

Research Article

Genotype by Environment Interaction and Grain Yield Stability of Food Barley (*Hordeum vulgare* L.) Genotypes in West Hararghe Zone, Eastern Ethiopia

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Abstract

Barley (*Hordeum vulgare* L.) is one of most important and commonly produced crops in Ethiopia. The experiment was conducted with the objective to determine the effect of genotype by environment interaction (GEI) on grain yield and to assess yield stability of Food Barley genotypes for the target environments. Fourteen genotypes, including Walashe were evaluated for two consecutive years in 2022 and 2023 at Arba rakate, Mechara and Daro Gudo. The experiment was laid in RCBD with three replications. The result revealed that there was significant difference among genotypes for grain yield across the testing environments. The mean grain yield of the genotypes across the six environments were 3341.2 kg/ha which ranged from 2768.4 kg/ha (G10) to 4045.6 t/ha (G13). The analysis of variance for AMMI also revealed significant variation for genotypes, environment and genotypes by environment interaction. The main effects of environment (E), genotypes (G) and GE interaction were highly significant at $P < 0.01$. Environment had the largest effect, explaining 58.7% of the total variability, while Genotypes and GE interaction explained 6.5% and 12.1% of total sum of squares, respectively. The larger contribution of the environment indicated that environments were very diverse. The first and second principal component accounted for 78.66% and 12.84% of the genotype by environment interaction ($G \times E$), respectively). Based on AMMI stability value (ASV), test G12, G13, G7 and G14 were the most stable ones. Genotype Selection Index (GSI) showed that in the present study the most stable and high yielding genotypes were G13, G7 and G14. Based on this analysis, test G13, G7 and G14 were the most stable ones with AMMI stability values (ASV) of 9.08, 24.754 and 19.59, respectively. In the present study, Genotype Selection Index (GSI) showed that the most stable and high yielding genotypes were G13, G7 and G14 whereas, G10, G2, G3, G1 and G9 were the least stable and low yielding genotypes. Therefore, G13 and G7 were identified as candidate genotypes to be verified for possible release.

Keywords

AMMI, Food Barley, Genotype by Environment Interaction, ASV, GSI, IPCA

1. Introduction

Barley has a long history as a domesticated crop, as one of the first to be adopted for cultivation and the crop is now virtually produced worldwide [44]. Barley is the fourth most im-

portant cereal crop in the world after maize, Wheat and rice [19], while in Ethiopia; It is the fifth most important cereal crop in Ethiopia in terms of area coverage, after tef, wheat, maize,

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and sorghum [11]. The world major producers are European Union, Russia, Australia, Canada, Turkey and United Kingdom [19]. Ethiopia is the first largest producer in Africa sharing about 25% of the barley production in the content, followed by Morocco and ranked 12st in the world with a share of 1.47% of the world's total production [19]. Barley accounted for 7.74% (23,391,098.8 quintals) of the total grain production, with cereal crops contributing 88.69% (about 302,054,260.58 quintals) [11]. Among cultivated cereals in Ethiopia, barley has a large number of accessions preserved in the Ethiopian gene. However, several reports indicated that barley production has been negatively affected by both biotic and a biotic stresses. Diseases that include net blotch and scald have significant contributed to reduce barley productivity in the country.

The development of superior varieties in terms of grain yield, quality, stress resistance, and yield stability is an important consideration in plant breeding programs. Barley breeding program has been focusing mainly on developing high yielding varieties, with good level of resistance to major biotic and a biotic stresses. However, yield is a complex quantitative trait, often controlled by many genes, influenced by prevailing environmental conditions, with each gene having a small effect. In order to identify the most stable and high yielding genotypes, it is important to conduct multi-environment trials [35]. Genotypic responses in trials involving many environments are crucial in cultivar evaluation and recommendation [32] because crop grain yield is not determined by genotype and management practices alone but by environmental Interaction (GEI).

In most of the plant breeding programs, GE interaction effects are of special interest for identifying the most stable genotypes for mega-environments and adaptation for specific targets. The existence of genotype by environment interaction (GEI) complicates the identification of superior genotypes adapted to a range of environments because of the demand for phenotypic uniformity across environments and seasons [20]. Breeders always look for high-yielding, widely adapted, and stable genotypes across a range of environments. It is also a priority for

breeders to develop improved genotypes that are superior not only in grain yield, but also performance in other agronomic traits over a relatively wide range of environments [9, 25]. Therefore, repeated testing of genotypes across a wide range of environments is an effective way to examine the GEI in developing high-performing and stable cultivars. The potential of genotype's adaptability and stability across different environments has been estimated using different statistical tools such as additive main effects and multiplicative interaction (AMMI) analysis [24], joint regression [23], genotype and genotype by environment interaction (GGE) biplot [52], and regression stability models [17]. AMMI and GGE biplot models are used to quantify the stability of genotypes across locations using the interaction principal component analysis (IPCA) [47, 51]; the most effective and commonly used multivariate models for the analyses of stability and adaptability [50]. These models also provide an opportunity for ranking genotypes and selecting suitable mega environments (MGEs). Stability is not the sole factor to consider when choosing genotypes, and stable genotypes may not always produce the best results in terms of yield. Furthermore, the genotype selection index (GSI) was developed for the selection of the best genotype, which has both high mean performance and stability. Therefore, the objective of this study was to determine the effect of genotype $\times$ environment interaction (GEI) on grain yield and to assess yield stability of Food Barley genotypes for study area.

2. Materials and Methods

2.1. Descriptions of the Study Area

The experiment was conducted in three locations, namely, Mechara, Arba rakate and Daro gudo (Table 1). These locations are the main multi-location variety testing sites for barley improvement program and representative of different barley growing agro-ecologies of west hararghe zone.

Table 1. Profile of the study area.

Environments	Altitude (m.a.s.l)	Rainfall (mm)	Average temperature (°C)		Latitude (°North)	Longitude (°East)
			Max	Min		
Mechara	1796	963	15	28	40.19	08.35
Arba rakate	2250	1120	13	28	40.87	9.07
Daro gudo	2300	1280	10	24	40.89	9.003

2.2. Experimental Materials

In this study, 14 barley genotypes including the standard checks were used. Among them, one was released variety and the rest 13 were genotypes/lines (Table 2). These genotypes

were promoted from a preliminary yield trial (PYT) experiment composed genotypes tested in 2021. The materials were collected from Sinana Agricultural Research Center national barley breeding program.

