Evaluation of Food Barley Genotypes for Grain Yield and Agronomic Traits in the Central Highlands of Ethiopia

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Abstract

The present study was undertaken to evaluate the performance of promising food barley genotypes for grain yield and yield related traits. The trial was conducted in 2017 and 2018 main cropping season using randomized complete block design with three replications. Variance analysis and GGE biplot were used to understand the nature of genotype × environment interaction (G × E) in a grain yield data collected from eighteen barley genotypes grown in eight environments (Location and year combinations). The combined analysis of variance (ANOVA) showed significantly higher genotype, environment and genotype by environment interaction effects for all the traits studied. Accordingly, genotypes EH1493 X HB1307 (G10) and HB 1307 X ND25160 (G2) showed the highest mean grain yield of 4558 kg ha⁻¹ and 4499 kgha⁻¹, respectively. GGE biplot showed that G10 was the winner genotype at BK18, DB18 and HO18 environments and it has good grain yield stability across the testing environments. Therefore, G10 is a potential candidate variety to be included in the variety verification trial for possible release.

Keywords: ANOVA, GGE biplot, grain yield, stability **DOI:** 10.7176/ALST/84-02 **Publication date:** December 31st 2020

INTRODUCTION

Barley (*Hordeum vulgare* L) is an important stable food crop and has high potential in narrowing food deficit and enables to achieve food security in Ethiopia. It sustains a livelihood of millions of people residing on the highlands and fetches a substantial income for farmers. It is widely grown in diverse rain-fed agro-ecological zones of Ethiopia at an altitude of 1400 to over 3600 m.a.s.l. The crop is more diversified and prominent in areas between 2300 to 3400 m.a.s.l (Zemede, 2002). Food barley is commonly cultivated in stressed areas where soil erosion, soil acidity, occasional drought or frost limits the choice of other crops. It is cultivated in different production systems, namely; early, late, *Belg* and residual moisture (Yirga *et al*, 1998).

Barley is the fifth important cereal crops after maize, tef, wheat and sorghum. It is produced on about 1 million hectares of land from which 2.0 million tons of grain are produced annually (CSA, 2018). The productivity of barley in Ethiopia is low (2.1 t/ha) as compared to world average of 3.1 t/ha. The low productivity is mainly attributed to abiotic stresses (soil acidity, frost, water logging, low moisture and low soil fertility) and biotic stresses (diseases, pests and weeds).

In general, barley remains an important crop in the Ethiopian agriculture because of its role in providing food for the rapidly growing population (3.0 % per year). Therefore, there is a need to focus on barley improvement and developing alternative varieties to the different production systems and agro ecologies. Variety development effort is a dynamic process as one breeding program is required to provide a large option of varieties for diverse environmental conditions. Moreover, available varieties become obsolete due to break down of disease resistance and poor performance. Hence, it is crucial to provide new improved varieties that could go with the improved production packages identified on a continuous basis. Increasing the productivity of food barley is very important for the resource poor smallholder farmers in Ethiopia to improve the output and income to satisfy the local food demand of the rapidly growing population.

The National Barley Research program at Holetta and Kulumsa in collaboration with D/Berhane regional research center has conducted a multi-location variety trial, including lines developed from local collections, introductions and local crosses with the main objective of identifying stable and superior varieties to be released for production and use in the future breeding.

MATERIALS AND METHODS

A total of eighteen food barley genotypes including three check varieties were evaluated using completely randomized block design with three replications. The experiment was executed at Holetta, Jeldu, Debrebirhan, Bekoji and Kofole during the main cropping season in 2017 and 2018 under rain-fed conditions. Descriptions of the testing sites are described in Table 1. The materials were evaluated for eight quantitative traits at eight locations across years (Table 2). The traits studied were days to heading (days), days to maturity (days), plant height (cm),

thousand kernel weight (gm), hectoliter weight (Kg hl⁻¹), grain yield (Kg ha⁻¹), scald and net blotch disease severity (%). A plot size of 1.2 m by 2.5 m was used to lay the experiment and the spacing between blocks and plots within blocks were 1.5 m and 0.4m, respectively. Analysis of variance (ANOVA) was carried out using R software to determine the effect of genotype, environment and their interaction on various traits of the food barley genotypes. Linear mixed effect model (lmer) of package lme4 was used for data analysis and the environments were considered as random and genotypes as fixed effects (R Core Team, 2017). The following ANOVA models have been used to test the performance of genotypes at each and combined locations, respectively (Singh and Ceccarelli 1996).

