

Multi-location assessment of yield and agronomic traits in food barley (*Hordeum vulgare* L.) genotype in north Shewa Zone, Oromia, Ethiopia

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ABSTRACT

The field test changed into performed on 14 food barley genotypes along with one local and one currently released well known check (Walashe) at Fitch Agricultural research center at 2023-2024 cropping seasons. The goal was to assess the significance of genotype through environment interaction, grain yield stability, and high yielded and disease resistance genotypes in north shewa zone. The seed changed into sown in randomized completed block design (RCBD) with 3 replications within the plot size of 1.2mx3m. Effective tiller per plant (PPT) Plant height (PH), spike length (SL), days to 50% heading (DH), days to 95% maturity (DM), thousand seed weight (TSW) and grain yield (GY), flag leaf length (FLL), peduncle length (PDL) and awn length had been accrued as agronomic traits. Combined evaluation of variance detected widespread distinction among principal effect of genotypes, year and locations for maximum agronomic developments considered. The interplay impact of genotype via year, location by year, genotype by location by year imposed giant impact particularly on yield however none in all traits. Amongst evaluated genotypes, G-12 with grain yield of 3574.8kg ha^{-1} had significantly better mean grain yield over the rest genotypes and recorded 12.6% yield benefit over standard check (Walashe). The mixed ANOVA and the AMMI analysis for grain yield throughout environments discovered significantly laid low with environments, which maintain 72.4% of the overall variation. The genotype and genotype through environmental interaction were great and accounted for 9.5% and 13% respectively. Principal component 1 and 2 accounted for 6.8% and 3.3% of the GEI respectively with a total of 10.1% variant. In typically, G-12 turned into recognized as promising genotype for grain yield, more stable, tolerant to diseases and can be used as parents for breeding purposes.

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

1. INTRODUCTION

Barley (*Hordium vulgare* L.) is identified as one of the international's most historical food crop, which is thought to have first domesticated about 10,000 years ago from its wild family within the Fertile Crescent of the close to East and center of diversity in Ethiopia [4]. In Ethiopia, Barley is the fifth crucial cereal crop after tef, Maize, Sorghum and Wheat in each general area coverage and annual production [6]. It's far cultivated at altitudes starting from 1500 to 3500 above sea level and predominantly grown at elevation ranging from 2000 to 3000 m.a.s.l. [21].

Being the maximum dependable and appropriate crop for the highland farmers [9], in a few areas it is cultivated in district seasons: belgs which relies on the quick rainfall duration from March to April and Meher which relies at the long rainfall length from June to September [5]. The maximum vital biotic and abiotic elements that lessen productiveness of barley in Ethiopia include; low yielding types, insect, disease, bad soil fertility, soil acidity and weed competition [5]. Slow increasing of these production constraints are held to be crucial for diminishing productivity of barley.

Multi-location assessment of various barley genotypes is among alternative intervention technique through which productivity of the crop could be alleviated. Subsequently, multi-environment yield trials are crucial in estimating genotype by environment interaction (GEI), figuring out superior and stable genotypes inside the final selection cycles [13; 15]. Enormous GEI results from versions within the quantity of differences amongst genotypes in various environments, called qualitative or rank adjustments, or versions inside the comparative ranking of the genotypes, called quantitative or absolute variations among genotypes [10]. The study of GEI is important in numerous agro-ecologies and enables to remark genotypes adapted to these numerous environments. The additive main effect and multiplicative interaction (AMMI) model also helped us better recognize the complicated patterns of genotypic responses to the environment [11]. Therefore, the principal objective of this study was to assess and identify food barley genotypes with high yielder, yield stability and disease tolerant/resistances across check locations and areas with comparable agro-ecologies.

