

EVOLUTION BARLEY GENOTYPES IN MULTI-ENVIRONMENT TRIALS BY AMMI MODEL AND GGE BIPLLOT ANALYSIS

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ABSTRACT

The uniformity of genotypes are significant for crop breeding program decisions to improve new varieties. The AMMI (Additive main effects and multiplicative interaction) analysis and Genotype x Environment Interaction (GEI) is make to estimation grain yield and understands GxE interaction patterns by researches as differential ranking of variety yields in multi-environment trials. Therefore, fifteen barley advanced line and six national cultivars and four foreign varieties (registered in abroad) were used in the study. The experiments were performed according to a complete randomized block design with four replications at five environments during two years. The stability and superiority of genotypes for yield and other traits were determined using AMMI and GGE biplot analysis. Factors (G, GE, and GEI) were found to be highly significant ($P < 0.01$) for grain yield. AMMI analysis indicated that the major contributions to treatment sum of squares were environments (98.52%), GE (0.45%) and genotypes (1.02%), respectively, suggesting that grain yield of genotypes were effected environmental conditions. The GGE biplot indicated that PCA 1 axes (Principal component) was significant as $P < 0.01$ and supplied to 49.36% of complete GxE interaction. The AMMI indicated that G8 and G23 desirable and stabile genotypes for grain yield in multi-environment. Moreover, E2 and E5 (irrigated environments) were high yielding, while E3 (drought stress) low yielding as forecast. On the other hand, GGE biplot indicated that three group were occurred among traits, first group (GY: grain yield, CC: crude cellulose, CD: cold damage), second group (PC: , HW: hectoliter weight, TGW: thousand grain weight, SH: seed humidity), third group (LOD: lodging, PH: plant height, HT: heading time). Moreover: the study showed that G3, G6, G7, G8, G13 and G21 were the best genotypes both grain yield and other traits. The results of AMMI model and GGE biplot indicated that G8 is suitable to recommend for release and G23 desirable origin for yield stability and G7 valuable source for quality to use in barley breeding program.

KEYWORDS:

Barley, GEI, AMMI, GGE biplot, Grain yield, Stability

INTRODUCTION

Turkey is important for barley grain, because it ranks 6th barley production in the world. In fact, Turkey has more barley production potential, but there are more limiting factors. Some of these limiting factors are lack of varieties with high yield potential and agronomic practices, fluctuations in product prices policy and etc. On the other hand, the environment conditions is changing from region to region and year by year. Therefore, it is an essential to improve modern varieties, which is stable and favorable under environmental and other factors. Barley has been cultivated for many years and has a wide range of adaptation, growing best on fertile, well-drained soils in Shout –Eastern Anatolia of Turkey. It is also grown mainly on rainfall conditions, but genotype x environment interaction (GEI) restricts the progress in yield improvement under rain fed and unpredictable climatic conditions [1]. Modern barley breeding is largely directed towards the development of genotypes characterized with increased yield potential, wide adaptation and high responses to agronomic inputs [2]. Some agronomic and technological traits such as lodging (LOG), plant height (PH), thousand kernel weight (TKW), hectoliter mass (HM) and grain protein content (GPC) have significant influence on barley grain yield and quality. The yield and other traits of each variety in any environment is a sum of environment (E) main effect, genotype (G) main effect and genotype by environment interaction (GE or GEI) [3]. Farmers need varieties that show high performance in terms of yield and other essential agronomic traits. Their superiority should be reliable over a wide range of environmental conditions and years. Different statistical analysis, such as correlation, path coefficient and principal component analysis (PCA) can be used to reveal associations between yield and other agronomic traits. The impact of AMMI and GGE Biplot methods has been clearly showed by different researchers using

multi-environment. These methods; provide the correlative size and significant effects of GEI and its interaction [4], This method enables better understanding of genotypes performance over several environments, and selection of stable and high yielding genotypes [5], Also it is important for testing promising lines under across environments to estimate stability and performance [6], and thus, it is useful for breeders and supporting breeding program decisions. The major objective of study reveal adaptation of barley genotypes using AMMI and GGE Biplot analysis to estimate the importance of GE interaction on yield, define the correlations

among traits and estimate performance of genotypes and recommend lines to release in breeding program.

