ORIGINAL ARTICLES

Registration of Two Food Barley (Hordeum vulgare L.)Varieties (HB 1965 and HB1966) for the Highlands of Ethiopia

[1]Thomas Tsige, [1]Tigist Shiferaw, [1]Wondimu Fekadu, [1]Berhane Lakew, [2]Shimles Gezahegn, [3]Kefyalew Taye, [2]Workineh Mekasa, [2]Anberber Haile, [1]Seid Ahmed

[1]Holetta Agricultural Research Center, P.O. Box 31, Holetta, Ethiopia
[2]Kulumsa Agricultural Reserach Center, P.O. Box 489, Assela, Ethiopia
[3]Debreberhan Agricultural Reserach Center, P.O. Box 112, Debreberhan, Ethiopia
Corresponding author: thomas.tsige@yahoo.com

ABSTRACT

Twelve food barley genotypes advanced from the local crossing program and germplasmsintroduced from ICARDA were evaluated in a multi-location variety trial to identify stable genotypes with high grain yield, desirable agronomic characters and good level of disease resistance. The experiment was conducted in a randomized complete block design with three replications at eleven environments during the 2014 and 2015 cropping seasons. Analysis of variance (ANOVA) depicted that SCFBRVT P#3/11 and FBRVTB P#24/11 exhibited the highest mean grain yield potential with good agronomic performance and good level of disease resistance across testing environments.The significant genotype by environment interaction (G×E) in the combined analysis of variance necessitated applying stability analysis in grain yield. Therefore, among the tested genotypes FBRVTB P#24/11 showed the highest mean grain yield and stabilityin most stability parameters considered in the experiment followed by SCFBRVT P#3/11. Accordingly, the two varieties, SCFBRVT P#3/11 and FBRVTB P#24/11 were promoted to variety verification trial in 2016, and released in 2017 under the name HB 1965 and HB1966, respectively. Both varieties showed good physical grain quality coupled with high grain yield potential of 5.3and 5.5 t/ha, respectively. The two varieties have shown good level of disease resistance to leaf blotches and scald, good lodging tolerance and high biomass yield. HB 1965 and HB 1966 are six rowed types suitable to the highlands of major barley growing areas of the country. Moreover, HB 1965 is an early maturing variety suitable for frost-prone areas and double cropping barley production systems,while HB1966 is a long maturing variety suitable for the cool highland barley growing areas.

Key words:, G×E, Food barley, Stability parameters

INTRODUCTION

Barley (*Hordeum vulgare* L.) is one of the major cereal crops grown in Ethiopia and its production is an old heritage with a large number of landraces and traditional practices(Zemede, 2000). Currently, its total area coverage in the main season isclose to one million hectarewith total annual grain production of about 2.05 million tons (CSA, 2018).

Barley improvement in Ethiopia was started in the 1950s through the introduction of exotic germplasm and collections of local landraces with an objective of improving grain yield potential, grain quality and resistant/tolerant to biotic as well as abiotic stresses (Hailu *et al.*, 1996). Despite the breeding endeavors, in the last decades varieties released by the federal and regional research centers were limited in quantity and standard quality attributes (Wondimu *et al.*,2013). Therefore, currently the barley research program carried out different breeding activities using landraces, foreigngermplasms andgenetic variability created locally throughhybridization.The objective of this paper is to present the results of a variety trial conducted at eleven environments in 2014 and 2015 cropping seasons with subsequent identification and release of two outstanding food barley varieties, namely HB 1965 (SCFBRVT P#3/11) and HB 1966 (FBRVTB P#24/11).

MATERIALS AND METHODS

A total of twelvefood barley genotypes, including two improved (Cross # 41/98 and EH 1493)and one local check were evaluated in seven testing locations (Adet, Bekoji, Debreberhan, Dabat, Holetta, Jeldu and Kofele) for two consecutive years (2014 and 2015) in a total of eleven location-year combination environments. The genotypes for this study were selected based on the previous field performances in the preliminary variety trial (Table 1).These test genotypes were derived from hybridization of elite genotypes and landrace selections. The experimental genotypes were grown in a randomized complete block design with three replications. A plot consisted of six rows spaced 0.2m apart and the row length was 2.5m, with area of $2m^2$ harvested from the four central rows for yield determination.

