

Multi-Location Evaluation of Yield and Yield Related Trait Performance in Food Barley (*Hordeum Vulgare* L.) Genotypes at Western Oromia, Ethiopia

Geleta Negash^{1*}, Wagar Raga², Biru Alemu²

^{1,2}Oromia Agricultural Research Institute (IQOO), Haro Sabu Agricultural Research Center (HSARC), P.O.Box 10, Kellem Wollega, Dembi Dollo

***Corresponding Author:** Geleta Negash, Oromia Agricultural Research Institute (IQOO), Haro Sabu Agricultural Research Center (HSARC), P.O.Box 10, Kellem Wollega, Dembi Dollo

Abstract: Barley is one of the founders, old world agriculture and the first domesticated cereal crop. This experiment was conducted on fifteen barley genotypes against checks at Haro Sabu Agricultural Research Center sub site in 2017-2018. The objective was to assess the magnitude of genotype by environment interaction, grain yield stability, high yielding, insect pest tolerant genotypes in the growing areas of western Oromia. Seeds were planted in RCBD with three replications. Eleven agronomic traits and four disease reaction data were evaluated. Analysis of variance detected significant difference among genotypes for most observed traits both separated and combined analysis. Observation attained significant differences over years and locations for almost all traits. The combine ANOVA and the AMMI analysis for grain yield across environments revealed significantly affected by environments, that hold 41% of the total variation. The genotype and genotype by environmental interaction, were significant and accounted for 10.46 % and 27.69 % respectively. Principal component 1 and 2 accounted for 15.74 % and 5.71 % of the GEI respectively with a total of 21.45 % variation. In general, G2 and G12 were identified as the best genotypes for yielding ability, stability, tolerant to diseases and use as parents in future breeding programs.

Keywords: AMMI, food barley, GGEI, performance, stability

Abbreviations: AMMI = additive main effects and multiplicative interactions, ANOVA = analysis of variance, GEI = genotype by environmental interaction, GGEI = genotype and genotype by environmental interaction, RCBD = Randomized Completed Block Design

1. INTRODUCTION

Barley (*Hordeum vulgare* L) ($2n = 2x = 14$) is one of the most important staple food crops in the highlands of Ethiopia. It is a cool season crop, the most dependable and early maturing cereal grain with relatively high yield potential including in marginal areas where other cereal crops cannot have adapted [14, 31]. The major barley production areas of the world include: Europe, the Mediterranean fringe of North Africa, Ethiopia and the Middle East, former USSR, China, India, Canada and USA [16]. Ethiopia is the second largest barley producer in Africa, next to Morocco, accounting for about 25 % of the total barley production in the continent [10]. However, there is great yield gap between national average yield (2.11 t/ha^{-1}) [7] and world average yield (3.04 t/ha^{-1}) (Foreign Agricultural Service/USDA April 2017 Office of Global Analysis). This production limitation may be attributed to primarily the low yielding ability of farmers' cultivars, which are the dominant varieties in use; the influence of several biotic and abiotic stresses; and poor promotion of improved barley production package technologies [1].

Environmental fluctuation and interaction is also the major limitation for food barley production and productivity. Genotype by environment interaction (GEI) is the differential responses of different genotypes across a range of environments [29]. In breeding, genotype x environmental interaction (G x E) cause many difficulties, while the environmental factors such as temperature, soil affect the performance of genotypes. Genotype x environment (GE) interaction reduces the genetic progress in plant breeding programs through minimizing the association between phenotypic and genotypic values [6]. Consequently, multi-environment yield trials are essential in assessing of genotype by environment

interaction (GEI) and identification of superior genotypes in the final selection cycles [30, 32]. Phenotypes are a mixture of genotype (G) and environment (E) components and interactions (G x E) between them. GxE interactions complicate process of selecting genotypes with superior performance. Therefore, multi-environment trails (METs) are widely used by plant breeders to evaluate the relative performance of genotypes for target environments [9].