MATERIALS AND METHODS

Plant genetic materials. The experimental material comprising sixteen lines, five regional and four international spring barley varieties (Table 1) were evaluated in seven rain-fed environments in different growing season (Table 2).

TABLE 1
The information's about genotypes, used in experiment.

Genotype	Pedigree of genotypes
G1	Hml02/ArabiAbiad//ER/Apm/3/Belford..TR-0AP-5AP-0AP-4AP-8AP-0AP
G2	Lignee527/Chn-01//Lignee527/As45ICB93-0813-0AP-5AP-0AP
G3	Hma-02//11012- 2/CM67/3/Arar/PI386540...ICB93-0247-0AP-9AP-0AP
G4	Beecher (foreign registered varieties)
G5	ŞAHİN-91(regional check)
G6	Assala-04(foreign registered varieties)
G7	SLB15-05/4/H.spont.96-3/3/Roho//Alger/Cere...-1ICB93-0700-0AP-10AP-0AP
G8	WI2291(foreign registered varieties)
G9	Alanda/4/Arar/3/Mari/Aths*2//M-Att-73-337-1ICB94-0512-14AP-0AP
G10	SUR-93(regional check)
G11	F2cc33ms/Ci07555//AlandaICB93-0436-0AP-2AP-0AP
G12	Rhn/Lignee527/3/Hma-02//11012-2/CM67ICB93-0251-0AP-10AP-0AP
G13	Hm02//110122/CM67.Sask.1800//Pro/CM67/3/D170/.. ICB94-0564-40AP-0AP
G14	National check(unblieved)
G15	TOKAK-157(national check)
G16	Arar/PI386540//Giza121/Pue/3/Lignee527//Chn-01ICB93-0394-0AP-3AP-0AP
G17	Arta/4/Arta/3/Hml-02//Esp/1808-4LICB96-0601-0AP-10AP-0AP
G18	Erdorado/4/ROD586/Nopal's'/3/PmB/Aths//BcICB93-0932-0AP-1AP-0AP
G19	Hml-02//WI2291/BgsICB83-1554-1AP-1AP-6AP-0AP-6AP-0AP
G20	VAMIK HOCA (national check)
G21	Hml-02//WI2291/BgsICB83-1554-1AP-1AP-6AP-0AP-22AP-0AP
G22	805145/Hma01/6/805132/4/Bera's'/Cel//Oksamu...ICB93-0209-0AP-5AP-0AP
G23	Moroc9-75(foreign registered varieties)
G24	Moroc9-75/WI2291/WI2269ICB93-1132-0AP-32AP-0AP
G25	AKHISAR (national check)

TABLE 2
Years, sites, codes, coordinate status of environment long term of precipitation.

Years	Sites	Code of sites	Altitude (m)	Latitude	Longitude	Annual rainfall (mm)
2004/2005	Diyarbakir	E1	500	36° 97' N	38°42' E	680.6
	Diyarbakir (Irrigated)	E2	501	36° 97' N	38°42' E	680.6
	Ceylanpinar (Drought stress)	E3	363	36° 51' N	40° 20' E	260.3
2005/2006	Diyarbakir	E4	496	36° 97' N	38°42' E	356.7
	Diyarbakir (Irrigated)	E5	497	36° 97' N	38°42' E	356.7

The experiment was conducted in a randomized block design with four replications at five environments (rainfall and irrigated) during 2004-05-2005-06 growing seasons. Totally, nearly 150 mm supported in per irrigated environments. The seeding rate was used 450 seeds m⁻². Plot size was 7.2 m² (1.2 × 6 m) consisting of 6 rows spaced 20 cm apart. Sowing was done by Wintersteiger drill. The fertilization rates for all plots were used 60 kg N ha⁻¹ and 60 kg P ha⁻¹ with sowing time and 60 kg N ha⁻¹ was applied to plots at the early stem elongation. Harvest was done using Hege 140 harvester up on 6 m².

Statistical analysis. The data grain yields of twelve (25) genotypes in five (7) environments were evaluated by AMMI analysis [7]. The AMMI and GGE biplots were used to identify the mega-environments and superior genotypes for grain yield

and other traits. All statistical analyses were performed using GenStat Release 14.1 (Copyright 2011, VSN International Ltd.) and GGE biplot software programs.