Plots were fertilized according to the recommendations of 41kg ha^{-1}N and 46 kgP_2O_5 ha^{-1}.Seeds were drilled at a rate of 85 kg ha^{-1} as uniformly as possible.A11 management practices were performed in accordance with the recommended food barley husbandry packages for the specific test locations and soil types. Observations were made on five important phenologic, agronomic and yield related traits including days to heading,days to maturity ,plant height,thousand seed weight and grain yield . Data on scald and net blotch disease severitywere also recorded by visually estimating the percentage of leaf area diseased and rated using the Saari and Prescott (1975) scale for disease severity.

Data on all the quantitative traitsweresubjected to analysis of variance using SAS (SAS Institute, 2002). The locations were considered as random and genotypes as fixed effects, and a mixed effect model ANOVA was used for statistical analysis. Bartlett's test for homogeneity of variance was carried out to ensure homogeneity of error variances of the individual experiments. Therefore,the analyses of variance for each environment and over locations were performed using the following model (Singh and Ceccarelli, 1995).

$Y_{ij} = \mu + g_i + b_j + e_{ij}$ and $Y_{ijk} = \mu + g_i + E_j + GE_{ij} + b_{k(j)} + e_{ijk}$

Where, Y_{ij} = observed value of genotype i in block j, μ = grand mean of the experiment, g_i = the effect of genotype i, b_j = the effect of block j,e_{ij} = error effect of genotype i in block j. Y_{ijk} = observed value of genotype i in block k of environment j, E_j = the environment effect, GE_{ij} = the interaction effect of genotype i with environment j, $b_{k(j)}$ = the effect of block in environment j, e_{ijk} = error (residual) effect of genotype i in block k of environment j.

Specifically, the scale data (0-9) obtained on disease severity were 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.

The stability of the genotypes for grain yield across the testing environments was investigated using different stability parameters. The following analyses were performed using GEA-R (2016) Version 4.0 software for different stability models. Including Wricke'secovalence (Wi) (Wricke, 1962), Nassar and Hühn's non-parametric measure of stability ($S^{(1)}$),average absolute rank difference of genotype on the environment and ($S^{(2)}$): variance ranges of environments (Nassar and Hühn, 1987), Shuckla'sstability variance (Shukla, 1972), Francis andKanenberg's (1978) variation coefficient (CVi), superiority index (PI) (Lin and Binns, 1988), and GGE bi-plots.The GGE biplot was done according to the method suggested by Yan *et al*. (2000).

Table 1. Lists of environments and genotypes used for the study

Location	Year	Environment Code	Genotypes	Genotype code
Adet	2015	AD15	1. MSFC P#15/11	G-1
Bekoji	2014	BK14	2. SCFBRVT P#3/11 (HB 1965)	G-2
Bekoji	2015	BK15	3. MSFC P#24/11	G-3
Debreberhane	2015	DB15	4. SCFBRVT P#7/11	G-4
Dabat	2015	DA15	5. SCFBRVT P#5/11	G-5
Holetta	2014	HA14	6. SCFBRVT P#8/11	G-6
Holetta	2015	HA15	7. SCFBRVT P#2/11	G-7
Jeldu	2014	JL14	8. SCFBRVT P#1/11	G-8
Jeldu	2015	JL15	9. FBRVTB P#24/11 (HB1966)	G-9
Kofele	2014	KF14	10. Cross # 41/98	G-10 –Std.chk
Kofele	2015	KF15	11. EH 1493	G-11- Stdchk
			12. Local Check	G-12