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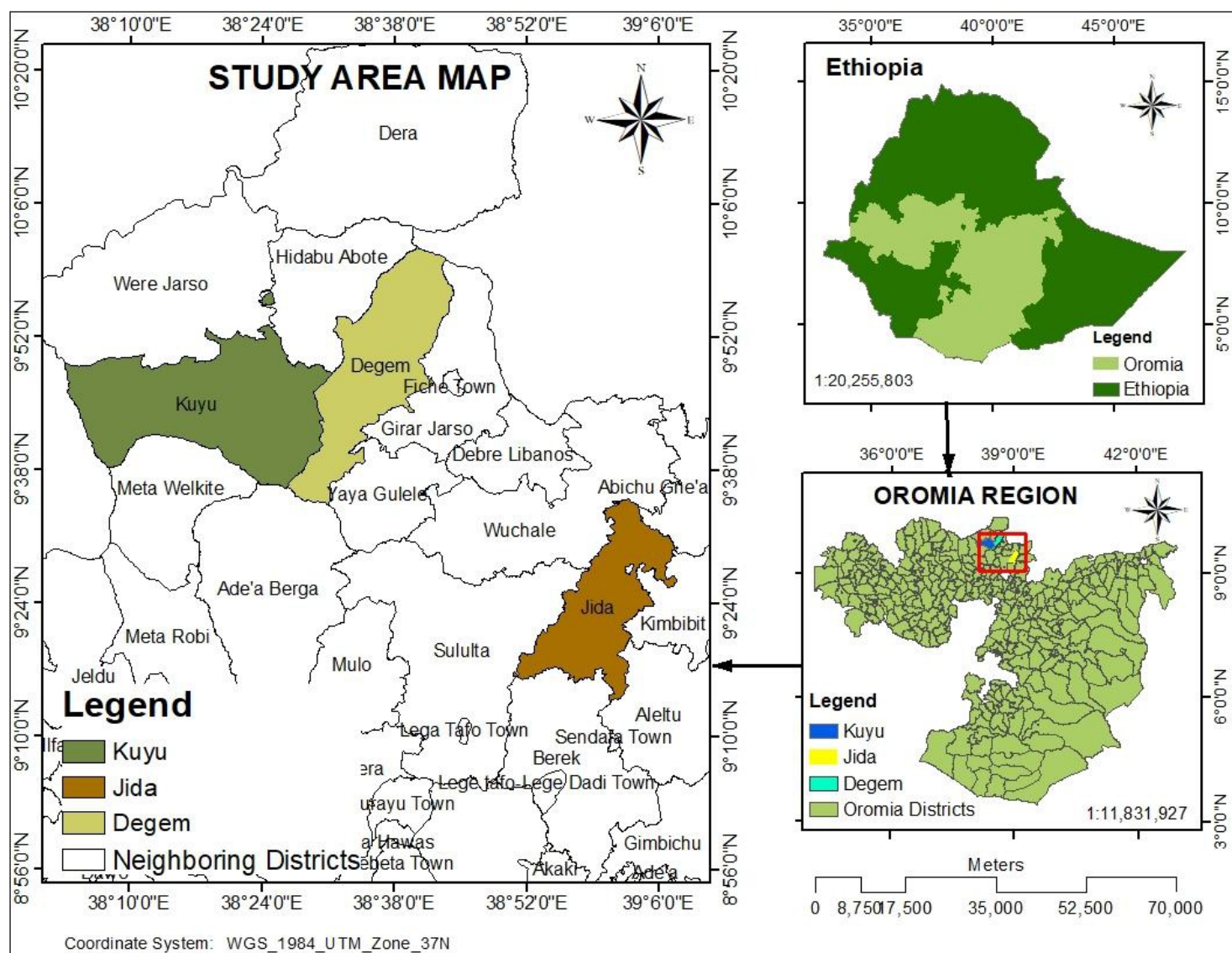
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2. Materials and Methods

Description of locations: The test was carried out at different rain fed locations in North shewa zone at Fitche agricultural research center at Degam, Kuyu and Jida sub site all through the 2023-2024 foremost cropping season, that represent distinctive agro-ecologies of the barley growing areas of the zones.

Map of experimental districts



2.1 Experimental materials: Fourteen (14) food barley genotypes, collectively with currently released standard check (Walashe), HB1307 and one farmer's cultivar, had been included within the trial evaluation. The genotypes were selected based totally on average performance and agro-ecology and were received from Ethiopia biodiversity institute (EBI), Sinana and Holeta agricultural research center.