 $Y_{ij}=\mu+G_i+B_j+e_{ij} \mbox{ and } Y_{ijk}=\mu+G_i+E_j+GE_{ij}+Bk_{(j)}+e_{ijk}.$

Where, Y_{ij} = observed value of genotype i in block j, Y_{ijk} = observed value of genotype i in block k of environment j, μ = grand mean of the experiment, G_i = the effect of genotype i, B_j = the effect of block j, $Bk_{(j)}$ = the effect of block k in environment j, e_{ij} = error effect of genotype i in block j, E_j = environment effect, GE_{ij} = the interaction effect of genotype i with environment j, e_{ijk} = error (residual) effect of genotype i in block k of environment j. In addition GGE bi-plots were performed to determine stability of the tested food barley genotypes using GGEBiplotGUI package of R-software (R Core Team, 2017). Table 1. Description of testing sites

No.	Testing sites	Altitude (m)	Rainfall (mm)	Longitude	Latitude
1	Holetta	2400	1100	38°38'E	9°00'N
2	Jeldu	2800	1200	38°03'E	9°17'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 g	enotypes and	environments	used for tl	ne experiment
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Entry	Genotype	Location	Year	Environment code
G1	EH 1493 x PPB 25	Bekoji	2017	BK17
G2	HB 1307 x ND 25160	Bekoji	2018	BK18
G3	HB 1493 x ND 25160	Kofele	2017	KF17
G4	EH 1493 x HB 42	Kofele	2018	KF18
G5	Cross # 41/98 x HB 42	Holetta	2017	HO17
G6	EH 1493 x Cross 41/98	Holetta	2018	HO18
G7	ARDU 12-60B x HB 1307	Jeldu	2018	JL18
G8	HB 1307 x PPB 25	Debreberhane	2018	DB18
G9	HB 1307 x Cross # 41/98			
G10	EH 1493 x HB 1307			
G11	Estayesh x Lab # 87			
G12	Cross # 41/98 X HB 1307			
G13	Tolese x HB 1307			
G14	HB 1307 X PPB 53			
G15	Shege X Cross #41/98			
G16	HB 1965			
G17	HB 1966			
G18	Local check			

RESULTS AND DISCUSSION

Combined analysis of variance showed that genotype, environment and the genotype x environment interaction had a highly significant effect on all the traits studied (Table 3). The significant genotype effect showed the existence of significant variability among the tested genotypes. Highly significant genotype x environment interaction effect observed in this trial showed the tested genotypes performed differently across the testing environments for the traits. Therefore, researches involved in the barley improvement program should have to see the adaptability of genotypes to different test environments. Similarly, significant difference among the testing environments also observed. In the present study all traits showed the higher contribution of the environmental component to the total sums of squares and similar results were reported by Abtew *et al.*, (2015).

Table 5. Weah square values for combined analysis of variance of 18 food barley genotype	Table 3. Mean sq	uare values for	combined an	nalysis of	variance o	f 18 foo	d barley genotype
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	DF	DHE	DMA	PLH	SC(DF)§	NB(DF)§	TKW	HLW	GYLD
Gen Env	17 7	89.6** 2206**	96.9** 8145 ^{**}	174** 5102**	602(17) ^{**} 22733(5) ^{**}	131(17)** 31876(5)**	151.5** 2104**	26.5** 1219**	1448234** 23019573**
Gen:env	119	11.5**	22.0**	51**	250(85)**	89(85)**	19.2**	7.3*	1443851**
Env:rep	16	8.3	13.7	155	383(12)**	154(12)**	10.4	7.9	2059673**
Residuals	272	7.5	8.8	33	138(204)	56(204)	9.9	5.5	657602
CV		3.3	2.1	5.1	36.1	21.1	7.5	3.7	19.4
Mean		82.7	140.8	113.5	32.5	35.6	42.1	64.1	4190.8