The data were graphically analyzed for interpreting GE interaction using the GGE biplot software [8]. GGE biplot methodology is composed of the biplot concept [9] and GGE concept [28]. The graphs generated based on (1) The AMMI 1 model showing Genotype × Environment means, (2) The relationship genotype by five environments (3) Mega environments “which-won-where” pattern to identify the best genotypes in each environment, (4) The relationship genotype by trait, (5) “which-won-where” pattern to identify the best genotypes for traits, (6) Ranking genotypes based on traits by mean and stability, (7) Comparison of genotypes based on traits by ideal genotype.

TABLE 3
The variance of AMMI analysis on grain yield of barley

Source of Variance	DF	Sum of square	Mean of squares	F Ratio	Explained (%)
Total	499	1672811221	3352329	*	
Treatments	124	1376927067	11104251	16.24	
Genotypes	24	73256998	3052375**	4.46	1.02
Environments	4	1174240077	293560019**	88.57	98.52
Block	15	49717401	3314493	4.85	
G × E	96	129429992	1348229**	1.97	0.45
Interaction PCA 1	27	78322324	2900827**	4.24	74.32
Interaction PCA 2	25	25054927	1002197	1.47	25.67
Residuals	44	26052741	592108	0.87	
Error	231	75323191	326074	*	
Total	253	598192454	1785649		

df, degrees of freedom; **, p<0.01; G, Genotypes; E, Environments.

TABLE 4
The average yield performance at each E and over environments (kg ha⁻¹)

Genotype	E1	E2	E3	E4	E5	Mean	IPCAG[1]	IPCAG[2]						
1	6400	ab	5981	Cg	1775	hl	6823	ab	6465	cg	5489	CH	1.231.897	-310.231
2	6165	ac	5977	dg	1725	il	6575	ae	6548	cg	5398	DI	1.229.528	-0.76983
3	6088	ac	7098	ac	2367	fg	5585	eh	6056	dh	5439	CI	-391.917	-758.455
4	5615	bc	6319	bg	1527	kl	6113	ag	5535	gh	5022	HK	656.333	-440.678
5	5185	bc	5906	eg	3479	ac	4846	hi	5550	gh	4993	HK	-2.380.875	1.533.825
6	5252	c	5996	cg	2031	gk	5454	fh	5596	fh	4866	JK	-274.420	420.782
7	6229	ac	7054	ad	2821	df	6525	ae	6967	ad	5919	AC	262.132	492.335
8	6785	a	6833	ae	3609	ab	6598	ae	7746	ab	6314	A	-251.015	976.883
9	6731	a	6754	af	2406	eg	6265	af	6925	ad	5816	AD	397.570	-651.351
10	6563	ab	5940	dg	3271	bd	5200	g ₁	5931	dh	5381	DI	-1.977.766	-344.622
11	6010	ac	6127	bg	1952	gl	7083	a	7275	ac	5690	CF	1.820.928	982.833
12	6363	ab	5698	Fg	1988	gl	5633	dh	5167	hi	4970	IK	-657.766	-1.309.028
13	5679	ab	6894	ae	2802	df	6385	af	6515	cg	5655	CG	0.18586	1.048.035
14	5758	ac	6373	bg	2163	gj	5931	bg	6696	Bf	5382	DI	520.771	472.686
15	6035	ac	5410	G	3867	a	4223	i	4181	i	4743	K	-4.357.536	-287.450
16	5260	c	5844	eg	2133	gj	6625	ad	6013	dh	5175	GK	652.828	1.437.251
17	6050	ac	6783	ag	2365	fg	6671	ac	6450	cg	5664	CG	581.509	257.437
18	5750	ac	6065	bg	2944	ce	6077	ag	6377	cg	5442	CI	-521.753	1.248.210
19	6363	ac	6488	ag	2256	fi	5473	fh	5611	eh	5238	FK	-734.648	-1.287.381
20	6050	ac	6288	bg	2377	eg	6867	ab	6819	ad	5680	CG	896.063	842.250
21	6210	ac	6775	af	3013	cd	6696	ac	6150	dh	5769	BE	-379.071	440.821
22	6796	a	6660	af	1613	jl	5590	eh	5892	dh	5310	DJ	178.579	-2.386.681
23	6333	ab	7581	A	2339	fh	6923	ab	7915	a	6221	AB	1.691.729	412.588
24	6631	ab	5906	eg	1773	hl	5773	ch	6235	cg	5264	EJ	316.581	-1.308.733
25	6400	ab	7160	ab	1421	i	6200	ag	6721	be	5580	CG	1.471.733	-1.404.343
Mean	6108	A	6396	A	2401	B	6085	A	6293	A				
CV (%)	12.0		12.3		16/8		11.8		12.6					
LSD	104ns		111.0*		56/8		102.0**		112.3**					