RESULTS AND DISCUSSION

Analysis Of Variance

The combined environment analysis of variance revealed that the variation in allquantitative traits among genotypes were significant. The mean square due to genotype by environment interaction was also significant indicating that the performances of the genotypes were not consistent across different testing environments. In addition to this, mean squares of environment proved highly significant ($p<0.01$) for all the traits considered (Table 2). Among the tested genotypes, SCFBRVT P#3/11(G-2) and FBRVTB P#24/11 (G-9) showed relatively higher mean grain yield at many testing environments.FBRVTB P#24/11 exhibited the highest mean grain yield value (5507 kg ha^{-1}) followed by SCFBRVT P#3/11 which scored5269 kg ha^{-1}, althoughthese were not significantly different from standard check (EH 1493), SCFBRVT P#7/11 and SCFBRVT P1#11(Table 3 and 4).Similarly, the individual environment analysisof variance illustrated that SCFBRVT P#3/11 had grain yield means ranging from3789kg ha^{-1} to 7192 kg ha^{-1}.Likewise, the mean grain yield value of FBRVTB P#24/11 varied from 3581 kg ha^{-1} to 7022 kg ha^{-1} at AD15 and JL15 environments, accordingly (Table 4).SCFBRVT P#3/11 exhibited the lowest mean days to maturity of129.52across experimental locations (Table 3), indicating its better adaptabilityto double cropping and frost prone areas. On the other hand, FBRVTB P#24/11 had a mean day to maturity of 136.20 (Table 3).

FBRVTB P#24/11showed better TKW with mean value 44.05g, but this is not significantly different from that of SIFBRVT

P#5/11 and the local check (Table 3).Regarding plant height, the local check scored the highest mean of 120 cmfollowed by FBRVTB P#24/11(109.94cm). This higher plant height of the local check is not an unexpected since this is true with the local barley landraces that are characterized by tall plant height and susceptibility to lodging (Getachew *et al.*, 2011).In addition,though not significantly different from most test genotypes, MSFC P#15/11, SIFBRVT P#8/11 and SCFBRVT P#3/11showed reduced plant height with means of 104.42cm, 105.47cm and 105.61cm, respectively (Table 3).

Scald and net blotch are among the important diseasesof barley in different parts of Ethiopia. As survey results and loss levels indicate, scald remains a significant disease in barley production (Bekele *et al.*, 2011).Therefore,the test genotypes included in the present experiment were evaluated against scaled and net blotch resistance, and the twelve test genotypes varied significantly in severity of scald and net blotch. SCFBRVT P#3/11 and FBRVTB P#24/11 showed resistant reaction for scald with scores of 8.50% and 16.57%,and moderately resistant reaction for Net blotchwith scores of 35.04% and 35.39%, respectively (Table 5).

Generally, FBRVTB P#24/11 (G-9) and SCFBRVT P#3/11 (G-2) were selected as the superior varieties among the tested genotypes in terms of grain yield, agronomic characters and disease resistance. Hence, they were released in 2017 under the name HB 1965 and HB1966, respectively. HB1965 (Awra-gebs×and IBON 64/91) was developed using a modified bulk pedigree selection method, while HB1966 (F2 S×S 121/99) was selected from segregants of ICARDA germplasms.

Table 2. Mean square analysis of variance for agronomic, grain yield and diseases of twelve food barley genotypes tested at eleven environments in 2014 and 2015 cropping seasons

Traits	Env. (DF=10)	Geno. (DF=11)	Rep. (Env.) (DF=22)	Geno.* Env. (DF=110)	(R^2)%
Days to heading	3217.05**	314.66**	19.46NS	38.96**	93.03
Days to maturity (DF) †	10867.96 (9)**	314.21(11)**	29.11(20)NS	44.43(99)**	98.17
Plant height (cm)	4066.06**	937.33**	157.57**	107.87**	86.55
Thousand kernel weight (g)	727.13**	289.07**	11.02NS	23.81**	85.21
Grain yield (kg ha^{-1})	39728674.4**	15326909.8**	1104321.6**	1945827.0**	88.09
Scald(DF)§	3673.81(8)**	4542.99(11)**	55.63(18)NS	411.46(88)**	95.53
Net blotch (DF)§	16125.76(8)**	707.66(11)**	104.83(18)NS	233.83(88)**	96.29

DF=degree of freedom, **, * significant at 5% and 1% probability level, ns=non significant, †these data were not recorded at JL2, §those data were not recorded DB15and DA15 and mean squares under those traits are angular transformed values.