The additive main effects and multiplicative interaction (AMMI) model have also led to more understanding in the complicated patterns of genotypic responses to the environment [13]. These patterns have been successfully related to biotic and abiotic factors. [20], proposed another methodology known as GGE-biplot for graphical display of GE interaction pattern of MET data with many advantages. GGE biplot is an effective method based on principal component analysis (PCA) which fully explores MET data. It allows visual examination of the relationships among the test environments, genotypes and the GE interactions. The first two principle components (PC1 and PC2) are used to produce a two dimensional graphical display of genotype by environment interaction (GGE-biplot). If a large portion of the variation is explained by these components, a rank-two matrix, represented by a GGE- biplot, is appropriate [21].

The objective of this study was to assess genotype performances, the magnitude of genotype x environment interaction for grain yield and to evaluate the stability for grain yield and tolerant to diseases of food barley genotypes.

2. MATERIALS AND METHODS

2.1. Description of Locations

The experiment was conducted at three different rain fed locations in Kellem and west Wollega zones of Haro-sebu agricultural research center at Belem research sub site (altitude 1759 masl, 09° 02' N, 035° 104'E), Mata (altitude 2016 masl, 08° 34' N, 034° 44'E) and Badesso (altitude 2054 masl, 08° 40' N, 034°47'E) in western Oromia, Ethiopia, during the 2017-2018 main cropping season, that represent the varying agro ecologies of the barley growing areas of the zones.

2.2. Experimental Materials

Fifteen regional variety trial of food barley genotypes, together with three checks, two standard checks (Abdane and Dinsho) and one farmer's varieties, were included in the trial (Table 1). The genotypes were selected based on average performance and agro-ecological adaptation. Genotypes were obtained from Ethiopia biodiversity institute (EBI) Sinana Agricultural Research Center and from farmers for the farmers' varieties.

Table1. List of food barley genotypes evaluated in 2017-2018 main cropping season

No	Codes	Genotypes Acc.No	Sources
1	G1	242573	EBI
2	G2	220677	EBI
3	G3	Abdane	SARC
4	G4	202820	EBI
5	G5	237021	EBI
6	G6	219142	EBI
7	G7	241675	EBI
8	G8	Local	Farmer
9	G9	225176	EBI
10	G10	4560	EBI
11	G11	233028	EBI
12	G12	219307	EBI
13	G13	64260	EBI
14	G14	233030	EBI
15	G15	Dinsho	SARC

G-genotype, Acc. No- accession number EBI- Ethiopia biodiversity institute, SARC- Sinana Agricultural Reaserch center

2.3. Experimental Design and Management

Randomized completed block design (RCBD) with three replications was used in all locations. Each experimental plot had six rows of 2.5 m long spaced and 20 cm apart with a plot area of 1.2 m x 2.5 m. Drill planting by hand was used with the same rate for all locations. Fertilizer was applied at a rate of 41 and 46 kg ha⁻¹ of N and P₂O₅, respectively, in the form of Urea and DAP. All P₂O₅ and half of N were applied during planting, while the rest half splits were applied at tillering stages. A seeding rate of 85 kg ha⁻¹ was used. First weeding was carried out 35 days after emergence and the second one at 30 days after the first weeding. Weeding was done up to four times for all locations. The data considered for analysis was from the candidates of the net plot, thus the four central harvestable rows. The harvested genotypes were sundried before being tested for moisture content where 12% was the preferred average moisture content using moisture tester. Grain yield data was then obtained by weighing the dried grain using a digital scale.

2.4. Data Collection Method

Ten plants were selected randomly before heading from each row (four harvestable rows) and tagged with thread and all the necessary plant based data were collected from these sampled plants.

2.5. Plot Basis

The following plant parameters were determined: Days to heading (DH), Days to maturity (DM), Lodging percentage (LDG), Thousand seed weight (TSW), Grain yield (GY), and the four major economically important food barley diseases such as scald, septoria (SEP), stem rust (SR), and leaf rust (LR)

2.6. Plant Basis

Plant height (PH), Productive tillers (PTR), Spike length (SL), Grain per spike (GPS), spike weight per plant (SWPP) and number of spike lets per spike (NSPS)