** , p<0.01; * , p<0.1

RESULTS AND ANALYSIS

The results of AMMI Analyses in grain yield: The variance of AMMI analysis showed that as $p < 0.01$, all factors had significant effect on barley grain yield of twenty five genotypes tested in five environments and total sum of squares explained 98.52% for environmental effects, 1.02% for genotypic effects and only 0.45% GEI effects (Table 3). The high addition of environment effects showed that there were important differences among environments for grain yield. On the other hand, the genotype effect were high than GEI effect. The results of AMMI analysis showed similar results of [14], [15], [16], showed 89.6%, 8.6% and 1.8%. Moreover, [17] and [18], reported that the environment effect had the highest effect than other factors on barley and soybean grain yield respectively. The results of Environment, Genotype and G x E effects obtained from this study illustrated similar results of the studies described above and the effect of environment > genotypes > GEI. The existence interaction of grain yield displayed by GGE biplot, especially when the interaction portioned between two interaction principal component axis

(PCA) (Table 3). This status of GGE biplot made it establish and the biplot calculate effects of genotype and environment. The results of mean square of the interaction axis PCA 1 was significant ($p < 0.01$), while PCA 2 was not significant ([2], [1]). Results of GGE biplot analysis also indicated that the PCA 1 axis accounted 74.32%, PCA2 accounted for 24.68% (Figure 2). GGE biplot showed existence interactions of G x E, so it was portioned between first and second IPCA (Interaction Principal Component Axes).

The barley grain yield variation is depending on genotypic and environment factors as shown Table 1 & Table 2. [6], [17], suggested that the AMMI model is the most accurate a model because it can predict using the first two IPCAs. The closer the IPCAs scores to zero meaning that genotypes are the most stable across their environments. Actually, these biplots is removed two types, model of AMMI 1 and model of GGE biplot [19], [20]. In AMMI 1, the genotype and environments means are plotted on coordinate, the IPCA scores of same genotypes and environments, which are on the ordinate.

TABLE 5
AMMI selections the first four genotypes for per environment and PCA scores.

Sites	Mean (kg/ha ⁻¹)	Score	1	2	3	4	PCA [1]	PCA [2]	Variance
E1	6108	-10.37	G22	G22	G9	G8	-1.036.521	-3.787.832	658088
E2	6396	3.39	G23	G23	G8	G9	339.099	-1.273.168	773853
E3	2401	-51.14	G15	G15	G8	G5	-5.114.178	2.267.291	1592343
E4	6085	30.02	G23	G23	G8	G11	3.001.789	1.307.939	896464
E5	6293	28.10	G23	G23	G8	G11	2.809.811	1.485.770	1115334

TABLE 6
The traits value of average for twelve genotypes.

Genotypes	Heading time (date)	Plant Height (cm)	Thousand grain weigh (g)	Hectoliter Weight (g/l)	Protein content (%)	Crude Cellulose (%)	Seed Humidity (%)	Lod-ging (%)	Cold damage (Scor.19)
1	109	95	37.7	62.5	11.2	4.3	10.7	40	3
2	109	101	36.8	61.8	12.3	4.9	10.5	50	5
3	108	94	40.8	65.8	12.9	5.4	10.8	0	5
4	106	101	40.8	61.6	12.4	4.6	10.6	15	4
5	115	109	43.8	65.2	12.4	4.2	11.0	25	2
6	108	89	41.3	64.9	13.2	6.0	10.6	0	6
7	107	95	44.7	66.2	13.0	5.3	10.8	0	4
8	108	94	39.2	64.3	13.1	5.0	11.0	5	6
9	108	85	37.0	58.7	12.2	4.4	10.5	30	3
10	119	110	40.8	64.6	12.4	5.1	10.8	55	3
11	112	99	38.6	62.3	11.3	4.7	11.0	13	4
12	108	103	39.2	61.4	11.5	4.5	10.8	53	3
13	108	95	42.3	66.6	12.8	5.1	10.7	5	4
14	108	100	36.9	60.7	12.4	4.2	10.5	15	3
15	115	100	42.2	64.4	12.7	4.9	10.7	75	1
16	112	89	33.8	61.0	11.7	5.6	10.7	85	4
17	113	96	35.6	60.3	11.7	5.2	10.8	40	5
18	113	96	37.8	64.7	12.6	5.0	10.7	15	5
19	115	100	39.9	64.3	12.5	4.2	10.9	55	4
20	112	104	38.2	62.9	12.2	4.7	10.8	15	5
21	106	90	42.4	65.3	12.5	5.5	10.8	5	5
22	114	90	38.5	61.6	11.2	4.7	10.5	30	5
23	114	86	41.4	63.0	11.9	4.5	10.6	0	5
24	111	94	38.1	63.9	12.7	4.6	11.1	50	4
25	113	100	43.3	61.9	11.8	4.7	10.7	38	3
Mean	111	96	39.7	63.2	12.3	4.9	10.7	28.5	3.9