Table 1: Passport data and description of food barley land-races used in the study

Genotype	Acc. No	Genus name	Species name	Region	Zone	Woreda/District	Locality	Sources
G-3	3541	Hordeum	vulgare	Amhara	AGEW AWI	BANJA	Askona, 7Km Injibara-Chagni junction	EBI
G-9	3575	Hordeum	vulgare	Amhara	MISRAK GOJAM	ENEMAY	Bichena	EBI
G-2	3579	Hordeum	vulgare	Oromiya	ARSSI	ROBE	Tena, 20Km Robi to Sedika	EBI
G-13	3594	Hordeum	vulgare	SNNP	SEMEN OMO	CHENCHA	Dorzie, 27Km Arba Minch to Chench	EBI
G-6	3657	Hordeum	vulgare	Oromiya	ARSSI	ROBE	Habe, 23Km from Kula	EBI
G-12	3661	Hordeum	vulgare	Amhara	AGEW AWI	BANJA	1Km Injibara to Addis Abeba	EBI
G-4	3671	Hordeum	vulgare	Amhara	MISRAK GOJAM	GUZAMN	Bueched, 9Km Debre Markos to A. A	EBI
G-14	3672	Hordeum	vulgare	Amhara	MISRAK GOJAM	AWABEL	Shafe, 21Km Debre Markos to Addis Abeba	EBI
G-1	3782	Hordeum	vulgare	Amhara	DEBUB GONDAR	FARTA	5Km E. of Debre Tabor	EBI
G-10	3796	Hordeum	vulgare	Amhara	DEBUB GONDAR	FARTA	Debre Tabor	EBI
G-8	3908	Hordeum	vulgare	Oromiya	ARSSI	SHERKA	19Km bekoji to Gobesa	EBI
G-5	HB1307							HARC
G-7	Walashe							SARC
G-11	local							FARMER

G-genotype, Acc. No- accession number EBI- Ethiopia biodiversity institute, SARC- Sinana agricultural research center, HARC-Holeta agricultural research center

2.2 Experimental layout and Trial management:

Randomized completed block design (RCBD) with 3 replications became used across location. Every experimental plot had six rows of 3m length and 20 cm apart with a plot area of 1.2 m x 3m. Drilling seed with the aid of hand changed into used with the same seed rate for every location. Fertilizer become applied at a rate of 100kg ha^{-1} and 100kg ha^{-1} of UREA and NPS and half of UREA was carried out at some stage in planting time, whilst the rest half of splits have been implemented at tillering stages. Seed rate of 125kg ha^{-1} was used. First weeding was executed 35days after emergence and the second at 30 days after the first weeding conducted. Statistics considered for analysis was from the candidates of the net plot, hence the 4 central harvest-able rows. The harvested genotypes were dried earlier than being tested for moisture content material where 12% changed into the desired average moisture content the usage of moisture tester. Grain yield data was then obtained with the aid of weighing the dried grain using a digital scale.

2.3 Statistics series technique: eight plants have been selected randomly earlier than heading from every row (4 harvest-able rows) tagged and all the vital plant based data had been collected from those sampled plants.

Plot based: the following plant parameters have been determined: Days to heading (DH), Days to maturity (DM), Thousand seed weight (TSW), Grain yield (GY), and the four main economically vital food barley disease which include scald, septoria (SEP), stem rust (SR), and leaf rust (LR).

Plant based: Plant height (PH), productive tillers (PPT), Spike length (SL), Flag leaf length (FLL), Peduncle length (PDL), and Awn length (Awl).

2.4 Statistical evaluation

Analysis of variance is calculated using the model:

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

Where in: 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 interplay.

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

2.5 AMMI model

in which: 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 principal component analysis (PCA) axis k , Y_{ik} and δ_{jk} are

the genotype and environment principal component score for axis k , N is the number of principal components retained in the model, and ε_{ij} is the residual term.

2.6 AMMI Stability Value (ASV)

ASV is the gap from the coordinate factor to the beginning in a two-dimensional plot of IPCA1 rankings in opposition to IPCA2 rankings inside the AMMI model [18]. Because the IPCA1 score contributes more to the GxE interaction sum of squares, a weighted value is needed. This weighted value calculated for each genotype and every environment in step with the relative contribution of IPCA1 to IPCA2 to the interaction sum of squares as follows:

$$ASV = \sqrt{[(SSIPCA1 / SSIPCA2) (IPCA1score)]^2 + (IPCA2score)^2}$$

Where: SSIPCA1/SSIPCA2 is the weight given to the IPCA1-value by dividing the IPCA1 sum of squares with the aid of the IPCA2 sum of squares. The larger the ASV value, either negative or positive, the more especially adapted a genotype is to a certain environments. Smaller ASV values imply more stable genotypes across environments [18].