3. STATISTICAL ANALYSIS

3.1. Analysis of Variance is Calculated using the Model

$$Y_{ij} = \mu + G_i + E_j + GE_{ij}$$

Where Y_{ij} is the corresponding variable of the i^{th} genotype in j^{th} environment, μ is the total mean, G_i is the main effect of i^{th} genotype, E_j is the main effect of j^{th} environment, GE_{ij} is the effect of genotype x environment interaction.

$$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^N \lambda_k Y_{ik} \delta_{jk} + \epsilon_{ij}$$

3.2. The AMMI Model used was

Where Y_{ij} is the grain yield of the i^{th} genotype in the j^{th} environment, μ is the grand mean, g_i and e_j are the genotype and environment deviation from the grand mean, respectively, λ_k is the eigenvalue of the principal component analysis (PCA) axis k , Y_{ik} and δ_{jk} are the genotype and environment principal component scores for axis k , N is the number of principal components retained in the model, and ϵ_{ij} is the residual term.

GGE-biplot methodology, which is composed of two concepts, the biplot concept [12] and the GGE concept [20], was used to visually analyze the METs data. This methodology uses a biplot to show the factors (G and GE) that are important in genotype evaluation and that are also the source of variation in GEI analysis of METs data [22]. The GGE-biplot shows the first two principal components derived from subjecting environment centered yield data (yield variation due to GGE) to singular value decomposition [20]. AMMI Stability Value (ASV): ASV is the distance from the coordinate point to the origin in a two-dimensional plot of IPCA1 scores against IPCA2 scores in the AMMI model [24]. Because the IPCA1 score contributes more to the GxE interaction sum of squares, a weighted value is needed. This weighted value was calculated for each genotype and each environment according to the relative contribution of IPCA1 to IPCA2 to the interaction sum of squares as follows:

$$ASV = \sqrt{[(SS_{IPCA1} \div SS_{IPCA2})(IPCA1score)]^2 + (IPCA2score)^2}$$

Where, SS_{IPCA1}/SS_{IPCA2} is the weight given to the IPCA1-value by dividing the IPCA1 sum of squares by the IPCA2 sum of squares. The larger the ASV value, either negative or positive, the more specifically adapted a genotype is to certain environments. Smaller ASV values indicate more stable genotypes across environments [24]. Genotype Selection Index (GSI): Stability is not the only parameter for selection as most stable genotypes would not necessarily give the best yield performance. Therefore, based on the rank of mean grain yield of genotypes (RYi) across environments and rank of AMMI stability value RASVi), genotype selection index (GSI) was calculated for each genotype as:

$$GSI_i = RASV_i + RY_i$$

A genotype with the least GSI is considered as the most stable [11]. Analysis of variance was carried out using statistical analysis system (SAS) version 9.2 software [25]. Additive Main Effect and Multiplicative Interaction (AMMI) analysis and GGE bi-plot analysis were performed using Gen Stat 15th edition statistical package [19]

4. RESULTS AND DISCUSSIONS

4.1. Combined Analysis of Variance

The mean square of analysis of variance (ANOVA) is presented in Table 2. Highly significant differences were detected among the main and the interaction effects ($P \leq 0.01$) for most of the parameters. The combined analysis of variance revealed that significant differences were recorded across location for all parameters except spike weight per plant. Year*genotypes effects were significant for most traits. Year*location *genotypes were significant for most traits such as days to heading, days to maturity, stem and leaf rust, spike length, grain per spike, thousand seed weight and grain yield.

Table2. Analysis of variance (ANOVA) for grain yield and yield related traits of food barley genotypes evaluated in 2017-2018 main cropping season

Source	DF	DH	DM	PTL	Scald	SEP	SR	LR	LDG
rep	2	20.69	12.51	1.51	0.31	0.08	0	0.06	0.01
Geno.	14	163.17**	163.73**	2.20**	0.3	0.17**	0.34**	0.36**	0.66*
loc	2	371.83**	179.45**	24.35**	9.08**	8.81**	17.68**	20.38**	16.77**
yr	1	2881.20**	2.7	138.96**	3.91**	1.07**	2.22**	2.80**	47.71**
geno*loc	28	22.81*	33.77**	0.6	0.78**	0.08*	0.21**	0.21**	0.44
geno*yr	14	120.10**	104.67**	1.66*	0.25	0.04	0.09*	0.1	0.56*
loc*yr	2	124.34**	15.63	16.23**	3.91**	1.07**	2.22**	2.80**	1.17*
geno*loc*yr	28	28.30*	34.11**	0.61	0.25	0.04	0.09**	0.10*	0.38