Table 3. Average performances of the twelve food barley genotypes for five agronomic and yield related traits acrosseleven environments during the 2014/15 and 2015/16 main seasons

No.	Genotype	Days to heading	Days to maturity†	Plant height (cm)	Thousand kernel weight (g)	Grain yield (kg ha^{-1})
1	MSFC P#15/11	81.36^{bcd}	133.83^{bc}	104.42^{ef}	39.98^{bc}	3369.4^{e}
2	SCFBRVT P#3/11	74.52^{e}	129.52^{d}	105.61^{def}	36.49^{e}	5268.8^{a}
3	MSFC P#24/11	83.85^{ab}	136.77^{b}	113.18^{bc}	40.14^{bc}	4053.8^{de}
4	SCFBRVT P#7/11	82.67^{b}	133.53^{bc}	108.30^{cde}	39.79^{bcd}	4980.1^{ab}
5	SCFBRVT P#5/11	82.06^{bc}	142.87^{a}	116.85^{ab}	46.33^{a}	4412.9^{bcd}
6	SCFBRVT P#8/11	86.47^{a}	136.24^{bc}	105.47^{def}	37.55^{de}	4381.2^{bcd}
7	SCFBRVT P#2/11	83.36^{b}	135.70^{bc}	101.97^{f}	41.33^{b}	4237.7^{cd}
8	SCFBRVT P#1/11	79.21^{cd}	133.13^{c}	106.94^{def}	41.34^{b}	4957.1^{ab}
9	FBRVTB P#24/11	78.85^{d}	136.20^{bc}	109.94^{cd}	44.05^{a}	5506.7^{a}
10	Cross # 41/98	81.79^{bcd}	134.90^{bc}	108.33^{cde}	39.20^{bcd}	4905.8^{abc}
11	EH 1493	81.36^{bcd}	133.87^{bc}	108.27^{cde}	38.82^{cde}	5199.0^{a}
12	Local Check	84.39^{ab}	135.00^{bc}	120.33^{a}	44.97^{a}	3362.2^{e}
	Mean	81.67	135.14	109.14	40.84	4550.2
	CV (%)	4.53	2.23	5.98	7.58	15.44
	LSD (0.05)	3.05	3.42	5.07	2.38	698.00

*, ** significant at P≤0.05 and P≤0.01, respectively, †these data were not recorded at JL2

Table4. Mean grain yield (kgha^{-1}) of twelve food barley genotypes across elevenenvironments(location x year combinations) during the 2014 and 2015 cropping seasons