2.7 Genotype selection Index (GSI)

Stability isn't only the best parameter for choice as maximum stable genotypes might not necessarily give the best yield performance. Therefore, based at the rank of mean grain yield of genotypes (RY_i) throughout environments and rank of AMMI stability value ($RASV_i$), genotype selection index (GSI) become calculated for each genotype as:

$$GSI_i = RASV_i + RY_i$$

A genotype with the least GSI is considered as the most stable [8]. evaluation of variance became completed using R software program (model 4.2.2).

3. RESULTS AND DISCUSSIONS

3.1 Combined analysis of variance

The mean square analysis of variance (ANOVA) is provided in table 2. Significant differences were detected a number of the essential and the interaction effects ($P \leq 0.01$) for most of the parameters evaluated. The mixed evaluation of variance found out that significant differences have been recorded across location for all parameters. Year*genotypes and year*location*genotypes have been excreted considerable effect in particular on grain yield however none significant for most traits.

Table 2: Analysis of variance (ANOVA) for grain yield and related traits of food barley genotypes evaluated in 2023-2024 main cropping season

S. V	DF	DH	DM	FLL	PDL	PH	PPT	Awl	SL	TSW	YLDkg ha^{-1}
rep	2	68.2**	0.6*	11.2*	5.6*	489.7*	0.7*	6.3*	30.2*	11.7**	14245.0**
Gen	13	1284.5**	662.2**	54.9**	90.5**	676.6**	4.0**	8.5**	11.9**	334.8**	2010230**
Loc	2	1146.2**	1328**	59.6**	26*	2928.5**	13.3**	60.3**	45.9**	3766.8**	16850072**
Yr	1	9450**	12138**	168**	168**	1512**	42**	378**	378**	368.2**	126633395**
Gen.Loc	26	30.3**	50.8**	11.2 ns	31.9 ns	32.22 ns	32.7 ns	12.22 ns	22.4 ns	10.4**	602647**
Gen.yr	13	0.43 ns	45.2 ns	12.1 ns	0.81 ns	1.04 ns	1.52 ns	32.11 ns	0.169 ns	0.065 ns	1124582**
Loc.yr	2	0.65 ns	0.34 ns	2.67 ns	0.77	1 ns	1.48 ns	22 ns	0.169 ns	0.065 ns	19447714**
Gen.Loc.yr	26	0.9 ns	0.48 ns	7.25 ns	0.95	1.18 ns	1.66 ns	13.2 ns	0.169 ns	0.065 ns	210442**
Res	138	4.236	7.794	3.828	6.464	74.77	0.5566	1.047	1.058	5.041	100328

Key: ns, **, none significant, significant at 5% and 1% respectively, Loc = location, rep = replication, Gen = genotypes, Yr = year, Loc *Gen = location by genotype, Gen*yr = genotype*year, Loc*yr = location*year, Gen*Loc*yr = genotype by location by year, Res = residual effect, S.V= source of variation, DF -degree of freedom, DH- Days to Heading; DM- Days to Maturity; PPT- productive tillers, PH- Plant Height; SL- spike Length; TSW- Thousand Seed Weight, YLDkg ha^{-1} Yield kilogram per Hectare. FLL = Flag leaf length, PDL = Peduncle length and Awl = awn length.

3.2 Yield overall performance throughout locations: mean performance for grain yield throughout location and year offered in table three. Study performed [14] indicated that, some genotypes continuously carried out excellent in a few environments and fluctuating across a few locations. for this reason, the average grain yield ranged from the lowest of 1037.1kg ha^{-1} at kuyu sub site in 2023 to the best of 3735.8kg ha^{-1} on similar site in 2024 with grand mean of 2875.8kg ha^{-1} .The average grain yield across environments ranged from the lowest of 2373kg ha^{-1} for G-3 to the highest of 3574.8kg ha^{-1} for G-12 which constantly changed into done and gave better yield over the examined environments.