Table2. Continue

Source	DF	PH	SL	SWPP	SPS	GPS	TSW	QTHA
rep	2	28.83	0.2	0.35	54.74	3.53	21.29	13.66
geno.	14	209.42**	2.06*	0.24	61.22**	126.71**	246.85*	823.16**
loc	2	4308.57**	2.60*	0.69	217.74**	119.41*	2933.84**	851.03**
yr	1	931.86**	0.02	0.4	84.90*	311.80**	8079.74**	9684.87**
geno*loc	28	51.28	0.99	0.42	18.95	48.69*	155.8	62.89**
geno*yr	14	133.98**	1.58*	0.39	36.70*	101.68**	139.09	81.29*
loc*yr	2	1603.92**	3.55*	0.94	88.44*	1264.39**	3855.68**	1132.38**
geno*loc*yr	28	79.04	1.46*	0.46	24.58	59.00**	176.35*	72.41*

Key: **, significant at 5% and 1% respectively, Loc *geno = location by genotype, Yr*Loc*geno = year by location by genotype, DF -degree of freedom, DH- Days to Heading; DM- Days to Maturity; PTL- productive tillers, SEP- septoria, SR- stem rust, LR- leaf rust, LDG- lodging, PH- Plant Height; SL- spike Length; SWPP- Spike Weight per plant, SPS-spike lets per spike, GPS-Grain per spike, TSW- Thousand Seed Weight, QTHA- Yield quintal per Hectare.

4.2. Yield Performance of Food Barley Genotypes Across Locations

Mean performance for grain yield across location and year presented in Table 3. Study by [18] indicated that genotypes constantly performed best in some environments and fluctuating across some

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locations. Accordingly, the average grain yield ranged from the lowest of 19.33 Qtha⁻¹ at Bedesso sub site in 2017 to the highest of 36.47 Qtha⁻¹ at Belem site in 2018 with grand mean of 29.29 Qtha⁻¹.

The average grain yields across environments ranged from the lowest of 23.5 Qtha⁻¹ for G9 to the highest of 37.5 Qtha⁻¹ for G2. This wide variation might be due to the genetic potential of the different genotypes. Therefore, G2 and G12 were constantly performed across the locations. The difference in yield rank of genotypes across the environments exhibited the high crossover type of genotypes x environmental interaction [22, 3].

Table3. Mean grain yield (Qtha⁻¹) of food barley genotypes evaluated at three environments

Genotype	Grain Yield in Qtha ⁻¹						Com.mean
	2017			2018			
	Belem	Bedesso	Mata	Mata	Belem	Bedesso	
Dinsho	27.88bc	14.71fg	22.043fg	35.27b	31.92def	32.98b	27.5def
G1	31.23ab	16.56d-g	29.35b-e	31.69b	35.55cde	30.18b	29.1cde
G10	25.19b-e	20.17b-f	21.55fg	35.06b	33.59c-f	30.197	27.6def
G11	21.45def	23.03bcd	29.61b-e	28.92b	29.143ef	29.80b	27.0efg
G12	17.87fgh	26.85ab	30.81a-d	37.73ab	43.94abc	46.95a	34.0ab
G13	14.58gh	22.02b-f	23.38efg	29.74b	30.85def	31.43b	25.3gh
Abdane	7.79i	12.35g	36.94a	42.66ab	40.88a-d	37.21b	29.6cde
G14	34.60a	31.38a	29.41b-e	33.34b	24.87f	30.72b	30.7bcd
G2	23.07c-f	24.52abc	24.99def	49.86a	50.48a	51.89a	37.5a
G4	30.72ab	22.76b-e	31.54a-d	31.13b	31.72def	30.38b	29.7cde
G5	26.59bcd	15.10fg	34.74abc	31.95b	46.37ab	34.98b	31.6bc
G6	29.55ab	16.11d-g	35.31ab	30.75b	35.81cde	30.13b	29.6cde
G7	19.66efg	15.31efg	33.48abc	37.88ab	34.60c-f	29.66b	28.4c-f
G9	12.96hi	11.69g	16.58g	32.88b	39.10b-e	27.50b	23.5g
Local	14.36gh	17.47c-g	28.203c-f	36.48ab	38.19b-e	34.34b	28.2c-f
Mean	22.50	19.33	28.53	35.02	36.47	33.89	29.29
CV %	16.32	23.26	14.84	23.53	17.14	17.16	19.33
R ²	0.88	0.71	0.74	0.41	0.64	0.68	79.3
LSD 5%	6.14	7.52	7.08	13.78	10.46	9.73	3.724
F-test	**	**	**	**	**	**	**