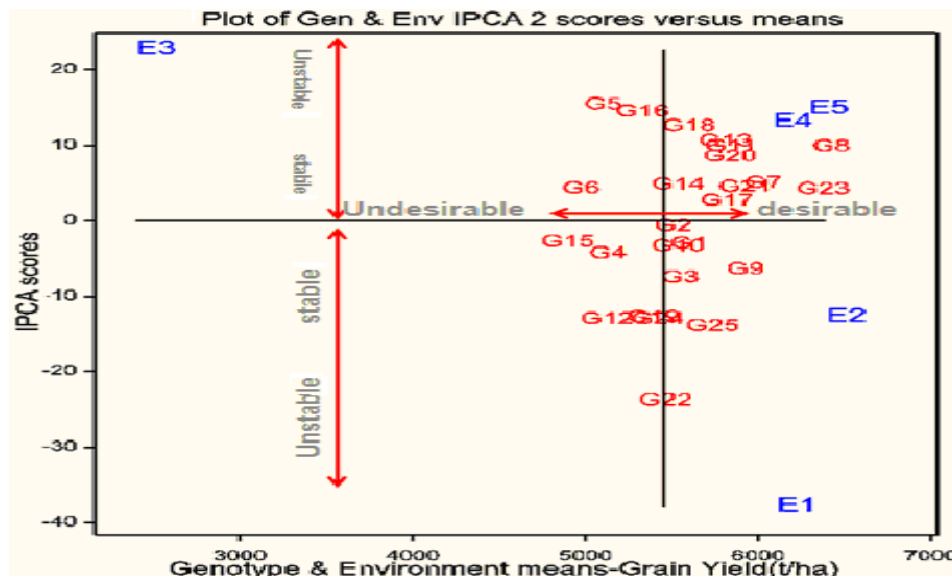


FIGURE 1

The AMMI 1 model showing grain yield (kg/ha⁻¹) of genotypes(G) in 5 environments(E).

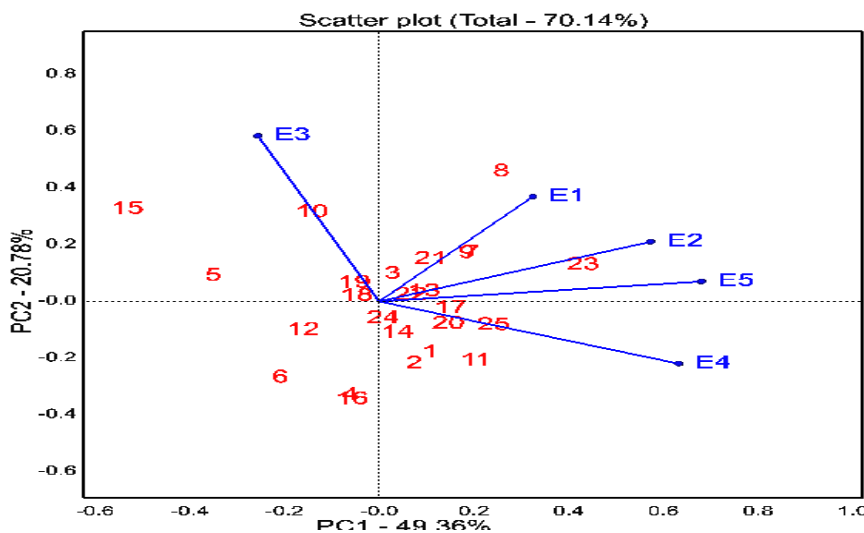


FIGURE 2

The relationship genotype by environments

For interpretation of AMMI, size and signal scores of the IPCA1 were observed, score near to zero were typical of genotypes and environments, which contribute little to the interaction that is they are stable [21].