Table 3: Mean grain yield (kg ha^{-1}) of food barley genotypes evaluated at five environments

	Year					
	2023		2024			
	Test Locations					
Genotype	Kuyu	Degam	Kuyu	Degam	Jida	Mean
G-1	720 ^{efg}	2671 ^{bcd}	3502 ^{abc}	3360 ^{bc}	3016 ^{abc}	2653.8
G-2	967 ^{c-f}	3362 ^{ab}	3638 ^{abc}	3165 ^{bc}	2761 ^c	2778.6
G-3	709 ^{efg}	2112 ^d	2659 ^c	2615 ^c	3770 ^a	2373
G-4	1429 ^{bc}	2602 ^{bcd}	4734 ^a	4614 ^a	3418 ^{abc}	3359.4
HB1307	1012 ^{c-f}	2129 ^d	4277 ^{ab}	4594 ^a	3417 ^{abc}	3085.8
G-6	851 ^{def}	2503 ^{bcd}	3680 ^{abc}	4949 ^a	2814 ^c	2959.4
Walashe	1581 ^b	2973 ^{a-d}	4307 ^a	3691 ^b	3078 ^{abc}	3126
G-8	1285 ^{bcd}	3687 ^a	3863 ^{abc}	3415 ^{bc}	3209 ^{abc}	3091.8
G-9	296 ^g	3115 ^{abc}	2831 ^c	3257 ^{bc}	2926 ^{bc}	2485
G-10	786 ^{d-g}	3310 ^{ab}	3674 ^{abc}	3481 ^b	3318 ^{abc}	2913.8
Local	1152 ^{b-e}	2503 ^{bcd}	4336 ^a	3145 ^{bc}	3709 ^{ab}	2969
G-12	2414 ^a	3618 ^a	4341 ^a	3700 ^b	3801 ^a	3574.8
G-13	795 ^{d-g}	2270 ^{cd}	2966 ^{bc}	2610 ^c	3166 ^{abc}	2361.4
G-14	522 ^{fg}	2182 ^d	3491 ^{abc}	3276 ^{bc}	3174 ^{abc}	2529
Mean	1037.1	2788.3	3735.8	3562.3	3255.4	2875.86
LSD5%	302.63	516.61	744.22	455.25	450.43	
CV%	17.4	11.1	11.9	7.6	8.2	

Key: G-genotype, CV- coefficient of variation, LSD- least significant difference

3.3 Agronomic performance: combined mean grain yield and other agronomic traits are organized in table4. From the evaluated genotypes, Genotype (G-12) became recorded medium days to heading, days to maturity, and plant height, which become an option to broaden resistant variety towards accommodations problems. It additionally recorded the highest thousand seed weight and grain yield. In the same way, G-4 was recorded medium days to heading, days to maturity, effective tillers and thousand seed weight. Those suggested that, there is remarkable flexibility for developing advanced types that suitable genotypes for various agro-ecologies with variable duration of growing length and high in grain yield repute. Furthermore, these genotypes (G-12 and G-4) have been recorded the best grain yield and that they had 12.6%, and 6.5% yield advantage over the standard check (walashe) respectively.

Table 4: Combined mean grain yield and other agronomic traits of food barley genotypes