Key: G- genotype, R², R-squire, CV- coefficient of variation, LSD- least significant different.

4.3. Agronomic Performance

Combined mean grain yield and other agronomic traits are presented in Table 4. Genotype (G12) was recorded medium days to heading, days to maturity, and plant height, indicated that, the possibility to develop resistant variety against lodging problems. And also it recorded the highest productive tillers per plant, thousand seed weight and grain yield. Similarly, Genotype (G2) was recorded medium days to heading, days to maturity, productive tillers and thousand seed weight and the highest spike length. These recommend great flexibility for developing improved varieties appropriate for different agro-ecologies with variable length of growing period and high in grain yield status. Moreover, these genotypes (G12 and G2) were recorded the highest grain yield and they had 14.95 %, and 26.58 % yield advantage over the best standard check (Abdane) respectively.

Table4. Combined mean grain yield and other agronomic traits of food barley genotypes

Gen/Vrt	DH	DM	PTL	LDG	PH	SL
Dinsho	57.4cd	89.6de	3.5b-e	2.0ab	90.2a-e	8.4bcd
G1	54.3ef	89.0def	3.5b-e	1.9abc	90.6a-d	8.5abc
G10	55.8de	90.4cde	3.8a-d	2.1a	92.8a-d	8.0cd
G11	56.3cde	92.6bc	3.9abc	1.5cd	89.5b-e	8.9ab
G12	58.8bc	94.3ab	4.4a	1.7bcd	93.6abc	8.7ab
G13	60.5b	96.4a	3.1e	1.9abc	89.5b-e	8.4bcd
Abdane	64.2a	96.5a	3.6b-e	1.5d	82.9f	7.9d
G14	54.9de	90.7cde	3.9abc	1.6cd	94.6ab	8.7ab
G2	57.2cd	93.2b	3.9ab	1.8a-d	90.3a-d	9.1a
G4	56.8cde	90.8cd	4.0ab	1.7bcd	91.0a-d	8.6ab
G5	55.4de	88.4ef	3.2de	2.0ab	87.7def	9.1a
G6	54.6e	90.2de	3.3cde	1.6cd	88.4cde	8.5bcd
G7	56.8cde	86.9f	3.5b-e	1.6cd	94.8a	8.4bcd
G9	60.5b	93.3b	3.8abc	1.8a-d	85.0ef	8.4bcd
Local	52.0f	87.1f	4.0ab	1.9abc	93.7ab	8.5abc
M ± SEM	57.03±0.41	91.29±0.34	3.69±0.08	1.78±0.05	90.31±0.67	8.54±0.06
CV%	6.76	3.74	25.01	31.54	8.78	10.75

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R ² %	78	75	67	69	66	47
LSD 5%	2.54	2.25	0.61	0.37	5.22	0.6
F test	**	**	**	**	**	**

