**	1.00						
NB	0.25	0.16	-0.33**	0.36*	1.00					
TKW	0.04	0.16	0.55**	-0.39*	-0.24	1.00				
HLW	-0.48**	-0.36*	0.02	0.13	-0.21	0.27	1.00			
GYLD	-0.39**	-0.33*	0.09	-0.25	-0.41**	0.06	0.08	1.00		
Protein	0.01	-0.01	0.51**	-0.51**	-0.21	0.39*	-0.11	-0.09	1.00	
Extract	-0.19	-0.10	-0.52**	0.49**	0.25	-0.19	0.45**	0.01	-0.62**	1.00

*, ** significantly different at $P < 0.05$ and 0.01 , respectively; DHE=days to heading (days); DMA= days to heading (days), PH=plant height (cm), SC=scald (%); NB=net blotch (%); TKW=thousand kernel weight(g); HLW=hectoliter weight(Kg hl⁻¹); GYLD=grain yield (Kg ha⁻¹)

GGE biplot

GGE biplot is an effective tool for analysing MET data. It had versatile graphical approach with different function (Yan, 2000, Yan, 2001, Yan *et al.*, 2007). The which won were patterns of GGE have a polygon drawn on the genotypes that are furthest from the biplot origin so that all other genotypes are contained within the polygon. Then the polygon subdivided into mega environments by perpendicular lines drawn from biplot origin (Yan *et al.*, 2007). In the present study the five locations falls in to four mega environments, which means Kofele and Debreberhane grouped in one mega environment and the remaining three falls into separate mega environments (figure 1). Accordingly, entry # 15 and 24 were the winning genotype at Holetta and Adadi locations. Similarly, entry # 29 and # 36 scored high mean grain yield value at Bekoji. On the other hand Entry # 22 was the best performing genotype in the mega environment, which contains Debreberhane and Kofele locations. Generally, the existence of different winning genotypes at different mega environments indicate the existence of GEI interaction and researcher should further investigate the different environmental variable which causes this variations.

Which Won Where/What

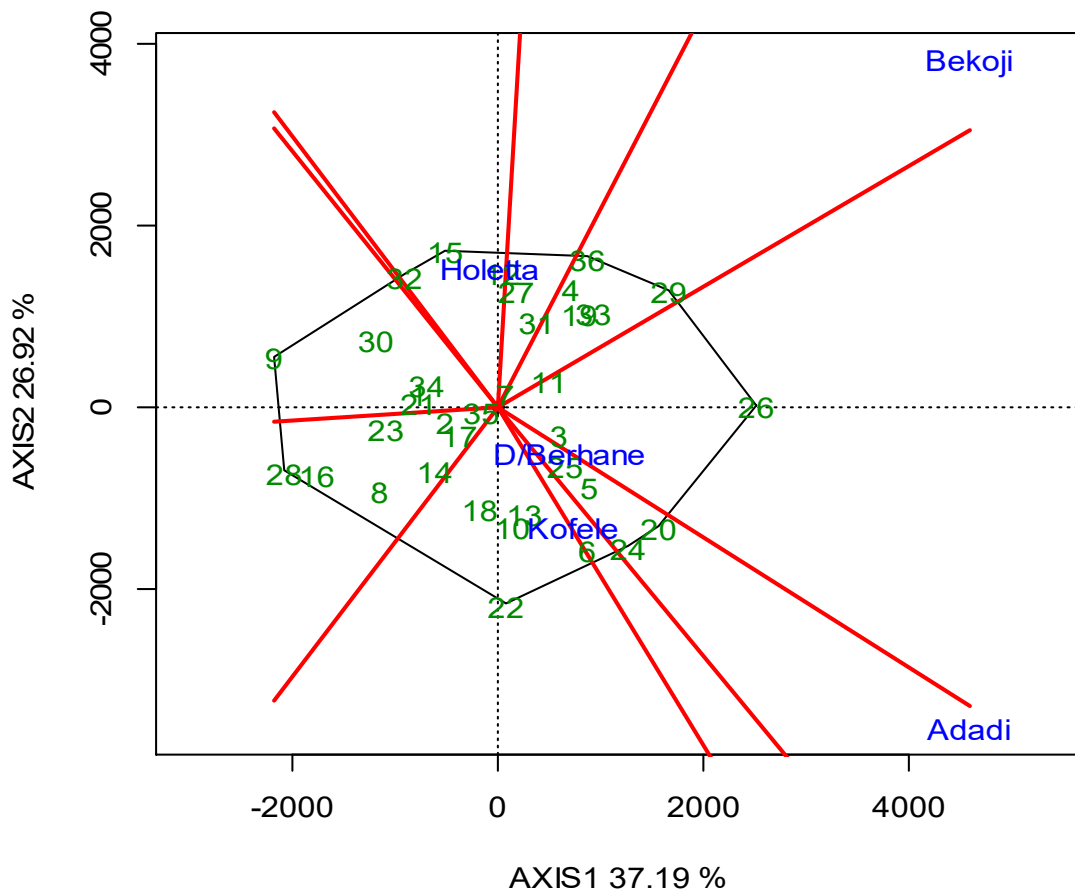


Figure 1: GGE biplot (the which won where view) using data from 36 barley genotypes (numbers) grown in five locations