Genotype	DH	DM	FLL	PDL	PH	PPT	SL	Awl	TSW	YLDkha ⁻¹	YLDA%
G-1	99.3 ^{ab}	147.8 ^{bcd}	18.6 ^a	9.4 ^{ef}	78.5 ^{cde}	2.3 ^{efg}	7.3 ^{def}	13.3 ^d	44 ^{ab}	2654 ^{defg}	
G-2	94.2 ^{bc}	145.3 ^{cd}	16.6 ^{cde}	13.6 ^{ab}	83.7 ^{bc}	2.9 ^{a-d}	7.7 ^{de}	13.7 ^{cd}	41 ^{bc}	2779 ^{cdef}	
G-3	74.7 ^e	132.1 ^e	15 ^{gh}	14.9 ^a	69 ^g	3.abc	7.6 ^{cde}	13.5 ^d	39.9 ^{bc}	2373 ^g	
G-4	86.3 ^d	143.3 ^d	12 ⁱ	7.2 ^g	77.9 ^{cdef}	2.8 ^{b-e}	7.7 ^{b-e}	14.2 ^{bcd}	38 ^{cd}	3359 ^{ab}	6.5
HB1307	102.5 ^a	153.1 ^{ab}	16.6 ^{def}	12.2 ^{bc}	90.2 ^{ab}	3 ^{abc}	8.95 ^b	13.8 ^{cd}	43.7 ^{ab}	3086 ^{bc}	
G-6	95 ^{bc}	147.5 ^{bcd}	18.3 ^{ab}	14.8 ^a	79.9 ^{cd}	3.3 ^{ab}	8. a-e	14.6 ^{bcd}	40.2 ^{bc}	2959 ^{cd}	
Walashe	86.2 ^d	144.3 ^d	17 ^{bcd}	12.8 ^{bc}	93.4 ^a	3.4 ^{ab}	8.9 ^{abc}	14.3 ^{bcd}	38.6 ^{cd}	3126 ^{bc}	0
G-8	91.3 ^{cd}	144 ^d	14.8 ^{gh}	11.3 ^{cd}	77.4 ^{c-f}	2.6 ^{c-f}	6.8 ^{ef}	14.2 ^{bcd}	37.6 ^{cd}	3092 ^{bc}	
G-9	101.1 ^a	147.3 ^{bcd}	18.abc	10.2 ^{de}	75. d-g	2.5 ^{c-f}	6.2 ^f	14.5 ^{bcd}	34.8 ^d	2485 ^{fg}	
G-10	99.2 ^{ab}	149.3 ^{a-d}	15.4 ^{e-h}	14.9 ^a	79.6 ^{cd}	1.8 ^g	7.5 ^{ef}	15.9 ^{ab}	46.3 ^a	2914 ^{cde}	
Local	92.8 ^c	146 ^{cd}	15.8 ^{d-g}	8 ^{fg}	71.3 ^{fg}	3.6 ^a	9.4 ^a	14.9 ^{abc}	36.1 ^{cd}	2969 ^{bcd}	
G-12	101.5 ^a	151.6 ^{abc}	15 ^{gh}	11.2 ^{cd}	76.3 ^{def}	2 ^{fg}	7.2 ^{ef}	13.6 ^d	48.6 ^a	3575 ^a	12.6
G-13	76.17 ^e	132.3 ^e	14. h	12.5 ^{bc}	72.6 ^{efg}	2.9 ^{b-e}	8.5 ^{a-d}	15.9 ^a	34.3 ^d	2362 ^g	
G-14	102.3 ^a	155 ^a	18.6 ^{ab}	12.8 ^{bc}	76.9 ^{c-f}	2.4 ^{d-g}	7. ef	13.9 ^{cd}	48.3 ^a	2529 ^{efg}	
Mean	93	146	16	12	79	3	8	14	41	2875.86	
LSD5%	5.9	6.8	1.5	1.7	6.9	0.6	1.3	1.3	4.9	382.7	
CV%	8.8	6.5	12.7	20.2	12.1	31.5	22.9	12.7	16.6	11	

Key: G- genotype, LSD- least significant difference, CV- coefficient of variation, DH- Days to Heading, DM- Days to Maturity, PPT- productive tillers, PH- Plant Height, SL- spike Length, TSW- Thousand Seed Weight, YLDkha⁻¹ - Yield kilogram per Hectare, FLL- Flag leaf length, PDL- Peduncle length, Awl-awn length and YLDA- yield advantage

3.4 Predominant disease reactions over location: maximum genotypes evaluated had considerably low reactions with their corresponding economically important disease. But, genotypes (G-9 and G-10) had been moderately susceptible to septorial, leaf and stem rust disease. On the other hand, genotype (G-12) was better tolerance to septorial, stem and leaf rust than the rest genotypes.

Table 5: Disease severity scale following a modified Cobb's scale using 0-9 scale of food barley genotypes evaluated in 2023-2024 main cropping season.

Genotypes	SEP	LR	SR
G-1	10r	60ms	10r
G-2	10r	20mr	10r
G-3	20mr	60ms	20mr
G-4	20mr	20mr	20mr
HB1307	20mr	10r	10r
G-6	10r	10r	10r
Walashe	20mr	60ms	10r
G-8	20mr	60ms	10r
G-9	60ms	60ms	60ms
G-10	60ms	65ms	60ms
Local	10r	10r	10r
G-12	10r	10r	10r
G-13	10r	20mr	10r
G-14	20mr	20mr	10r

Key: G- genotype, SR-stem rust, LR-leaf rust, SEP-septorial, r-resistance, mr- moderately resistant, ms- moderately susceptible

3.5 AMMI analysis for grain yield: The additive main effects and multiplicative interaction analysis of grain yield showed that, environment and genotypes via environment interaction had been tremendously significant ($P \leq 0.01$). This is similar to the report [17]. This suggests that one of the simple elements that affect GEI could either be genotypic or environmental in nature [7; 2] also report that 74.3% of the interaction sum of squares was defined by way of IPCA1.