Table4. *continue*

Gen/Vrt	SWPP	SPS	GPS	TSW	QTHA	YLD AV
Dinsho	1.3b	17.38bcd	24.06cde	46.61ab	27.5 ^{def}	-7.09
G1	1.42ab	18.41a-d	25.96bcd	39.97bcd	29.1cde	-1.71
G10	1.56ab	18.96abc	24.87cde	37.08cd	27.6def	-6.67
G11	1.35ab	19.69ab	22.13e	43.23bc	27.0efg	-8.81
G12	1.37ab	16.63cde	24.80cde	50.8a	34.0ab	14.95
G13	1.4ab	20.86a	32.76a	40.78bcd	25.3gh	-14.42
Abdane	1.44ab	14.39e	28.96a	42.65bc	29.6cde	0
G14	1.38ab	19.79ab	25.85bcd	42.68bc	30.7bcd	3.78
G2	1.41ab	16.03cde	22.49de	43.32bc	37.5a	26.58
G4	1.44ab	20.28ab	24.79cde	43.18bc	29.7cde	0.36
G5	1.28b	17.38bcd	24.71cde	44.24ab	31.6bc	6.84
G6	1.71a	17.99a-d	24.58cde	40.94bcd	29.6cde	0.03
G7	1.36ab	15.88de	26.66bc	40.6bcd	28.4c-f	-3.94
G9	1.53ab	16.19cde	23.37cde	35.03d	23.5g	-20.77
Local	1.27b	17.82bcd	23.82cde	40.76bcd	28.2c-f	-4.82
M ± SEM	1.41±0.02	17.85±0.06	25.32±0.12	42.13±0.1	29.29±0.72	
CV%	40.87	25.17	22.08	25.31	19.33	
R ² %	0.39	0.49	0.63	0.64	79.3	
LSD 5%	0.3804	2.95	3.68	7.01	3.724	
F test	ns	**	**	**	**	

Key: G-genotype, M-mean DH- Days to Heading; DM- Days to Maturity; PTL- productive tillers, LDG- lodging, PH- Plant

Height; SL- spike Length; SWPP-Spike Weight per plant, SPS-spike lets per spike, GPS-Grain per spike, TSW- Thousand Seed Weight, QTHA- Yield quintal per Hectare, YAD- yield advantage, CV- Coefficient of variation, R²-R-square, LSD- least significant.

4.4. Major Disease Reaction of Food Barley Genotypes Across Environments

Most genotypes evaluated had significantly low scores with their corresponding economically important disease reactions. However, genotypes (G1, G5, Dinsho and Abdane) were less tolerance to scald disease. Similarly, genotypes (G11, G5 G7 and Abdane), were less tolerance to septoria and stem rust. On the other hand, genotypes (G12 and G2) were better tolerance to scald, septoria, stem and leaf rust (Table 5).

Table5. *Combined mean of disease reactions (1-5 scale) of food barley genotypes evaluated in 2017-2018 main cropping season.*

Geno/Vrt	SCALD	SEP	SR	LR
Dinsho	1.6abc	1.3bcd	1.2f	1.3fg
G1	1.6a	1.3bcd	1.5abc	1.4ef
G10	1.3bcd	1.4bc	1.6a	1.6a-d
G11	1.2d	1.4ab	1.4de	1.5cde
G12	1.3d	1.2de	1.2f	1.3fg
G13	1.4a-d	1.3cde	1.4cde	1.5de
Abdane	1.6ab	1.4ab	1.6a	1.7ab
G14	1.3bcd	1.2e	1.4bcd	1.3g
G2	1.4a-d	1.4abc	1.4cde	1.4efg
G4	1.3a-d	1.3b-e	1.4de	1.5cde
G5	1.6abc	1.5a	1.5ab	1.8a
G6	1.4a-d	1.3b-e	1.3ef	1.6b-d
G7	1.3cd	1.4ab	1.4cde	1.4efg
G9	1.4a-d	1.3b-e	1.6a	1.6abc
Local	1.3a-d	1.3cde	1.6a	1.5de
Mean ± SEM	1.40±0.04	1.33±0.02	1.42±0.03	1.49±0.03

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CV%	32.99	16.08	14.08	16.58
R ² %	64	77	89	86
LSD 5%	0.3	1.97	0.13	0.16
F test	**	**	**	**

Key: G-genotype, CV- Coefficient of variation, LSD- least significant difference, R²-R-Square, SR-stem rust, LR-leaf rust, SEP-septoria, SEM- standard error of mean .1-5 scale where 1= resistant, 5= susceptible

4.5. AMMI Analysis for Grain Yield

The additive main effects and multiplicative interaction analysis (Table 6) of grain yield showed that environment, and genotypes by environment interaction were highly significant ($P \leq 0.01$). This is similar to the report of [23]. This indicates that one of the basic factors that affect GEI could either be genotypic or environmental in nature [8, 2] also reported that 74.3% of the interaction sum of squares was explained by IPCA1.