Mean vs stability view of GGE biplot presented in Figure 2. The projection of a cultivar from y-axis and x-axis showed their average performance and stability, respectively (Yan, 2001). Genotype 26 had the highest yield (as it had the large projection from y axis) and the most stable genotype (as it had zero projection from x-axis). But this genotype was not the winner in any of the test locations (Figure 1). Similarly, Genotype 29, 20 and 24 are the next high yielding genotypes but they had relatively less stability. Genotype 3 (M 135), 11 (HB 1307) and 7 (IBON 2013 P# 33) showed better stability with moderate average yield. Genotype 9 and 22 are least yielding and the most unstable genotypes, respectively.

Additionally, in Figure 2 the distance of the environment from the plot origin showed its discriminating ability (Yan, 2001). Hence, Debreberhane was not discriminating and representative environment. Then Kofele and Holetta was moderately discriminating and representative. Nevertheless, Bekoji and Adadi had large distances both from the origin (discriminating) and from the Y axis (not representative).

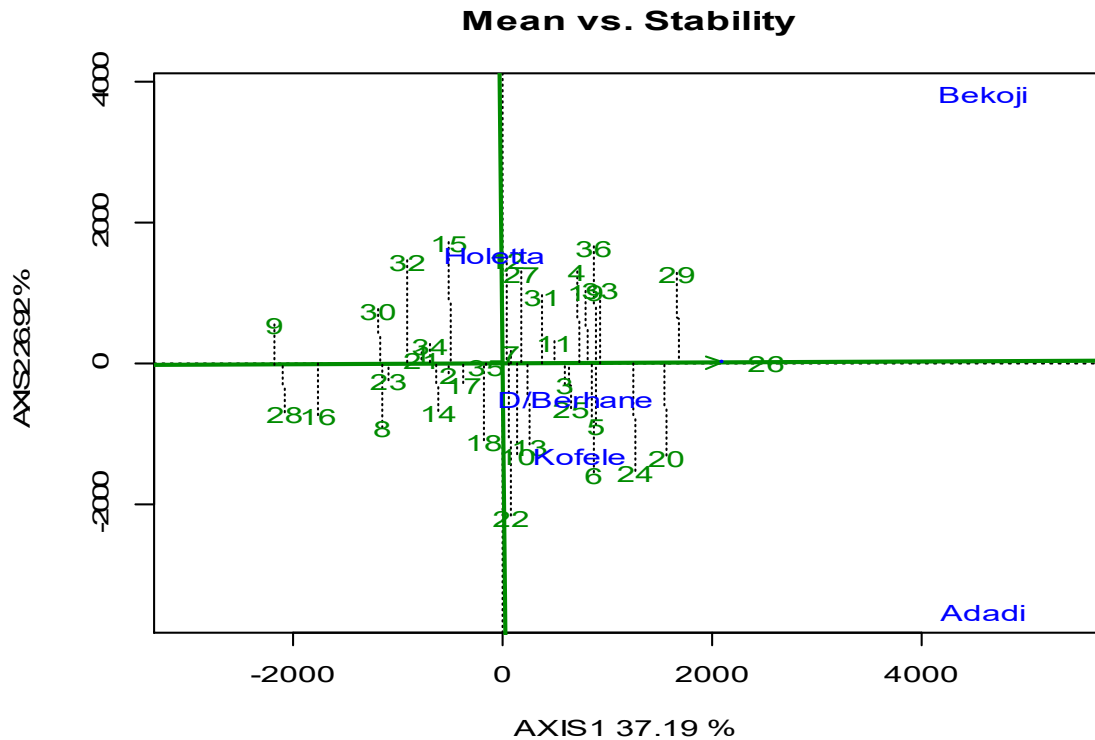


Figure 2: Mean vs stability view of GGE biplot using data 36 barley genotypes (numbers) evaluated at five locations

4. CONCLUSION

In this experiment all traits showed substantial genotype and genotype by location interaction effects, which indicated the performances of test genotypes were different across test locations. Most tested genotypes had an acceptable values for most important malt quality traits (protein and extract). Specifically, the candidate genotype (MBHIBYT-22) had the highest mean grain yield with good malt quality character. This genotype also had good stability; it could be recommended for further verification. Among good malt barley genotypes entry # 15 (G 13-64 Belgium) was specifically adopted to Holetta. Whereas, entry # 24 (IBON-HI 13/14 P# 41) can be recommended for Adadi location. Entry #22 (IBON-HI 14/15 P# 129) were specifically adopted to Kofele and Debreberhane locations. Additionally, hectoliter weight and protein content can be used as indirect selection criteria to improve malt extract in the malt breeding program.

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