DF=degree of freedom, DHE=days to heading, DMA= days to maturity, PLH=plant height, SC=scaled, NB=net blotch, TKW= thousand kernel weight, HLW= hectoliter weight, GYLD= grain yield, **, * Significant at 5% and 1% probability level, ns=non significant, §these traits were not recorded at DB18 and JL18 mean squares under those traits are angular transformed values

Based on the average data over eight environments, G10 (4558 kg ha-¹) and G2 (4499 kg ha-¹) scored the highest mean grain yield, though not significantly different from the recently released standard check varieties (HB1965 and HB 1966). Accordingly, G10 and G2 had 9.75 and 8.33% grain yield advantage over the highest yielding check variety (HB 1966) (Table 4). The highest mean hectoliter weight (HLW) and thousand kernel weight (TKW) values was scored by G7. The two high grain yielding genotypes (G10 and G2) also had higher HLW and moderate TKW values. Regarding disease related traits most test genotypes showed moderate tolerance to scald and net blotch disease. The check variety HB 1965 and 1966 scored 21.2 and 26.7% severity for scald and 33.3% and 32.8% severity for net blotch. Similarly, the candidate genotypes G10 and G2 also showed moderate scald (36.2, 29.0%) and net blotch (39.0, 37.2%) resistance, respectively. The ranges of plant height values of 106-115 cm were recorded with the lower end corresponding check variety HB 1965 while the upper end corresponds to the local check variety, this longer plant height is in agreement with the inherent nature of most local varieties. Furthermore, the phenological traits showed lower variability with, five and seven days differences in mean days to heading and maturity respectively (Table 4). Based on agronomic and grain physical quality traits (HLW and TKW), G10 is the top ranking genotype. Thus, G10 and the other two promising varieties, namely G2 and G7 can be used for future breeding program as donor parents.

Table 4. Means from the combined analysis of variance on 8 traits of 18 food barley genotypes tested at 8 environments.