The AMMI model showing Genotype x Environment means of grain yield. In the AMMI model, x-axis represents the genotypes and environment main effect and y axis represents the effects of interaction (Figure 1).

The environment and genotypes indicated much more variability in both main effect and interaction. According to AMMI, majority of genotypes (G2, G3, G7, G8, G9, G11, G13, G17, G18, G20, G23 and G25) and majority environments (without E3) showed good performance, because of they took place above on axis (mean yield). It is believed that these genotypes and environments were high

yielding and desirable. On the other hand, G4, G5, G6, G12, G10, G15, G16 and E3 demonstrated low performance, because they located under axis (mean yield). So, these cultivars and environments, which located under axis (mean yield) were low yielding and undesirable. Additionally, E4 and E5 had both high yield potential and positive IPCA1 scores; it means that this two environment are desirable. While G8 and G23 had highest grain yield amongst genotypes, G17 was very stable with low and positive IPCA scores (Table 5).

According to [5], the genotypes have small IPCA1 values are more stable, [22] the basic static concept of stability shows minimal variance of stable genotype across different environments. Therefore, G17 can be recommended to all environments, while G8 and G23 for high yield potential environments (special environment). Similar outputs were recorded by [23], in barley.

The relationship genotype by five environments. The GGE biplot analysis was used for estimation of discriminating power and representativeness of an environment as a test one for assessing genotypes. GGE biplot allows visualizing environment vectors lengths, which are proportional to standard deviations of genotype yields in corresponding environment (Fig. 2).

If the marker of a test environment is close to the biplot centre, i.e. has a short vector, all genotypes in it are similar, and this environment is not informative about their differentiation. In the study, all environments had nearly same long vectors, so they had same discriminating power and characterized by same discriminating power. The cosine of the angle between environment vectors is used for assessment of approximation between them: the smaller the angle between environment vectors is the larger correlation between them [21]. Correspondingly, there is a strong correlation between environments E1, E2, E4 and E5, while there is no correlation between E3 and other environments.

Mega environments “which-won-where” pattern to identify the best genotypes in each environment. Dividing the target environment into meaningful mega-environments and deploying different cultivars for different mega-environments is the only way to utilize positive GE and avoid negative GE and the sole purpose for genotype by environment interaction analysis [11]. A mega-environment is defined as a group of environments that consistently share the same best cultivar(s) [18]. This definition explain the following biplot based on the multi-environment trials (MET) data of barley yield illustrates two points: 1) A mega-environment may have more than one winning genotypes (Sector 2), and 2) even if there exists a universal winner (G23, G8, G15), it is still possible, and beneficial, to divide the target environments into meaningful mega-environments (Figure3).

Mainly, these six lines divide the biplot into six sectors. The environments located only three sectors; other sector did not related with any environment just covered special genotypes. On the other hand, E2, E4, E5, took places in the same sector consist of G11, G17, G23, G25 and G23 was high yielding and represented of vertex these three environments. The second sector consists of E1 with G3, G8, G21 and G21 took places of vertex of this sector. The third sector consists of E3 with G5, G10, G12, G15 and also G15 located the vertex of sector. Consequently, G23 had high yielding at three environments (E2, E4, E5), while G8 for E1 and G15 for E3 [24], reported that there is a strong correlations between environments, which located in same sector [25], the large variation due to location indicated strong influence of environments and existence of mega-environment among trial conducting locations, this suggests the usefulness of GGE biplot technique for identifying mega-environments among barley growing locations. Same [12], reported that the GGE biplot graphic analysis complements the AMMI biplot stratification, defining mega-environments and the cultivars that optimize performance in such mega-environments.

The GGE Biplot Analysis of genotypes by traits. In this analysis, the results of traits were examined by GGE Biplot analysis using different figures. The biplot of the principal component analysis illustrates relationships between the studied barley traits and genotypes at five environments (Figure 4- Figure 7). First PCA explained 27.53% of total variation, while second PCA explained 25.52%. Together, both axes accounted for 53.7% of the total variation in the data. According to the biplot figures, the relations between genotype and traits by traits were examined. The GGE Biplot showed that the breeders could select best genotypes for all traits and specific genotype for specific trait in breeding program.