No.	Genotype	AD15	DA15	DB15	BK14	BK15	HA14	HA15	JL14	JL15	KF14	KF15
1	MSFC P#15/11	2356^{def}	5126^{ab}	4762^{d}	3682^{bc}	3962^{c}	1716^{e}	1988^{f}	3422^{cdef}	5500^{def}	1899^{e}	2291^{fg}
2	SCFBRVT P#3/11	4076^{ab}	5788^{ab}	7192^{a}	4938^{a}	5441^{ab}	3789^{bc}	5002^{ab}	3867^{abcd}	6848^{bcd}	5697^{ab}	4921^{bcd}
3	MSFC P#24/11	2653^{cdef}	5343^{ab}	5192^{cd}	3146^{c}	5236^{ab}	2331de	3260de	4997^{a}	6960^{abc}	2607de	2748^{efg}
4	SCFBRVT P#7/11	4318^{a}	5612^{ab}	6403^{abc}	4762^{ab}	5157^{ab}	3472^{bc}	4158^{bcd}	2967^{def}	6307^{cde}	6837^{a}	4282^{cde}
5	SCFBRVT P#5/11	1739^{efg}	5179^{ab}	5821^{bcd}	4951^{a}	4305^{c}	4327^{ab}	1840^{f}	2758^{def}	5351^{ef}	4596^{bc}	6633^{a}
6	SCFBRVT P#8/11	1111^{g}	4754^{bc}	4740^{d}	4681^{ab}	5175^{ab}	4048^{bc}	3778^{cde}	2428^{f}	6073^{cde}	4550^{bc}	5484^{abc}
7	SCFBRVT P#2/11	1490^{fg}	6296^{a}	6241^{abc}	4371^{ab}	4207^{c}	3863^{bc}	4269^{bc}	2539^{ef}	6744^{bcde}	3005de	3588^{def}
8	SCFBRVT P#1/11	3595^{abc}	4860^{bc}	6581^{ab}	4621^{ab}	5149^{ab}	3025^{cd}	4294^{bc}	3720^{bcde}	6772^{bcde}	5513^{ab}	6396^{ab}
9	FBRVTB P#24/11	3581^{abc}	6204^{a}	6886^{ab}	4910^{a}	5925^{a}	5203^{a}	5657^{a}	3660^{bcde}	7022^{abc}	4655^{bc}	6591^{a}
10	Cross # 41/98	2875^{cde}	5625^{ab}	4574de	4715^{ab}	5630^{a}	3848^{bc}	4486^{bc}	4853^{ab}	8335^{a}	3806^{cd}	4541^{cd}
11	EH 1493	2077^{defg}	6166^{a}	6387^{abc}	5442^{a}	5825^{a}	3525^{bc}	4376^{bc}	4223^{abc}	8164^{ab}	4816^{bc}	5148^{abcd}
12	Local Check	3152^{bcd}	3754^{c}	3434^{e}	3083^{c}	4707^{bc}	1865^{e}	3054^{e}	4344^{abc}	4167^{f}	3384^{cd}	1937^{g}
	Mean	2770	5392	5684	4442	5060	3418	3869	3665	6520	4207	4522
	CV (%)	20.17	14.16	13.03	14.83	9.56	19.39	14.05	18.37	13.08	20.10	18.05
	LSD (5%)	1165	1293	1255	1116	819	1122	942	1220	1444	1465	1580

Table 5. Mean percent severity of scaled and net blotch of twelve food barley genotypes testedduring the 2014 and 2015 cropping seasons

No.	Genotype	Scald*	Net blotch*
1	MSFC P#15/11	72.68(67.59[a])	30.83(28.20[cd])
2	SCFBRVT P#3/11	8.50(11.15[e])	35.04(43.77[ab])
3	MSFC P#24/11	10.83(11.70[e])	43.67(50.13[a])
4	SCFBRVT P#7/11	6.61(14.76[de])	48.92(40.11[abc])
5	SCFBRVT P#5/11	15.59(21.85[cde])	30.86(25.19[cd])
6	SCFBRVT P#8/11	11.50(14.55[de])	44.05(52.19[a])
7	SCIFBRVT P#2/11	28.47(32.79[bc])	32.79(33.44[bc])
8	SCFBRVT P#1/11	8.48(6.76[e])	32.95(39.81[abc])
9	FBRVTB P#24/11	16.57(17.29[cde])	35.39(30.31[bcd])
10	Cross # 41/98	24.36(28.39[bcd])	30.39(16.83[d])
11	EH 1493	26.62(29.00[bcd])	35.14(38.81[abc])
12	Local Check	31.85(40.44[b])	54.70(44.00[ab])
Mean		22.02(24.66)	37.97(36.50)
CV (%)		(26.83)	(18.47)
LSD (0.05)		(16.62)	(15.11)

*Numbers in parenthesis are angular transformed values and those data were not recorded at DB15 and DA15 environments.