Trt#	Genotype	DHE	DMA	PLH	SC§	NB§	TKW	HLW	GYLD
G1	EH 1493 x PPB 25	80.9 ^{de}	144.3 ^a	109.7 ^{c-f}	30.0 ^{cde}	35.5 ^b	45.6 ^{ab}	64.6 ^{bc}	4037 ^{abc}
G2	HB 1307 x ND 25160	82.4 ^{a-e}	142.0 ^{abc}	109.8 ^{c-f}	29.0 ^{cde}	37.2 ^{ab}	43.0 ^{b-e}	64.7 ^{abc}	4499ª
G3	HB 1493 x ND 25160	84.8 ^{abc}	143.7ª	116.1ª	26.2 ^{de}	36.8 ^{ab}	45.6 ^{ab}	63.8 ^{bcd}	4103 ^{abc}
G4	EH 1493 x HB 42	80.7 ^e	141.2 ^{a-d}	111.3 ^{a-e}	31.2 ^{b-e}	32.8 ^b	44.0 ^{a-d}	64.5 ^{bc}	4331 ^{abc}
G5	Cross # 41/98 x HB 42	85.2 ^{ab}	144.8 ^a	113.6 ^{abc}	28.4 ^{cde}	35.5 ^b	43.9 ^{a-d}	64.4 ^{bc}	4270 ^{abc}
G6	EH 1493 x Cross 41/98	82.8 ^{a-e}	141.5 ^{a-d}	113.2 ^{abc}	35.6 ^{a-d}	36.2 ^b	43.7 ^{bcd}	64.3 ^{bc}	4262 ^{abc}
G7	ARDU 12-60B x HB	80.2 ^e	142.4 ^{ab}	113.1 ^{a-d}	35.7 ^{a-d}	35.6 ^b	47.9ª	66.7ª	3693 ^{bc}
	1307								
G8	HB 1307 x PPB 25	82.1 ^{b-e}	143.1 ^{ab}	110.9 ^{b-e}	32.9 ^{bcd}	34.5 ^b	43.8 ^{bcd}	64.5 ^{bc}	4326 ^{abc}
G9	HB 1307 x Cross #	83.9 ^{a-d}	142.3 ^{ab}	108.3 ^{def}	29.5 ^{cde}	34.5 ^b	42.7 ^{b-e}	64.9 ^{abc}	4219 ^{abc}
	41/98								
G10	EH 1493 x HB 1307	82.1 ^{cde}	141.9 ^{a-d}	109.9 ^{c-f}	36.2 ^{a-d}	39.0 ^{ab}	42.4 ^{b-e}	65.5 ^{ab}	4558ª
G11	Estayesh x Lab # 87	85.5ª	143.6ª	113.2 ^{a-d}	44.5 ^a	32.2 ^b	40.0 ^{de}	64.4 ^{bc}	4408 ^{ab}
G12	Cross # 41/98 X HB	80.6 ^e	139.4 ^{bcd}	110.4 ^{b-f}	36.7 ^{a-d}	34.5 ^b	41.4 ^{cde}	65.0 ^{abc}	4279 ^{abc}
	1307								
G13	Tolese x HB 1307	82.2 ^{b-e}	138. ^{cd}	111.2 ^{a-e}	31.2 ^{b-e}	38.4 ^{ab}	39.4°	64.6 ^{bc}	4101 ^{abc}
G14	HB 1307 X PPB 53	83.3 ^{a-e}	141.4 ^{a-d}	107.2 ^{ef}	38.4 ^{abc}	34.5 ^b	41.5 ^{cde}	65.3 ^{ab}	4153 ^{abc}
G15	Shege X Cross #41/98	84.3 ^{abc}	143.3 ^{ab}	111.2 ^{a-e}	41.7 ^{ab}	34.4 ^b	40.9 ^{de}	65.0 ^{abc}	4357 ^{abc}
G16	HB 1965	80.2 ^e	138.0 ^d	105.6^{f}	21.2 ^e	33.3 ^b	40.1 ^{de}	62.0 ^d	4035 ^{abc}
G17	HB 1966	82.1 ^{b-e}	143.9ª	109.2 ^{c-f}	26.7 ^{de}	32.8 ^b	44.1 ^{abcd}	64.0 ^{bcd}	4153 ^{abc}
G18	Local check	85.0 ^{abc}	142.7 ^{ab}	114.9 ^{ab}	30.0 ^{cde}	43.4 ^a	45.1 ^{abc}	63.1 ^{cd}	3659°

DHE=days to heading, DMA= days to maturity, PLH=plant height (cm), SC=scaled (%), NB=net blotch (%), TKW= thousand kernel weight (g), HLW= hectoliter weight (Kg hl⁻¹), GYLD= grain yield (Kg ha⁻¹), §these traits were not recorded at DB18 and JL18

Separate analysis for each of the test environments showed consistently large variation among test varieties for grain yield (Table 5). G10 and G2 gave consistently highest grain yield in all test environments exceeding the

check varieties. These genotypes scored mean grain yield ranged from 3628-5440 kg ha⁻¹ and 3577-5389 kg ha⁻¹, respectively, and this showed both genotypes could have a potential to be selected for variety verification trial. (Table 5). The two standard check genotypes HB 1965 and HB1966 had relatively lower grain yield than the candidate genotypes across test environments. Beside G7 and local check G18 recorded lower mean values in all locations.