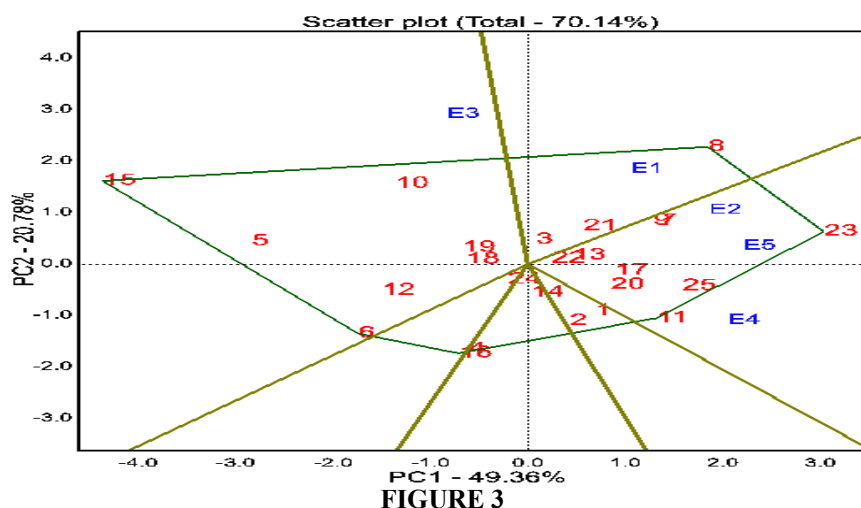


FIGURE 3 which genotype performed better in which environment for grain yield of barley