Stability Parameters

Wricke'secovalence (Wi^2) and Shukla's stability variance were calculated as stability parameters for each of the food barleygenotypes evaluated in the experiment (Table 6). Genotypes with low Wricke'secovalence (Wi^2) and Shukla's stability variance would be considered as stable. Accordingly, the lowest Wi^2 andShukla's stability values were noted for SCFBRVT P#3/11, EH 1493 and FBRVTB P#24/11 in their mean grain yield performance.Similarly, based on Francis and Kanenberg's (1978) coefficient of variability (CVi), both genotypes (SCFBRVT P#3/11and FBRVTB P#24/11) had high stability since both genotypes showed low CVi values. Furthermore, the smallest estimate of Non parametric Nassar and Hühn (1987) stability measure indicates the relative stability of genotypes.The genotypes MSFC P#15/11, SCFBRVT P#3/11and FBRVTB P#24/11 had relatively small non parametric measure of stabilityboth in $Si^{(1)}$(average absolute rank difference of genotype on the environment) and $Si^{(2)}$(Variance ranges of environments). However, MSFC P#15/11 showed the lowest grain yield performance and as a resultit was not considered for release.In addition, superiority of a genotype may be assessed by the superiority index (Pi) which is defined as the deviation of the i^{th} genotype relative to the genotype with maximum performance in each environment (Lin and Binns, 1988). Genotypes with lower Pi values are considered more superior and productive in a given set of environments than genotypes with higher Pi. Again, the most stable genotypes according to the Pi values wereSCFBRVT P#3/11and FBRVTB P#24/11(Table 6).

GGE refers to genotype main effect (G) plus genotype-by-environment interaction (GE). The graphical approach for analyzing multi environment trials (METs) is called GGE biplot (Yan *et al*., 2000). Specifically, the which-won-where view of the GGE biplot(Yan *et al*., 2000) is an effective visual tool in mega-environment analysis.In the graph polygon is formed by connecting the markers of the genotypes that are farthest away from the biplot origin such that all other genotypes are contained in the polygon. In addition, the graph contains a set of radiate lines perpendicular to eachside of the polygon. Theseperpendicularrays divide the biplotinto several sectorsand the winning genotype for each sector is the one located on the respective vertex (Yan and Tinker, 2006). In addition environments in the same sector are considered as a single mega environment. Therefore, environment HA14, HA15, BK14, BK15, DA15, DB15, KF14 were considered as single environment, and for this G-9 and G-2 were the respective vertex genotype. This indicates that the high yielding genotypes (G-9 and G-2) are the wining genotypes for that mega environment. G-5 and G-3 were the highest yielding genotypes in KF-15 and JL-14 environments respectively. (Figure 1). The existence of different winning genotypes in different environments confirmed the presence of crossover GXE interaction.

Ranking of genotypes relative to the ideal genotype are the one among the many uses of GGE biplot. In the biplot (Figure 2), the genotype found in the center of concentric circle on the AEC (Average environment coordinate) x-axis designed to be equal to the longest vector of all genotype and its projection on the AEC y-axis was obviously zero, meaning that it is absolutely stable. Therefore, G-9 is the ideal genotype (both stable and high yielding). In addition, G-2, G-11 and G8 were the next ideal genotypes found closer to G-9. Generally, based on the stability parameters and GGE biplots considered in this experiment, SCFBRVT P#3/11and FBRVTB P#24/11 wereidentified as the most stable genotypes.