Table 2. Description of Genotypes and their source.

Code	Genotypes	Source	Code	Genotypes	Source	Environment
G1	FBSNPlot100	SARC	G8	FBSNPlot79	SARC	E1 = Mechara 2022
G2	FBSNPlot44	SARC	G9	FBSNPlot76	SARC	E2 = Mechara 2023
G3	FBSNPlot39	SARC	G10	FBSNPlot81	SARC	E3 = Arba rakate 2022
G4	FBSNPlot54	SARC	G11	FBSPL104	SARC	E4 = Arba rakate 2023
G5	FBSPL106	SARC	G12	FBSNPlot13	SARC	E5 = Daro Gudo 2023
G6	FBSPL75	SARC	G13	FBSPL89	SARC	E6 = Daro Gudo 2023
G7	FBSPL63	SARC	G14	Walashe	SARC	

SARC = Sinana Agricultural Research Center

2.3. Experimental Design and Crop Management

The experiment was set up using a Randomized Complete Block design (RCBD) with three replications. Each experimental plot measured 5 m² (2.5m × 2m) and had ten rows that were 20cm between rows a part. Seed rate of 125 kg ha⁻¹ and fertilizer rate of 100 kg ha⁻¹ NPSB and 100 kg ha⁻¹ N. All of the N fertilizer (urea) was applied to the row in two applications to reduce losses and maximize efficiency: one third at planting and the other two-thirds 35 days later, during the crop's maximum growth period at full tillering stage, following weeding, and during light rainfall to reduce N loss to the atmosphere. All additional crop management practices and recommendations were uniformly implemented to all varieties as previously recommended for the Food Barley.

2.4. Data Collection

Data on grain yield and yield-related traits were collected on plot and plant basis from each plot, respectively. Data for plant height (cm), Spike length (cm), Number of seed per spike and thousand seed weight (gram) were collected on the basis of ten sample plants, which were randomly taken from each plot, and the average of ten sample plants was used for analysis. Grain yield (g) of each plot was measured on clean, dried seed and the measured. A grain yield value (kg) per plot was converted to kilogram per hectare for analysis. Additionally, major Barley disease and insect pests Leaf Rust and Shoot fly data were assessed for each genotype following 1-5 scales.

2.5. Statistical Analysis

Various statistical software applications were utilized to analyze the data. In accordance with the usual technique recommended by [31], the analysis of variance for each location and the combined data over location were carried out using a mixed linear model to evaluate the differences among genotypes in their performance for yield and yield-associated traits. Analysis of variance (ANOVA) of the individual location as well as pooled data over locations, AMMI, and GGE biplot analysis were performed using R statistical software [38]. The least significant difference (LSD) test was used to compare genotype means. For GGE biplots, GEA-R (Genotypic × Environment Analysis with R Widows) Version 4.1 [3] was utilized.

The Additive Main Effects and Multiplicative Interaction (AMMI) Model Analysis

AMMI combines ANOVA and principal component analysis (PCA) into a single study with additive and multiplicative parameters. Additive effects were obtained by applying the AMMI model with six growing environments (E), fourteen barley genotypes (G), and the multiplicative term is about G × E interactions. Following the fitting of multiplicative effects for the genotype by environment interaction using principal component analysis, AMMI analysis is used to fit the additive effects of genotypes and environments [34, 54] and is analyzed using the model below [24, 26]:

$$Y_{ij} = \mu + G_i + E_j + (\sum K_n V_{ni} S_{nj}) + Q_{ij} + e_{ij}$$

Where, Y_{ij} - is the observed yield of genotype i in environment j , μ - is the grand mean, G_i - the additive effect of the i th genotype

(genotype means minus the grand mean), E_j - is the additive effect of the j th environment (environment mean deviation), K_n - is the eigenvalue of the PCA axis n , V_{ni} and S_{ni} - are scores for the genotype i and environment j for the PCA axis n Q_{ij} = is the residual for the first n multiplicative components, e_{ij} - is the error.

Stability analyses

The AMMI stability parameters [27, 54] and GGE biplot were computed for grain yield and GEI analysis of variance using R Software. Accordingly, interaction principal com-

ponent axis (IPCA) scores of genotype, environment, and AMMI stability value from the AMMI model were computed as the standard procedure set by each model.

AMMI stability value

The relative contributions of IPCA1 and IPCA2 principal component analysis scores to the interaction sum of squares were used to calculate each genotype's AMMI Stability Value (ASV). [37] state that the ASV was calculated using the following formula:

$$ASV = \sqrt{[SS_{IPCA1} / SS_{IPCA2} (IPCA1 \text{ score})]^2 + [IPCA2 \text{ scores}]^2}$$

Where ASV is the AMMI stability value, SS_{IPCA1} / SS_{IPCA2} is the weight given to the IPCA1 value, by dividing the IPCA1 sum of square by the IPCA2 sum of square. R Software was used to get IPCA1 and IPCA2 values then ASV was calculated using Microsoft Excel following the given formula. The larger the IPCA score is, either negative or positive, the greater the adaptability of the specific genotype for the certain environment and lower ASV value indicate greater stability in different environments [20].

Genotype Selection index

The Genotype Selection index (GSI) was computed by adding the rankings derived from the AMMI stability value and the yield. Similar to ASV R Software was used for the ranking of both AMMI stability value and grain yield and ordering by using Microsoft Excel. It combines stability and mean yield into a single criterion; genotypes with high yield and stability are favored when both parameters have low values [10]. This is how the yield stability is determined:

$$TGSI = RASV + RY$$

Where RASV is the ranking of AMMI stability value and R is the rank of barley genotypes based on grain yield across environments. This index is the rank of ASV and yield [20].

GGE biplot analysis

The GGE biplot is a graphical tool which displays, interprets and explores two important sources of variation, namely genotype main effect and GE interaction of MET data [52] by using GEA-R (Genotypic by Environment Analysis with R Widows) Version 4.1 [3]. For this study, the GGE biplot method outlined by [48] was used to display the G and GE interaction patterns in the data. GGE biplot analysis considers that only the G and GE effects are relevant and that they need to be considered simultaneously when evaluating genotypes. The model for the GGE biplot based on singular value decomposition (SVD) of the first two principal components is:

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{j2} + \varepsilon_{ij}$$

Where Y_{ij} is the measured mean of genotype i in environment j , μ is the grand mean, β_j is the main effect of the environment j , $\mu - \beta_j$ being the mean yield across all genotypes in environment j , λ_1 and λ_2 are the singular values (SV) for the first and the second principal component (PCA1 and PCA2) respectively, ξ_{i1} and ξ_{i2} are eigenvectors of the genotype i for PCA1 and PCA2 respectively, η_{1j} and η_{2j} are eigenvectors of environment j , for PCA1 and PCA2 respectively, ε_{ij} is the residual associated with genotype i in environment j .