Table6. Additive main effect and multiplicative interaction analysis of variances (AMMI) for grain yield of 15 food barley genotypes evaluated at six environments

Source of variation	DF	SS	EX.SS%	MS
Total	269	27580	100	102.5
Treatments	89	21830	79.15	245.3**
Genotypes	14	2886	10.46	206.1**
Environments	5	11308	41.00	2261.7**
Block	12	361	1.31	30.1 ^{ns}
GEI	70	7636	27.69	109.1**
IPCA 1	18	4340	15.74	241.1**
IPCA 2	16	1575	5.71	98.4**
Residuals	36	1721	6.24	47.8
Error	168	5390		32.1

Key: DF = degree of freedom, SS = sum of squares, MS = mean squares, IPCA = Interaction Principal Component Axis, EX.

SS% = Explained Sum of square ns *, ** non-significant, Significant at the 5% and 1% level of probability respectively

The environment and genotype mean are presented in Fig.1 and Table 7. This bi-plot helped in the interpretation of the interaction effects among genotypes and environments; and in the assessment of the adaptability of genotypes. Genotype (G12 and G2) with a lower IPCA1 score were stable genotypes. Genotypes which are characterized by mean greater than grand mean and the IPCA scores nearly zero are considered as generally adaptable to all environment. However, the genotypes with high mean performance and with large value of IPCA scores are considered as having specific adaptability to the environments [26]. Study by [5] reported that the larger the IPCA scores, either negative or positive, the more specifically adapted a genotype is to a certain environments; yet the smaller the IPCA scores, the more stable the genotype is over all environments. Genotypes (G14 and G4) had grain yield above the grand mean; and similar IPCA1 scores with locations Bedesso and Belem implying that their interactions were positive; the higher yields of these genotypes were found, particularly, at these locations. Hence, they were the best adapted genotypes for these locations.

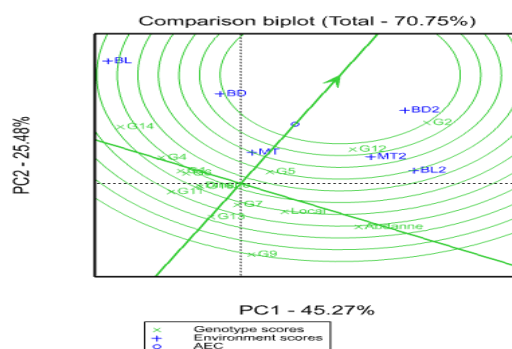


Figure1. GGE bi-plot based on genotype-focused scaling for comparison of genotypes for their yield potential and stability

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Key: G- genotypes, BD-bedesso, BL- Belem, MT- Mata, Number followed the lactations indicate the year (1=2017, 2= 2018)

Table7. Mean grain yield ($Qtha^{-1}$) per location and year from the AMMI additive GE model

Genotype	BD1 (E1)	BD2 (E2)	BL1 (E3)	BL2 (E4)	MT1 (E5)	MT2 (E6)	Mean	IPCAg1	IPCAg2
Abdane	10.46	37.1	10.94	46.12	33.92	39.3	29.64	2.72	-1.89
Dinsho	20.32	31.73	23.58	32.18	24.62	32.38	27.47	-0.66	0.69
G1	19.71	29.86	28	33.17	31.85	31.97	29.09	-1.32	-0.7
G10	21.38	32.55	23.63	32.07	23.29	32.83	27.63	-0.63	1.09
G11	19.14	29.32	25.11	30.93	26.77	30.67	26.99	-1.13	0.07
G12	23.97	43.49	20.55	44.63	28.26	43.24	34.02	1.55	1.06
G13	17.71	31.61	18.29	31.81	20.78	31.79	25.33	0.07	1.01
G14	29.28	30.95	37.27	28.11	27.12	31.59	30.72	-3.05	1.36
G2	28.39	50.62	19.86	49.83	27	49.11	37.47	2.52	2.14
G4	22.37	29.97	31.08	31.81	31.21	31.81	29.71	-1.88	-0.25
G5	16.82	33.99	23.64	41.12	37.43	36.75	31.62	0.25	-1.83
G6	17.56	28.93	28.15	34.82	36.19	32	29.61	-1.25	-1.75
G7	14.86	31.35	20.78	37.32	32.58	33.7	28.43	0.18	-1.36
G9	12.36	31.76	10.64	34.09	19.8	32.06	23.45	1.39	0.51
Local	15.69	35.14	15.98	38.99	27.14	36.11	28.17	1.24	-0.16
Environment									
Mean	19.33	33.89	22.5	36.47	28.53	35.02	29.29		
IPCAe1	-1.71	2.10	-4.34	2.81	-0.71	1.85			
IPCAe2	2.42	1.51	0.06	-0.89	-3.69	0.58			