Table 6. Results of various stability parameters for grain yield

No.	Genotype	Shuckla's variance (σ^2)	Variation coefficient CVi (%)	Wricke'sEco valence (Wi)	Superiority Measure (Pi)	Non parametric Nassar&Huehn	
						$Si^{(1)}$	$Si^{(2)}$
1	MSFC P#15/11	640918	41.31	5967852	4429435	0.35	2.40
2	SCFBRVT P#3/11	233853	21.4	2575642	497691	0.44	3.20
3	MSFC P#24/11	1023769	38.31	9158274	2831900	0.64	10.30
4	SCFBRVT P#7/11	926807	28.06	8350255	961067	0.56	7.80
5	SCFBRVT P#5/11	1483212	36.71	12986965	2132777	0.85	15.60
6	SCFBRVT P#8/11	693570	33.15	6406613	1952489	0.65	9.30
7	SCFBRVT P#2/11	746611	38.83	6848623	2238259	0.65	10.70
8	SCFBRVT P#1/11	523057	25.54	4985675	759730	0.51	7.00
9	FBRVTB P#24/11	450038	21.85	4377185	418257	0.36	3.70
10	Cross # 41/98	647724	26.92	6024565	1218128	0.53	8.40
11	EH 1493	308049	27.98	3193940	775878	0.40	5.40
12	Local Check	1349275	26.79	11870824	4485514	0.67	9.70

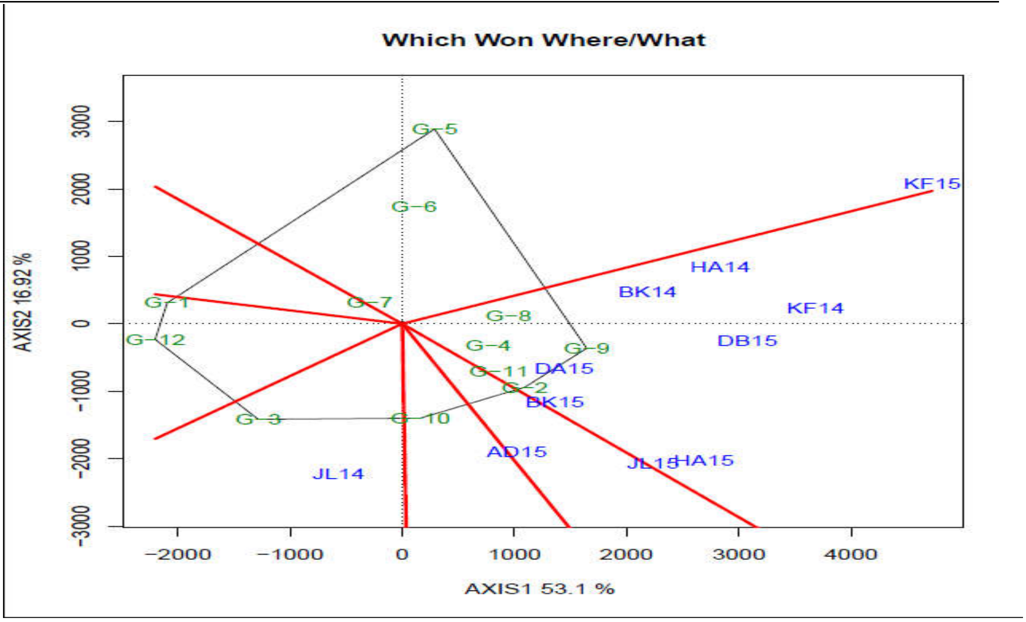

Figure 1. The which-won-where view of the GGE biplot of grain yield of Food barley genotypes based on the G × E data