3. Results and Discussion

3.1. Combined Analysis of Variance

Table 3. Combined analysis of variance for grain yield and related traits of food barley genotypes across three locations.

Source of Variation	DF	DH	DM	PH	SL	NSPS	TSW	GY
Location	2	1216.6**	2411.6**	15604**	46.896**	6664.9**	639.74**	120.1**
Replication	2	24.2	91.2*	65.6	0.638	172**	17.57	0.9
Genotype	13	222.7**	405.4**	775.9**	14.595**	1679.8**	267.68**	2.35**
Year	1	4723.3**	5525.4**	408.3*	17.413**	1326.2**	326.63**	31.4**
Location: Genotype	26	25.5	29.2	204.3**	0.845*	189.1**	94.28**	0.46
Genotype: Year	13	49.4**	53.5*	147.6**	1.269**	99.6**	31.8	1.821**

Source of Variation	DF	DH	DM	PH	SL	NSPS	TSW	GY
Location: Year	2	1962.1**	79	609.4**	39.618**	699.7**	240.03**	2.058*
Loc: Genotype: Year	26	18.6	62.4**	52.9	1.071**	121.4**	9.04	0.812**
Residuals	166	20.1	29.1	60.4	0.514	35.2	30.14	0.631

The results of the analysis of variance indicated that there was genetic variability in the food barley genotypes that were evaluated, with very highly significant differences ($p < 0.001$) seen among the genotypes (Table 3). The results of the analysis of variance for phenology, agronomic, yield, and yield components showed that there was a considerable variation between locations, suggesting that the locations had a major impact on the genotypes under test that were examined for the traits. Days to maturity, spike length, seeds per spike and grain yield were all substantially impacted ($p \leq 0.001$) by genotype, environment, and GEI, as shown in Table 3. In comparison to the other variables, Days to heading, plant height and thousand seed weight of the test genotypes also slightly influenced with GEI ($p \leq 0.05$). This is in agreement with the findings of [15, 29] the presence of variability of genotypes to these traits provides ample chance for the selection of high-yielding varieties.

3.2. Mean Performance of Traits

On average, grain yield of the genotypes ranged from 1320.9 to 5932.6 kg ha⁻¹. The average environmental grain yield ranged from 1320.9 kg ha⁻¹ at E2 to 5932.6 kg ha⁻¹ at E6. The environmental variability brings differences in quantitative traits of the tested genotypes (Table 4). The mean traits of genotypes indicated that G12, G4 and G2 were early

to head while G14 was late to head (Table 5). In terms of genotypes maturity, G4 and G3 were early matured with 99 days each, as compared to G14 that are late maturing genotypes having 116 days each. Genotypes that had longest spikes lengths were G7, G13, G3 and G4. For G12 and G5, the NSPS varied from 22.2 to 51.3).

The mean grain yields of the top six genotypes G13, G7, G14, G12, G5 and G4 were higher than the grand mean, whereas the mean yields of the remaining genotypes were lower. These high-yielding genotypes had unique morphological traits such as intermediate Days to heading and maturity, intermediate Plant height, taller Spike length, no of seeds per spike, and heavier Thousand-kernel weight. In line with this study, [29, 40] found that high grain yield was associated with mainly due to thousand seed weight, taller spike length and increased Number of seed per spike. Generally, the result signifies that the studied phenological, yield, and yield components of barley genotypes were influenced by environmental factors, and it indicated the presence of genetic variability among the tested genotypes. This result is comparable to that of [14], who found that the GEI, genotype, and environment variation were significant for 18 genotypes in six environments. This finding is consistent with the findings of several other researchers' previous works [18, 36, 45].

Table 4. The average yield (kg ha⁻¹) performance of 14 barley genotypes across six environments.

Genotypes	E1	E2	E3	E4	E5	E6	Overall Mean
G1	2100 ^{b-e}	1320.9 ^c	3440 ^{cd}	3801.7 ^{a-c}	4733.3 ^{ab}	4514.3 ^{bc}	3318.4 ^{cd}
G2	2066.7 ^{b-e}	1462.9 ^c	4153.3 ^{a-d}	2051.5 ^d	4833.3 ^{ab}	3217.3 ^{de}	2964.2 ^{de}
G3	2373.3 ^{a-d}	1467.6 ^c	4353.3 ^{a-d}	2524.7 ^{cd}	4806.7 ^{ab}	2753.4 ^e	3046.5 ^{c-e}
G4	2846.7 ^{ab}	1471.2 ^c	4426.7 ^{a-d}	2922.7 ^{b-d}	4793.3 ^{ab}	4096.2 ^{b-d}	3426 ^{cd}
G5	2553.3 ^{a-c}	1529.9 ^c	5466.7 ^a	2467 ^{cd}	4266.7 ^{ab}	4365.5 ^{b-d}	3441.5 ^{cd}
G6	2246.7 ^{a-e}	1676.9 ^{bc}	3353.3 ^d	2406.7 ^{cd}	4126.7 ^{ab}	3920 ^{c-e}	2955 ^{de}
G7	2816 ^{ab}	1731.4 ^{bc}	4860 ^{a-c}	3802.2 ^{a-c}	5380 ^a	5236.2 ^{ab}	3971 ^{ab}
G8	2513.3 ^{a-c}	1751.6 ^{bc}	4213.3 ^{a-d}	3474.3 ^{a-d}	4513.3 ^{ab}	3564.8 ^{c-e}	3338.5 ^{cd}
G9	1533.3 ^{de}	1752.8 ^{bc}	4160 ^{a-d}	2906.6 ^{b-d}	4993.3 ^{ab}	4386.8 ^{b-d}	3288.8 ^{c-e}
G10	1453.3 ^e	1836.3 ^{a-c}	3693.3 ^{b-d}	2400.5 ^{cd}	3620 ^b	3606.9 ^{c-e}	2768.4 ^e
G11	2620 ^{a-c}	1886 ^{a-c}	3606.7 ^{cd}	2725.3 ^{b-d}	4093.3 ^{ab}	4290.7 ^{b-d}	3203.7 ^{c-e}