G- genotypes, E-environment, BD-bedesso, BL- Belem, MT- Mata, IPAG- interaction principal axis to genotypes, IPAE-interaction principal axis to environment, Number followed the lactations indicate the year (1=2017, 2= 2018)

4.6. Stability Analysis for Genotypic Performance

AMMI Stability Value (ASV). In table 8 shows, AMMI stability values for grain yield. considering the AMMI stability value (ASV) that takes into account the scores of the IPCA2, genotypes with least ASV scores are the most stable, whereas genotypes with high ASV score are unstable [11, 5, 17]. Accordingly, genotypes (Dinsho, G11 and G13) were appeared to be among those showing low ASV and were the most stable. On the contrary, genotypes G14 and Abdane revealed the highest ASV and were thus considered to be unstable. Stability by itself should, however, not be the only parameter for selection, as the most stable genotype would not necessarily give the best yield performance [28]. Therefore, the study indicated that, Dinsho, G11 and G13 were recorded the lower ASV (Table 8), but recorded lower yield (27.47, 26.99 and 25.33 $Qtha^{-1}$ respectively) than the grand means (29.29 $Qtha^{-1}$). So if Dinsho, G11 and G13 will be selected based on ASV per se, there will be a risk of yield reduction. The stable genotype was followed with mean grain yield above the grand mean and this result was in agreement with [15], who has used ASV as one method of evaluating grain yield stability of bread wheat varieties in Tigray and similar reports been made by [4], [27] in barley in Tigray and bread wheat using AMMI stability value. A genotype with the least of genotype selection index (GSI) is considered as the most stable genotype [11]. Accordingly, G2, G12 and G5 were more stable genotypes with the low of genotype selection index (GSI) and higher mean grain yield (Table 8).

Table8. AMMI stability value, AMMI rank, Yield, yield rank and genotype selection index (GSI)

Genotype	ASV	ASV RANK	YLD	YLD RANK	GSI
G2	5.49	13	37.47	1	14
G12	3.12	10	34.02	2	12
G5	3.07	9	31.62	3	12
G14	5.54	15	30.72	4	19
G4	3.15	11	29.71	5	16
Abdane	5.50	14	29.64	6	20
G6	3.57	12	29.61	7	19
G1	2.48	8	29.09	8	16

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G7	2.28	6	28.43	9	15
Local	2.08	4	28.17	10	14
G10	2.09	5	27.63	11	16
Dinsho	1.59	1	27.47	12	13
G11	1.88	3	26.99	13	16
G13	1.68	2	25.33	14	16
G9	2.46	7	23.45	15	22

G- genotype

5. CONCLUSION AND RECOMMENDATIONS

Although the GEI of grain yield partitioned in to different IPCAs using AMMI model analysis, the first principal component axis for interaction alone explains most of the interaction sum of squares. The sign and magnitude of IPCA scores showed the relative contribution of each genotype and environment for the genotype and environment interactions. It helps to summarize the pattern and magnitude of GEI and main effects that reveal clear insight into the adaptation of genotypes to environments. This shows that genotypes (G2 and G12) are less contributors to the interaction effect and have consistent performances across locations whereas genotype, G14 with higher ASV scores and unstable genotype. Therefore, G2, and G12 were identified as the best genotypes in terms of yielding ability and stability, tolerant to diseases for advancement, release and use as parents in future breeding programs.

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