Table 6: AMMI for grain yield of 14 food barley genotypes evaluated at six environments

Source of variation	DF	SS	EX.SS%	MS
Genotypes	13	26132984	9.5	2010230**
Environments	4	199228966	72.4	49807241**
Block	10	1502029	0.5	150203*
Interactions	52	35759864	13	687690**
IPCA 1	16	18722881	6.8	1170180**
IPCA 2	14	9193302	3.3	656664**
Residuals	22	7843681	2.9	356531

Key: DF = degree of freedom, SS = sum of squares, MS = mean squares, IPCA = Interaction Principal Component Axis, EX. SS% = Explained Sum of square *, **, Significant at the 0.5% and 0.1% level of probability respectively

The environment and genotype mean are supplied in Fig.1 and table 7. This bi-plot helped within the interpretation of the interplay outcomes among genotypes and environments; and in the assessment of the adaptability of genotypes. Genotypes which can be characterized by using mean, more than grand mean and the IPCA scores almost zero are taken into consideration as normally adaptable to all environment. But, the genotypes with high mean overall performance and with large value of IPCA scores are taken into consideration as having specific adaptability to the environments [19]. Study carried out [3] stated that, the larger the IPCA scores, either negative or positive, the more particularly adapted a genotype is to a certain environments; yet the smaller the IPCA scores, the greater stable the genotype is over all environments. Primarily based on those, genotype (G-8) had grain yield above the grand mean; and similar IPCA1 scores with location Degam and kuyu implying that their interactions were effective; the higher yield of this genotype become observed, in particular, at these locations. Therefore, it is the best adapted genotypes for those locations.

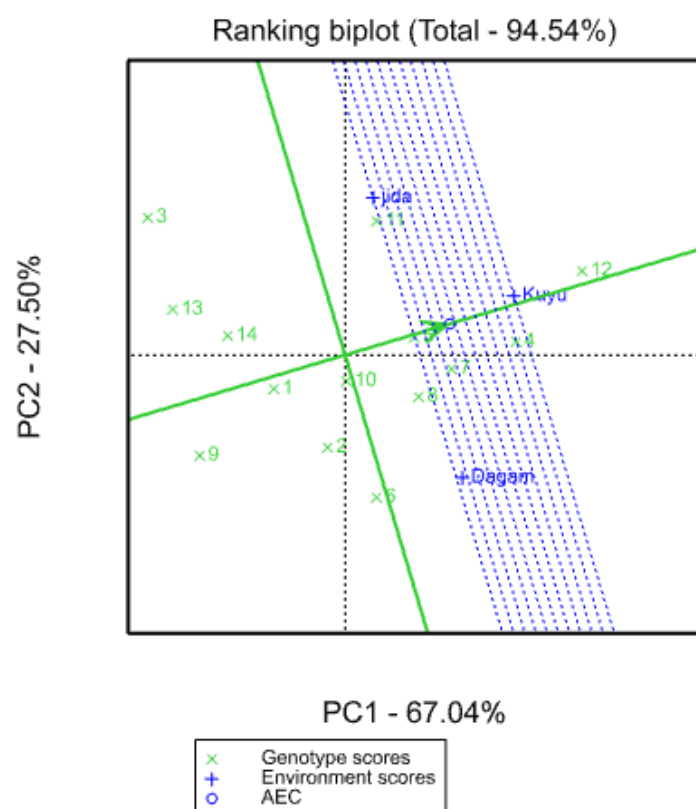


Fig. 1: GGE bi-plot based on genotype-focused scaling for comparison of genotypes for their yield potential and stability