Genotypes	E1	E2	E3	E4	E5	E6	Overall Mean
G12	2146.7 ^{a-e}	1900.8 ^{a-c}	5106.7 ^{ab}	3090.7 ^{a-d}	5266.7 ^a	3353.2 ^{c-e}	3477.5 ^{b-d}
G13	2986.7 ^a	2343.6 ^{ab}	3700 ^{b-d}	4583.9 ^a	4726.7 ^{ab}	5932.6 ^a	4045.6 ^a
G14	1766.7 ^{c-e}	2568 ^a	3820 ^{b-d}	4253.6 ^{ab}	4620 ^{ab}	4159.4 ^{b-d}	3531.3 ^{a-c}
Mean	2287.3	1764.28	4168.1	3100.8	4626.7	4099.8	3341.2
CV	22.4	25.23377	20.4	30.35248	21.17	17.2	23.76
LSD	859.76	747.1856	1425.6	1579.599	1643.7	1183.7	522.6

Table 5. Mean values of agronomic, disease, insect, and grain yield and yield related components of 14 barley genotypes.

Genotypes	DH	DM	PH	SL	NSPS	TSW	SHF	LR	GY kg/ha
G1	61.2 ^{c-e}	106.1 ^{bc}	72.9 ^e	6.9 ^g	40.9 ^{de}	47.8 ^{d-f}	3 ^b	3.33 ^a	3318.4 ^{cd}
G2	59 ^{e-g}	102.1 ^{de}	76.2 ^{c-e}	7.1 ^{fg}	28.4 ^g	50.9 ^{cd}	3.2 ^{ab}	2.83 ^{a-c}	2964.2 ^{de}
G3	61 ^{c-e}	99.1 ^{ef}	92.4 ^a	8.8 ^c	38.6 ^e	50.4 ^{c-e}	2.06 ^c	2.67 ^{b-d}	3046.5 ^{c-e}
G4	57 ^{fg}	98.2 ^f	91.9 ^a	8.7 ^c	38 ^e	50.5 ^{c-e}	2.06 ^c	2.83 ^{a-c}	3426 ^{cd}
G5	65.1 ^{ab}	107.8 ^{bc}	81.3 ^{bc}	8.4 ^c	51.3 ^a	47.6 ^{d-f}	3 ^b	3.17 ^{ab}	3441.5 ^{cd}
G6	61.3 ^{c-e}	108 ^{bc}	80.1 ^{b-d}	7.8 ^d	49.2 ^{ab}	45.7 ^{fg}	3 ^b	2.67 ^{b-d}	2955 ^{de}
G7	59.6 ^{d-f}	105.2 ^{cd}	83.3 ^b	10 ^a	29.7 ^{fg}	57.5 ^a	1.44 ^d	1.33 ^{fg}	3971 ^{ab}
G8	62 ^{cd}	107.3 ^{bc}	83.4 ^b	7.3 ^{e-g}	45.6 ^{bc}	47.2 ^{ef}	2.89 ^b	2.67 ^{b-d}	3338.5 ^{cd}
G9	65.3 ^{ab}	108.1 ^{bc}	82.5 ^b	7.6 ^{de}	26.2 ^{gh}	46.3 ^{fg}	3.11 ^{ab}	2.17 ^{de}	3288.8 ^{c-e}
G10	62.8 ^{bc}	107.4 ^{bc}	76.6 ^{c-e}	7.5 ^{d-f}	48.8 ^{ab}	42.8 ^g	3.56 ^a	3.33 ^a	2768.4 ^e
G11	66 ^a	109 ^b	74.7 ^e	7.6 ^{de}	48.9 ^{ab}	50.6 ^{c-e}	2.94 ^b	2.33 ^{c-e}	3203.7 ^{c-e}
G12	56.6 ^g	99.9 ^{ef}	88.7 ^a	8.4 ^c	22.4 ^h	52.5 ^{bc}	1.78 ^{cd}	3 ^{ab}	3477.5 ^{b-d}
G13	66.1 ^a	106.7 ^{bc}	73.7 ^e	9.5 ^b	32.4 ^f	55.3 ^{ab}	1.44 ^d	1.17 ^g	4045.6 ^a
G14	68 ^a	116.3 ^a	75 ^{de}	7.7 ^d	44.7 ^{cd}	49.2 ^{c-f}	1.83 ^{cd}	1.83 ^{ef}	3531.3 ^{a-c}
Mean	62.2	105.8	80.92	8.1	38.93	49.57	2.52	2.52	3341.2
CV	7.13	4.99	9.68	8.86	15.25	11.1	30.2	29.17	23.76
LSD	2.92	3.48	5.15	0.47	3.9	3.61	0.5	0.596	522.6

DH = days to heading, DM = days to Maturity, PH = plant height, SL = Spike Length, NSPS = number of seed per spike, TSW = thousand seed weight, GY = Grain Yield (kg/ha), SHF = Shoot fly, LR = Leaf Rust

3.3. AMMI Analysis

Table 6 displays results from the AMMI analysis of variance for grain yield (ton ha⁻¹) of 14 different barley genotypes tested in six different environments. Grain yield was significantly influenced by both the environment and genotype ($p \leq 0.001$) when the additive component of the study was taken into account. The environment explained the greatest portion of the variation in grain yield in this study (58.7%), followed by the GEI (12.1%) and genotypes (6.5%). Previous research

on barley [14, 29, 40], wheat [2, 7] and Finger millet [6, 15] supports this finding by showing that the environment was the main factor influencing variation in grain yield, followed by GEI. The current study found that environments accounted for the highest difference in grain yield, indicating the existence of several environments that can be further subdivided into mega environments. The present findings are consistent with the findings of [30], who observed that the variation in grain yield between environments suggests that the environments had an impact on the total grain yield of the test genotypes. The GEI demonstrated a substantial ($p \leq 0.001$) impact on

grain yield in relation to the multiplicative component.