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Trt	Genotype	BK1	HO1	KF1	BK1	DB1	HO1	JL1	KF1	Mea
#		7	7	7	8	8	8	8	8	n
G1	EH 1493 x PPB 25	4906	3300	3094	4437	3906	4611	4438	3634	4037
G2	HB 1307 x ND 25160	5389	3783	3577	4920	4389	5094	4921	4117	4499
G3	HB 1493 x ND 25160	4957	3350	3145	4488	3956	4661	4488	3685	4103
G4	EH 1493 x HB 42	5214	3608	3403	4745	4214	4919	4746	3943	4331
G5	Cross # 41/98 x HB 42	5133	3526	3321	4664	4132	4837	4665	3861	4270
G6	EH 1493 x Cross 41/98	5096	3489	3284	4627	4095	4800	4628	3824	4262
G7	ARDU 12-60B x HB	4540	2934	2728	4071	3539	4244	4072	3268	3693
	1307									
G8	HB 1307 x PPB 25	5197	3590	3385	4728	4196	4901	4729	3925	4326
G9	HB 1307 x Cross # 41/98	5069	3462	3257	4600	4068	4773	4601	3797	4219
G10	EH 1493 x HB 1307	5440	3833	3628	4971	4439	5144	4972	4168	4558
G11	Estayesh x Lab # 87	5250	3644	3439	4782	4250	4955	4782	3979	4408
G12	Cross # 41/98 X HB 1307	5142	3536	3331	4673	4142	4847	4674	3871	4279
G13	Tolese x HB 1307	4965	3359	3154	4496	3965	4670	4497	3694	4101
G14	HB 1307 X PPB 53	5005	3399	3193	4536	4004	4709	4537	3733	4153
G15	Shege X Cross #41/98	5195	3589	3383	4726	4194	4899	4727	3923	4357
G16	HB 1965	4908	3301	3096	4439	3907	4612	4440	3636	4035
G17	HB 1966	5026	3419	3214	4557	4025	4730	4558	3754	4153
G18	Local check	4463	2857	2651	3994	3463	4168	3995	3192	3659

Stability of the test genotypes across environments

The discussion in the previous variety trials based mostly on genotype main effect (G) and genotype-byenvironment interactions (GE) are treated as noise or a confounding factor (Yan and Tinker, 2006). But recently various methods developed to study GxE interaction and determine whether or not a genotype is stable in performance over a range of environments. The GGE biplot method consists of a set of biplot interpretation methods to evaluate genotype and test-environment (Yan *et al.*, 2007). The "Mean vs stability" view of GGE biplot helps to evaluate genotypes based on their mean performance and stability (Figure 1). The graph consists of xaxis passes through the biplot origin and the marker of the average environment, which is defined by the average PC1 and PC2 scores of overall environments. The stability and average performance of the genotypes was measured by their projection to the Y- axis and X axis, respectively (Yan, 2001). Therefore, G10 had both the highest average yield and stability. Then G-2 scored the second highest mean grain yield performance, but relatively it lacks stability and more adapted to specific environment, HO18. Similarly G11 (Estayesh x Lab # 87) had better mean grain yield and more adapted to environment, JL18. Among the check varieties G17 (HB 1966) revealed moderate mean grain yield and good stability. The local check variety G18 had the lowest average yield and the least stable variety (Figure 1).

The "which-won-where" pattern of a genotype by environment data set is an important feature of GGE biplot. The Biplot contain a polygon drown on genotypes that are furthest from the biplot origin so that all other genotypes are contained within polygon and these genotypes located on the vertices of the polygon performed either the best or the poorest in one or more environments (Yan and Tinker, 2006). The "which-won-where" view of the GGE biplot is an effective visual tool in mega-environment analysis (Yan *et al.*, 2007). G10 was the winner in environments DB18, BK18 and HO17. G2 was more adapted to the testing environment HO18. G11 was the highest yielding genotype in environments JL18. The check genotype G17 (HB1966) was a vertex genotype with no testing location specifically adapted to it. The local check variety (G18) was relatively low yielding genotype at all environments (Figure 2).



Figure 1. Mean grain yield performance and stability of genotypes based on the $G \times E$ data



Figure 2. The which-won-where view of the GGE biplot of grain yield of Food barley genotypes based on the G \times E data

CONCLUSION

In the present study, the eighteen food barley genotypes showed significant genetic, environmental and genotype by environment interaction effects for all traits considered in the experiment. Genotypes, G10 and G2 showed the highest mean grain yield potential at all environments. These genotypes showed moderately resistant to scald and net blotch, and acceptable TKW and HLW values. Based on "Mean vs stability" view of GGE biplot, G10 was the highest yielding and stable genotype. While G2 was the second highest yielding genotypes but it is relatively unstable. Similarly "Which won where" pattern of GGE biplot confirmed that G10 gave consistently highest mean grain yield across the test environments and G2 specifically adapted to HO18 environment. Therefore, based on mean performance and stability, G10 is the best potential variety identified for possible variety verification trial

for the mega and other similar environments. In addition, G10 and the other two Genotypes, G2 and G7 will be included in the food barley crossing program as potential parents for their good yield potential and physical grain quality traits.

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