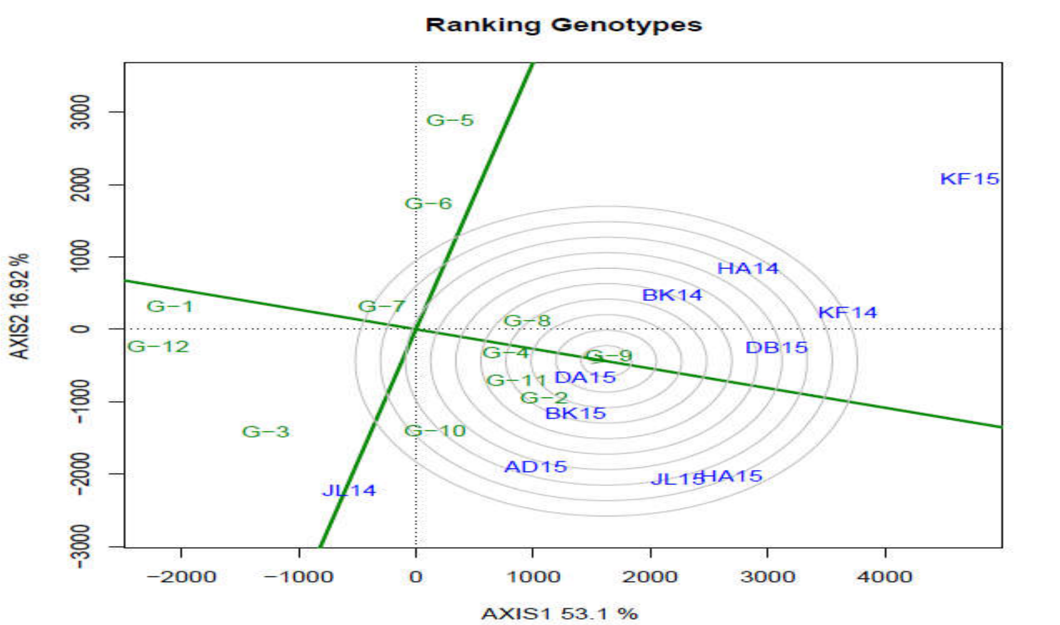

Figure 2. Ranking of genotypes based onboth mean performance and stability for food barley G × E data

CONCLUSIONS

The combined analysis of variance showed significant variation among the food barley genotypes tested for all the quantitative traits assessedin the experiment.In addition,all of the traits revealed significant G×E interaction. The two test genotypes, FBRVTB P#24/11 (G-9) and SCFBRVT P#3/11 (G-2) scored the highest mean grain yield values among the test genotypes. Besides their high yielding potential, the two genotypes are stable in their mean grain yield performance across the test environments. SCFBRVT P#3/11 (G-2) is an early maturing variety suitable for frost prone areas and for double cropping barley production systems.On the other hand, FBRVTB P#24/11 (G-9) is a late maturing variety with high plasticity that could serve as an alternative potential variety for the highland-long crop growing cycle areas. Therefore,FBRVTB P#24/11 (G-9) and SCFBRVT P#3/11 (G-2) were identified as superior varieties to be promoted to variety verification trial in 2016 cropping season ,and eventually released in 2017 under the name HB 1965 and HB1966, respectively.HB1965 is derived from a cross between a landrace line - Awra-gebs and ICARDA germplasm - IBON 64/91 using a modified bulk pedigree selection method, while HB1966 (F2 S×S 121/99) was identified from segregants of ICARDA germplasms.The detailed descriptors and recommendation practices of the two released food barley varieties are summarized on Table7.

Table 7. Agronomic and morphological descriptors of two six-row food barley varieties HB1965 and HB1966released in 2017

Description	HB1965	HB1966
Pedigree and source	Awragebs/IBON64/91 – Local cross	F2 SxS 121/99 – ICARDA selection
Adaptation	Highland potential, 2000 -2800 masl, Rainfall 500-700mm	Highland potential, >2400 masl, Rainfall 500-1000mm
Fertilizer rate (kg/ha)	41/46 (N/P_2O_5) / ha recommended to the area	41/46 (N/P_2O_5) / ha recommended to the area
Seed rate (kg/ha)	125	125
Days to heading	75	80
Days to maturity	132	137
Plant height (cm)	106	111
1000 seed weight (g)	35	42
Test weight (kg/hl)	60	62
Grain color	White	White
Yield in research fields (t/ha)	3.0-5.0	3.5-5.4
Yield in farmers' fields (t/ha)	2.5-3.5	3.0-4.0
Resistant to leaf diseases	Resistant to scald and net blotch	Resistant to scald and net blotch

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