Based on Table 6's AMMI results, the variance in the treatment sum of squares was explained by GEI effects, which accounted for 12.1% of the variation. Our results corroborate the findings of [40], who found that the GEI accounted for 10.47% of the total variation in barley. Because the environment contributed more to GEI than to genotype influence, there was a bigger variation in GEI for the observed yield variation. Two significant IPCAs were retrieved from the interaction component by the AMMI model (Table 6). Additionally, the AMMI's multiplicative component showed that the mean square for IPCA1 was very significant ($p \leq 0.001$). Thus, of the 73.19% total GEI sum of squares, IPCA1 and IPCA2 accounted for 54.32% and 18.87% of the interaction sum of squares, respectively. Variations in barley grain yield are caused by a combination of environmental and genetic variables (treatment = G + E + GE) determine the variation in barley grain yield.

Table 6 indicates that the split of the GEI (GEI = IPCA1 + IPCA2) resulted in two potential interaction principal component axes (IPCA) [14]. Moreover, the mean square of IPCA1 was higher than that of IPCA2, suggesting that GEI caused variations in the genotypes' grain yields. This result is

consistent with previous findings on barley from [18, 33, 40, 43]. According to these authors, environmental variations accounted for the majority of the variation in grain yield, with a bigger variation explained by the means. Furthermore, the findings showed that IPCA1 and IPCA2, the first two interaction principal components, were crucial in understanding the interaction. The two IPCAs in this investigation were accounted greater than 50% of the sum of square interaction. Consequently, the AMMI model with the first and second multiplicative components was sufficient for cross-validation of the GEI-explained variance in grain yield, which can be shown using a biplot; the remaining terms were residual. The outcome was consistent with the findings of multiple authors who used the first two principal components of GEI for GGE biplot analysis of various crops [29] (IPCA1 = 85.68%, IPCA2 = 11.66%, IPCA1&2 = 97.34%), [7] (IPCA1 = 45.5%, IPCA2 = 24.7%, IPCA1&2 = 70.2%), [15] (IPCA1 = 56.2%, IPCA2 = 43.7%, IPCA1&2 = 99.9%), [2] (IPCA1 = 50.24%, IPCA2 = 22.65%, IPCA1&2 = 72.89%), which demonstrated a similar magnitude of GEI variance revealed by the first two principal components of GEI and indicated that AMMI was the best predictive model with the first two multiplicative terms.

Table 6. Additive main effect and multiplicative interaction analysis of variance for grain yield kg/ha of 14 Food Barley genotypes across six environments.

Sources	DF	SS	MS	Total Variation Explained (%)	GXE Explained (%)	Cumulative (%)
Genotypes	13	30.5	2.347**	6.5		
Environments	5	275.7	275.7**	58.7		
Block	12	14.8	1.234	3.2		
Interactions	65	56.7	0.873**	12.1		
IPCA 1	17	30.8	1.814**		54.32	54.32
IPCA 2	15	10.7	0.71		18.87	73.19
Residuals	33	15.2	0.461			
Total	251	469.4	1.87			

3.4. AMMI Stability Value and Genotype Selection Index

The ASV measure was suggested by [37] to address this issue because the AMMI stability model does not account for the quantitative stability measure, which is necessary to quantify and rank genotypes according to their yield stability. Actually, ASV is the separation between zero and the IPCA1 scores versus IPCA2 scores in a two-dimensional scatter graph. The IPCA1 score has to be weighted by the proportionate difference between IPCA1 and IPCA2 scores to

composite for the relative contribution of IPCA1 and IPCA2 total GE sum of squares because it contributes more to the GE sum of scores (Table 7). Afterward, the distance from zero was determined using Pythagoras' theorem [37]. The genotype that has the lowest ASV is considered to be the most stable; as a result, this model classifies genotypes G12, G13, G14, and G7 as stable in that order. Similar to this, [4] observed that the yield response and stable genotype dynamics are always parallel to the mean response of the tested environment. Research on barley by [14, 29, 40], finger millet by [6] and Field Pea by [41] all confirm this conclusion. The most unstable genotypes in this investigation were G1, G10,

G3, G2 and G9. These genotypes are adapted to specific and favorable environments. Similar this, [10] found that genotypes that had higher AMMI stability value and IPCA score were more particularly suited to a particular environment. The most stable genotypes might not always produce the best results, so stability principles by themselves might not be the main selection factor. According to [6, 20], stability should not be the sole criterion for selection, as the genotypes with the highest levels of stability may not always produce the highest yields. Therefore, there is a need for approaches that incorporate both mean yield and stability in a single index.

Genotypes with the least GSI values are considered as the most stable with high grain yield [6, 8]. Consequently, GSI-discriminated genotypes G13, G12, G7, and G14 were the most stable and high mean yield performance (Table 7). Similarly, [28] indicated that both yield and stability should be considered simultaneously to exploit the useful effect of GEI. Conversely, genotypes such as G10, G3, G2, G1, G9, G6, G8 and G11 exhibited high GSI values and yields below the grand mean, suggesting that these genotypes exhibited unstable performance in all tested environments.

Table 7. Mean grain yield, and stability parameters for 14 food barley genotypes.

Genotype	Mean	IPCAg1	IPCAg2	ASV	rASV	RGY	GSI
G1	3.318	-0.39592	0.00594	5240.942	14	8	22
G2	2.963	-0.4824	-0.06266	605.4	11	12	23
G3	3.046	0.32207	-0.14088	1276.22	12	11	23
G4	3.426	0.03917	0.05456	56.564	7	6	13
G5	3.443	-0.2147	0.25921	65.23	8	5	13
G6	2.956	0.2094	0.45725	36.19	5	13	18
G7	3.971	0.06108	0.19608	24.754	4	2	6
G8	3.339	0.28415	-0.28165	79.4	9	7	16
G9	3.288	-0.48541	0.08568	445.48	10	9	19
G10	2.768	0.25485	0.00626	3201.1	13	14	27
G11	3.203	0.29097	0.40753	56.26	6	10	16
G12	3.477	0.01842	-0.41801	4.983	1	4	5
G13	4.046	0.03148	-0.29653	9.08	2	1	3
G14	3.531	0.06684	-0.2728	19.59	3	3	6
Grand mean	3.34						

3.5. GGE Biplot Analysis

The biplot displays the genotypic main effect (G) and GEI effect of genotype under different environmental dataset [52]. The application of the biplot for partitioning through GGE biplot analysis showed that PC1 and PC2 accounted for 78.66% and 12.84% of the GGE sum of squares, respectively (Figure 1A).