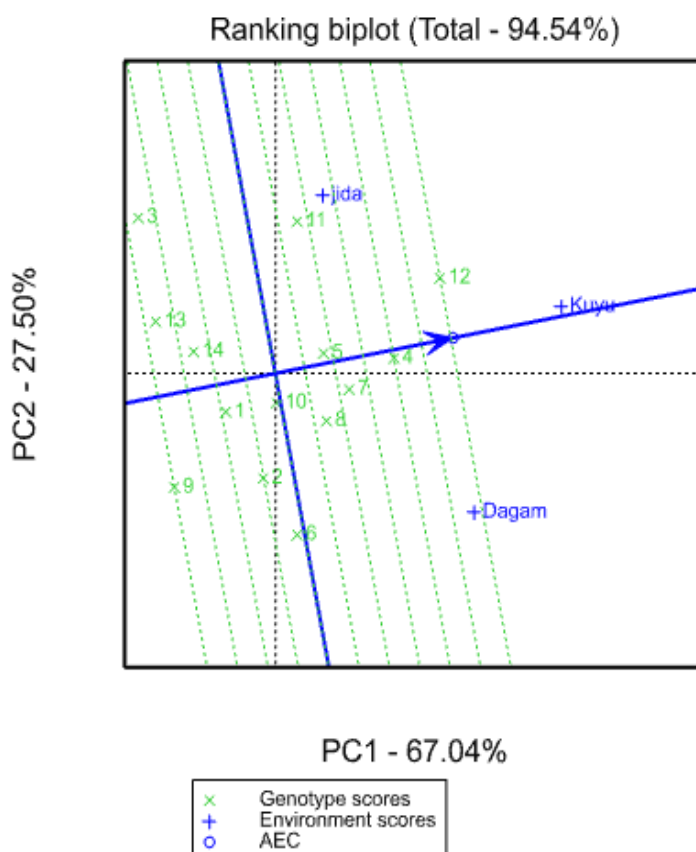


Fig. 2: GGE bi-plot based on tested environments-focused comparison

3.6 Stability evaluation for genotypic performance: The AMMI stability values (ASV) for grain yield is offered in table7. Considering the AMMI stability value that takes into consideration, the scores of the IPCA2, genotypes with least ASV scores are the most stable, at the same time as genotypes with high ASV score are unstable [3; 8]. Consequently, genotype (G-12) became regarded to be amongst the ones showing low ASV and became the more stable. At the opposite this, genotype (G-6) revealed the highest ASV and become hence taken into consideration to be unstable. Stability by way of itself be supposed to, however, no longer be the best parameter for choice, as the most stable genotype could no longer essentially provide the first-class yield performance [16]. So, the study indicated that, G-1 was recorded the lowest ASV, however recorded decrease grain yield of 2654kg ha^{-1} than the grand means of 2875.8 kg ha^{-1} . The stable genotype became accompanied with mean grain yield above the grand mean and this result was in agreement with [12], who has used ASV as one method of comparing yield stability of bread wheat types and comparable reports been made with the aid of [1] in barley and bread wheat using AMMI stability value. A genotype with the least of genotype selection index (GSI) is considered because the maximum stable genotype [8]. Primarily based on that reason, G-12 became more stable genotype with the low of genotype selection index (GSI) and better yield.

Table 7: AMMI stability value, AMMI rank, Yieldkg/ha, yield rank and genotype selection index (GSI)

Genotype	ASV	ASV rank	YLD	YLD rank	GSI	IPCAG1	IPCAG2
G12	24.5	8	3575	1	9	11.97	2.07
G4	41.3	12	3359	2	14	-20.2	3.77
Walashe	3.9	2	3126	3	5	-1.63	-2.09
G8	27.4	10	3092	4	14	11.87	-12.91
EH1307	50.1	13	3086	5	18	-24.29	8.19
Local	17.8	5	2969	6	11	2.86	16.84
G6	54.8	14	2959	7	21	-26.24	-12.13
G10	15.6	4	2914	8	12	6.44	-8.46
G2	24.7	9	2779	9	18	9.65	-14.88
G1	2.7	1	2654	10	11	0.43	-2.59
G14	10.2	3	2529	11	14	-3.46	7.42
G9	22	6	2485	12	18	8	-14.8
G3	34.1	11	2373	13	24	13.61	19.88
G13	24.4	7	2362	14	21	10.99	9.7
Grand Mean			2875.86				

Conclusions and recommendations

Grain yield partitioned in to one-of-a-kind IPCAs the use of AMMI model evaluation, that the first principal component axis for interaction alone explains most of the interplay sum of squares. The sign and magnitude of IPCA scores showed the relative contribution of every genotype and environment for the genotype by environment interactions. It facilitates to summarize the pattern and significance of GEI and fundamental outcomes that screen clean insight into the adaptation of genotypes to environments. This suggests that, genotype (G-12) is less contributors to the interaction effect and has consistent performances throughout locations. Consequently, it was identified as promising genotype in phrases of yield capacity and stability, tolerant to disease and endorsed for development, launch and use as parent's materials in purpose of breeding programs.

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