3.5.1. Ranking Genotype Based on Their Mean Performance and Stability

91.5% (PC1 = 78.66%, PC2 = 12.84%) of the GGE variation is explained by the two principal components of the GGE biplot. The barley genotypes were ranked using the aver-

age-tester axis (ATC abscissa) in the GGE biplot (Figure 1A) with the horizontal line representing their average performance over the three locations. Higher mean yield across environments is indicated by the single-arrowed line, which represents the average environment coordinate (AEC) abscissa, also known as the average environment axis (AEA) (Figure 1A). G7, G13, G14, G12 and G5 were therefore high yielding on this graph, whereas G10, G6 and, G2, G3 and G11 were low yielding. AEC coordinates separate genotypes with better grain yields from those with below-average grain yields. G10, G6 and G2, G3 and G11 genotypes thus had below-average mean grain yield, whereas G7, G13, G14, G12, G5, and G4 genotypes exhibited above average mean grain yield. The genotypes in Figure 1A that were farthest from the AEA abscissa in either direction show increased GEI and

decreased stability. The genotypes with the highest yields and least stability are G12, G1 and G9, whereas G10 and G2 have the lowest yields and are the least stable. The best genotypes for selection are those with good stability and high mean yield. It was determined that the best broadly adapted genotypes across environments were those that produced the highest yields and were the most stable, namely G7, G13, G14, and G12. Because of their low yields, genotypes G10, G6 and G2 were not taken into consideration for production in the current study. According to this study, a number of researchers [1, 5, 18, 22, 42, 45, 53] reported the relative contributions of stability and mean grain yield for the identification of desired genotypes after the GGE biplot procedure.

3.5.2. Which-Won-Where Polygon View of GGE Biplot

Stability analysis of the genotypes based on their IPCA scores using the GGE biplot analysis and the polygon view of the GGE biplot showed the best performing genotypes and interaction patterns among genotypes and environments (Figure 1B). There are eight sectors in this polygon. The

genotypes G7, G13, G14, G8, G3, G10, G6 and G9 that are situated at a polygon's corner are hence vertex genotypes with the longest vectors. Vertex genotypes within each sector indicate the genotypes with the highest yields within that sector relative to other sectors in the environment. These genotypes were among the most environment-responsive in the directions that they responded to. However, the low-yielding genotypes G3, G10, G6 and G9 were spread out among all over the test locations and showed poor yields at each site. Compared to corner genotypes, genotypes inside the polygon exhibit lower location responsiveness. The graph was divided into eight sectors by the rays of the line graphs, as illustrated in Figure 1B two environments were within one sector, while the remaining environment were within another. This resulted in the identification of two mega-environments, where in genotype G14 performed well in two winning environment Arba Rakate and G7 and G13 in the Daro Gudo and Mechara winning environments. Several authors [16, 33, 36, 43, 45, 52, 53] have reported and found mega environments and the feasibility of selecting stable genotypes using GGE biplot models.

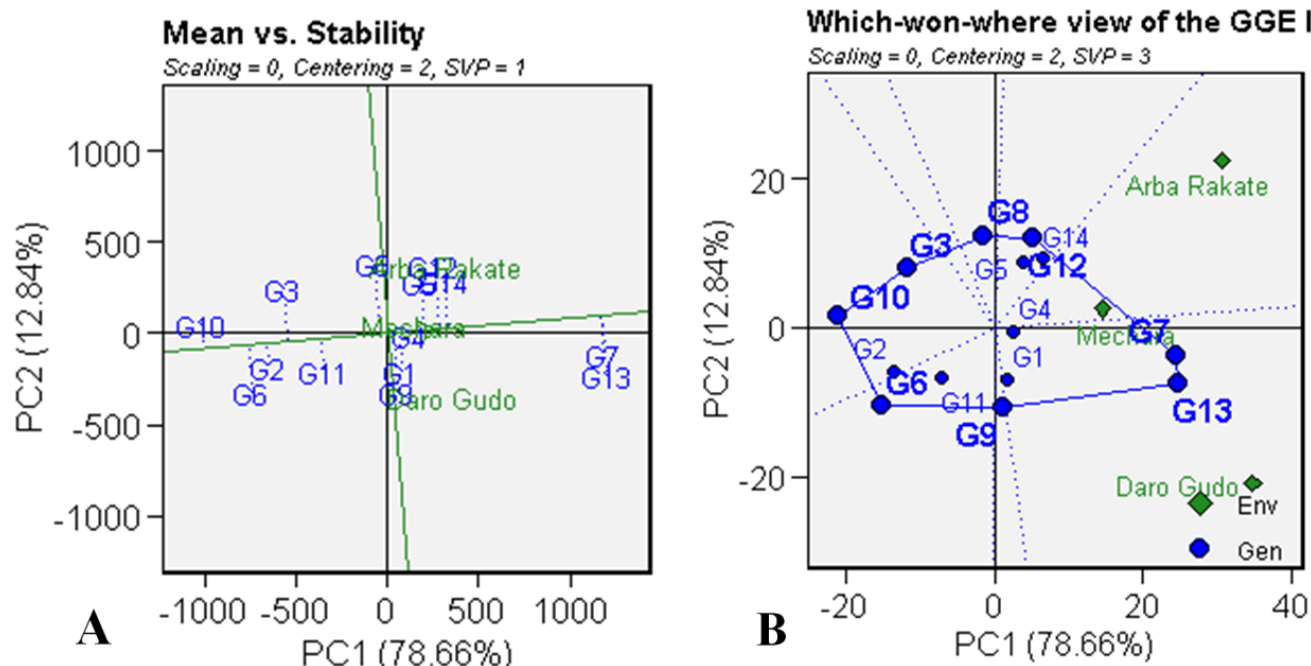


Figure 1. (A) GGE biplot showing “mean versus stability” of 14 barley genotypes, (B) Which-won-where pattern of genotype plus genotype $\times$ environment interaction effect (GGE) biplot.

3.5.3. Discriminating Ability of Testing Environments

Discriminating ability is an important measure of a test environment and the most equally important measure of test environment is its representativeness of the target environment [12, 13, 39, 50]. An ideal environment should be highly differentiating of the genotypes and at the same time repre-

sentative the target environment [50]. The concentric circles on the biplot help to visualize the length of the environment vectors, which is proportional to the SD within the respective environments [50] and is the measure of the discriminating ability of the environments. Therefore, based on our study, Daro gudo and Arba rakate was the most discriminating environment, but least representatives (Figure 2A). Based on representative nature, Mechara were representative (smaller

angels with AEA) environments, but least discriminating environments. Discriminating, but not-representative environments (Daro gudo and Arba rakate) are useful for selecting specifically adapted genotypes if the target environment can be divided into mega-environment [13, 48]. Numerous authors [18, 33, 43, 45] to determine representative and discriminating test settings for genotypes of various crops employed GGE biplot.

3.5.4. Evaluation of Environments Relative to the Ideal Environments

An ideal environment is one which highly discriminating

the tested varieties and at the same time be representative of the target locations [46] and desirable environments are close to the ideal environment. Accordingly, nearest to the first concentric circle, the environment Daro gudo was the ideal environment to select widely adapted food barley genotypes, whereas, Mechara was far from the ideal environment and considered as unstable and it is, therefore, not a representative environment for the other three environments included in this study. The order of the test environments is Daro Gudo>Arba rakate>Mechara (Figure 2B).

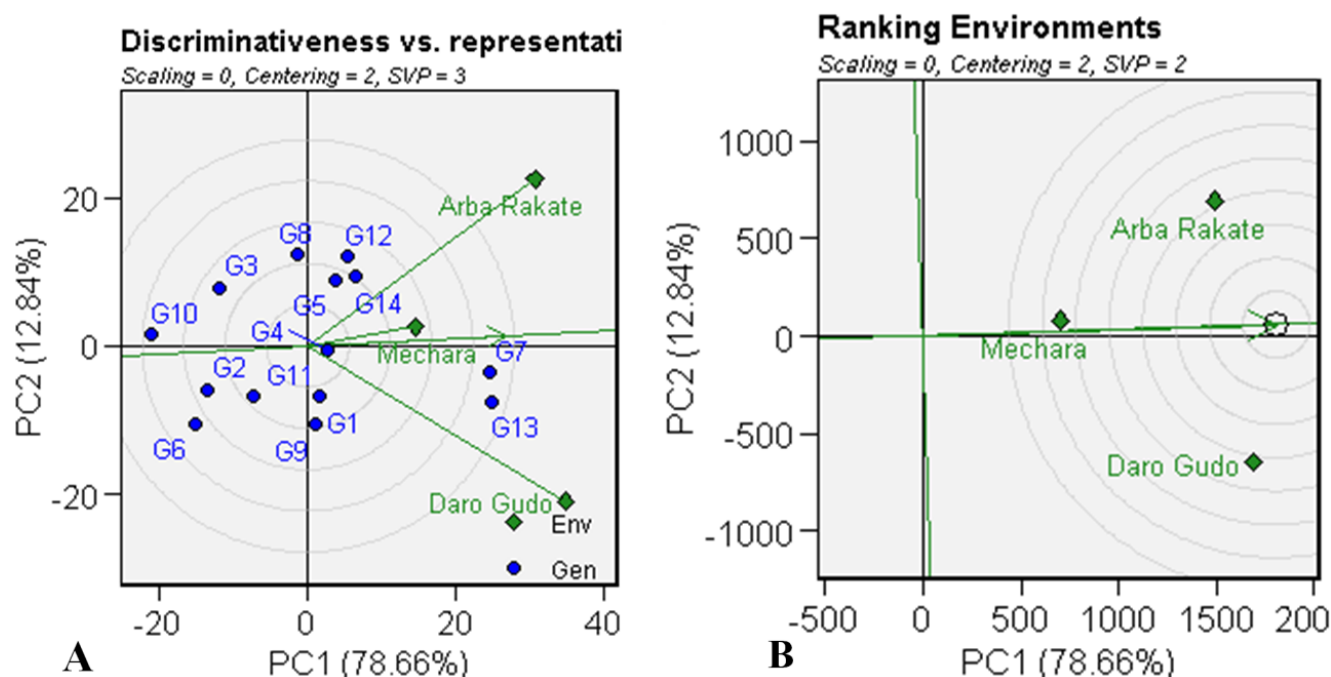


Figure 2. (A) GGE biplot showing rank of test locations based on discriminating ability and representativeness, (B) Ranking of the Test Environments.

3.5.5. Comparison of Genotypes Relative to the Ideal of Genotypes

The AEC approach was used in the GGE biplot methodology to estimate genotype yield and stability [49]. According to [21], the optimal genotype has the highest mean grain yield and is stable in all situations. The genotypes that are closest to the ideal genotype are considered desirable. The biplot's first concentric circle is home to the ideal genotype, which is utilized as a benchmark for selection. Consequently, G7, G13, and G14 are the genotypes that are closest to the optimal genotype. Compared to other genotypes, they are the most desired ones. According to [21, 33, 45], this finding is consistent. The AEC approach was used to determine the genotypes G10, G6, and G2 were the most unstable genotypes, which are regarded as undesirable due to their distance from

the ideal genotype (Figure 3A). The genotype that exhibits the highest yield and stability in various settings is considered the optimal genotype. According to [48], genotypes in the GGE biplot with high PC1 scores have high mean yields, while those with low PC2 scores have yields that are consistent across environments. The AEC is the line that goes through the biplot origin and is determined as the mean of the PC1 and PC2 scores for all environments [46]. According to [4], the AEC is shown as a single arrow pointing in the direction of high stability. Thus, to illustrate the difference between genotypes and the ideal genotype, concentric circles were created starting from the middle and pointed with an arrow [50]. Based on this, the genotypes G7, G13, and G4 are seen to be the most desirable, as they are the closest to the ideal genotype. Conversely, if a genotype is extremely far from the first concentric circle, namely, G10, G2, and G6, are considered unfavorable (Figure 3A).

3.5.6. Relationship Among Test Environments

Figure 3B is the environmental-vector view of the GGE biplot, which is based on the environment-centered (centering = 2) GE without any scaling (scaling = 0), and it is environment-metric-preserving (SPV = 2) [50]. This biplot explained 91.5% of the total variation of the environment-centered genotype by environmental interaction. Based on this biplot, Arba Rakate and Mechara were positively correlated (an acute angle), while Daro Gudo and Arba Rakate were slightly negatively correlated (an obtuse angle) Figure 3B. The larger

obtuse angle between Daro Gudo and Arba Rakate might be an indication of strong crossover, implying that the GEI is moderately large. The distance between two test environments measures their dissimilarity in discriminating the variety; hence, the test environments clearly fall into two groups, in which Arba Rakate and Mechara form the first group and Daro Gudo form the second group alone. Positively associated environments (Arba Rakate and Mechara) implied that the same information could be generated about the variety, hence the potential to reduce testing costs by dropping one of the two [50].

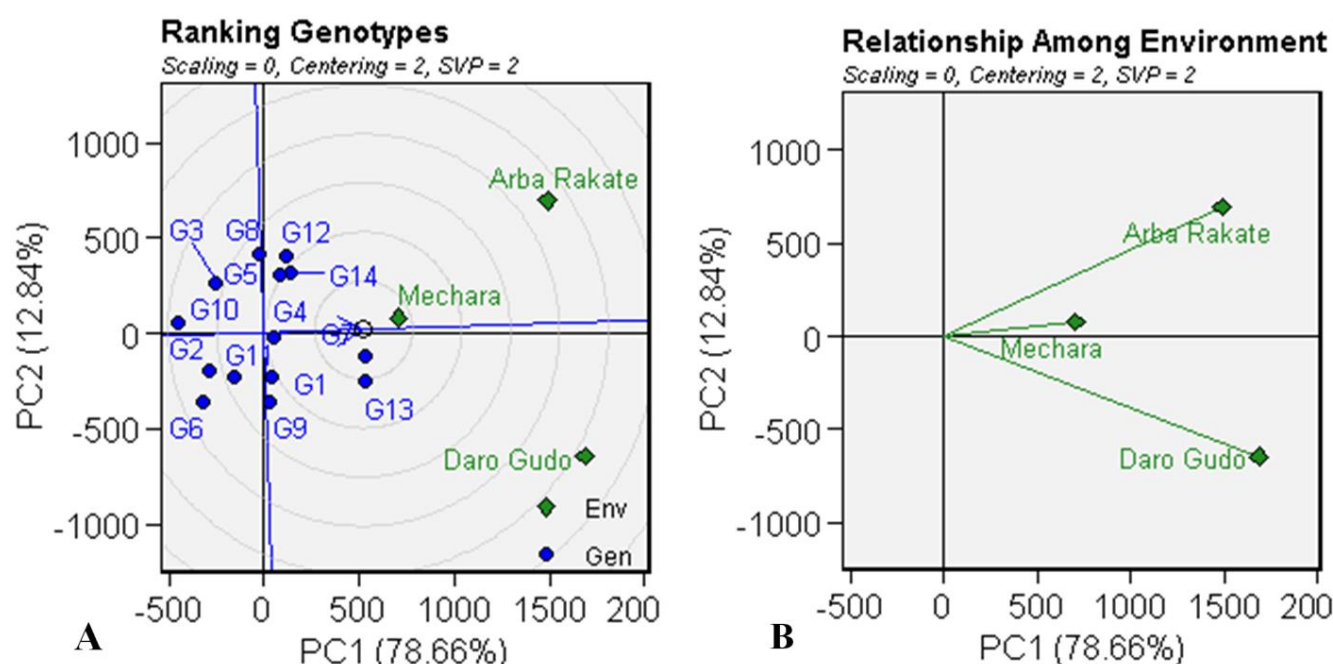


Figure 3. (A) Comparison of genotypes relative to the ideal genotype, (B) Biplots of the correlation between environments.

4. Conclusions and Recommendations

A broad range of variation exists between genotype, environment, and GEI, as demonstrated by the combined analysis of variance, which revealed that genotype, environment, and GEI are highly significant among the genotypes for all traits. The E and G main effects accounted for 58.7% and 6.5% of the treatment sum of squares, respectively. According to the AMMI analysis of variance, 12.1% of the treatment sum of squares was explained by the GEI. The more variance attributed to the environments is a sign of environmental diversity. Two IPCAs were sufficient to cross-validate the GEI-explained variance in grain yield because they accounted for 91.5% of the interaction sum of squares. The genotypes G13, G7, and G14 were shown to be stable and high yielding in all conditions using the AMMI and GGE biplot techniques. In addition, the genotypes G13, G7, and G14 were shown to have high yielding and stable

performance in a variety of environments, and they can be suggested for use in a variety of settings based on the genotype selection index and AMMI stability value. When compared to other genotypes, G7, which ranked highest among the genotypes in the GGE biplot analysis and was positioned in the center of the concentric circles, was the optimal genotype in terms of stability and high yield performance when compared to the other genotypes. G13 and G14 genotypes are also regarded as attractive genotypes. The best genotype in this study for high yielding capacity was genotype G7, which was located in the first concentric circle. This genotype can be utilized as a benchmark for assessing the development of barley varieties in future breeding programs. Genotypes, such as G10, G6, G3, G11 and G17 were found to have the least stable performance and should only be suggested for particular situations due to their high YSI and ASV values. The current study offers important information on the genotypes of barley yield stability and the ideal environments for upcoming improvement programs in west hararghe zone. The genotypes G13, G7,

and G4 were generally found to be stable and high yielding, making G13 and G7 ideal for possible release, while G14 was found to be suitable for cultivation in a wider range of environments based on GGE biplot and AMMI analysis.

Abbreviations

AEC	Average Environment Coordinate
AMMI	Additive Main Effect and Multiplicative Interaction
ANOVA	Analysis of Variance
ASV	Ammi Stability Value
E	Environment
G	Genotype
GEI	Genotype by Environment Interaction
GSI	Genotype Selection INDEX
GY	Grain Yield
IPCA	Interaction Principal Component Analysis
MET	Multi Environment Trials
RASV	Rank of Ammi Stability Value
RGY	Rank of Grain Yield
SSIPCA	Sum of Square Interaction Principal Component Analysis

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Author Contributions

Gabisa Bekela: Conceptualization, Data curation, Formal Analysis, Funding acquisition, Investigation, Methodology, Project administration, Resources, Software, Supervision, Validation, Visualization, Writing – original draft, Writing – review & editing

Abubeker Terbush: Conceptualization, Data curation, Formal Analysis, Funding acquisition, Investigation, Methodology, Project administration, Resources, Software, Supervision, Writing – review & editing

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Data Availability Statement

The data used to support the findings of this study are included within the article.

Conflicts of Interest

The authors declare no conflicts of interest.

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Biography



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Desu Assegid: Crop breeding and genetics, Sorghum, Maize, Wheat, Barley, Tef, Rice, Finger millet