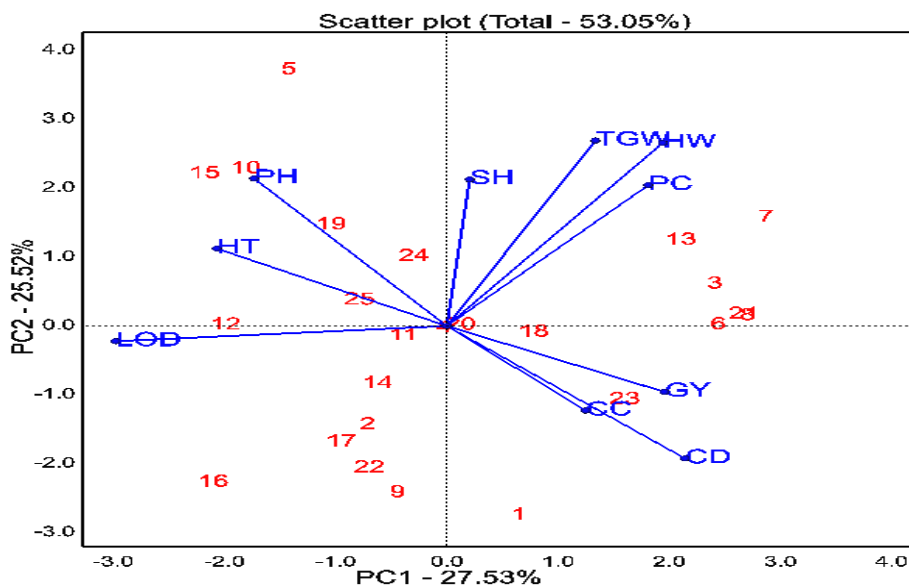


FIGURE 4

The relationship genotype by trait in five environments

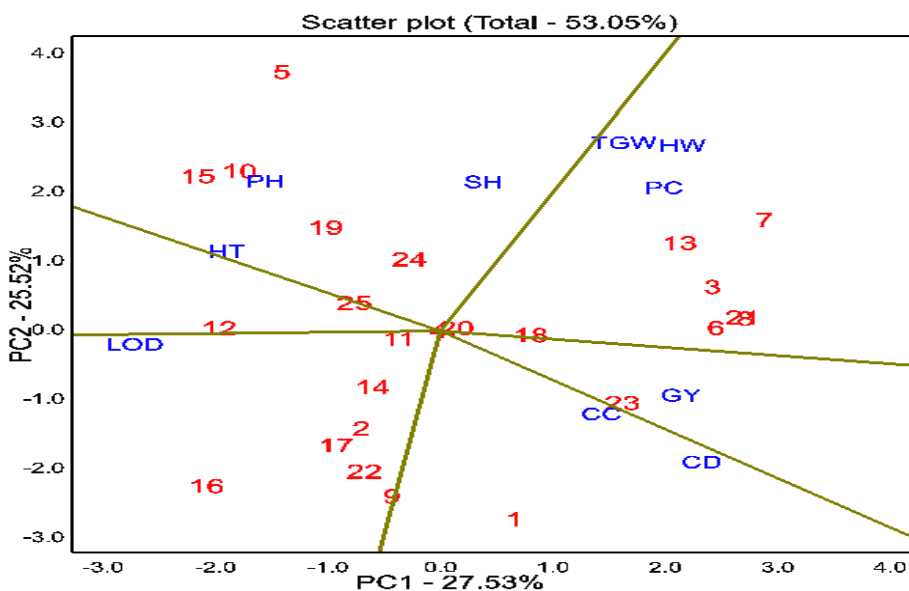


FIGURE 5

GGE biplot showing which-won-where of genotypes based on traits

The relationship each genotype by each trait. Both the genotype vectors and the traits vectors are drawn in Figure. 4, so that the specific interactions between a genotype and a trait (i.e., the performance of each genotype in each environment) can be visualized (Fig.4).

Figure 4, can be used (1) to rank the genotypes based on performance in any trait, and (2) to rank traits on the relative performance of any genotype. The interpretation of performance a genotype in a trait is better than average if the angle between its vector and the trait's vector is $<90^\circ$; it is poorer than average if the angle is $>90^\circ$; and it is near average if the angle is about 90° [8]. When the angle between two genotypes is $>90^\circ$, then this two genotype are different as genetic. Therefore, the results of traits showed that there is high variation

among genotypes. According to results, G3, G4, G6, G7, G13 and G21 are desirable for all traits, and so they can be recommended for release. On the other hands, some national cultivars (G5, G10, G15), G12 and G18 had been late maturity time, very tall and lodging scores, so these genotypes is not recommend for these environments. The cultivar which located near to the biplot center have less contribution to G or GE, while genotypes having longer vectors show the most contribution of G and/or GE [8]. So, G7 with the longest vectors is the best genotypes, while some other genotypes (G11, G18 and G20) have short vector. The genotypes are far from center of Biplot graphs, are specific genotypes for specific environment. There are negative correlation between two traits, are opposite to each other on graph and the angles of vector is

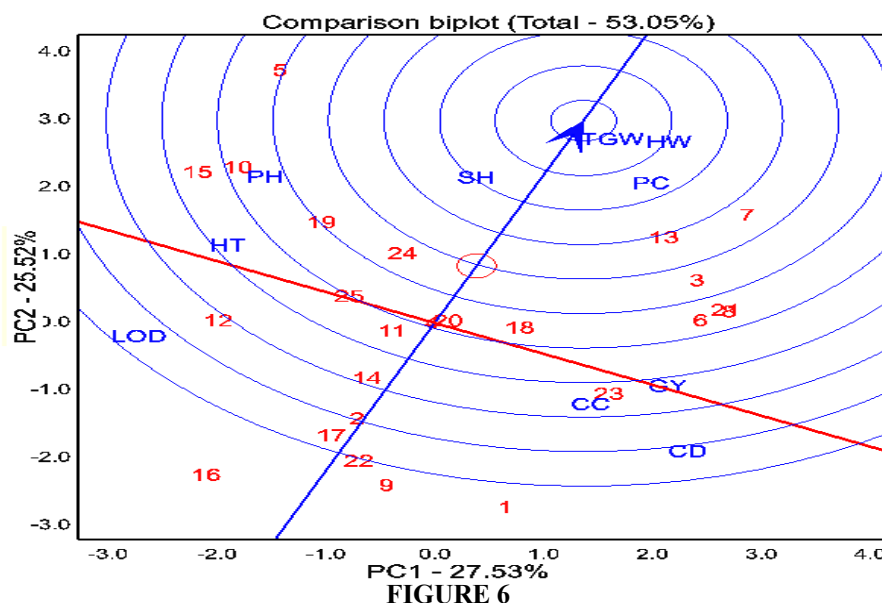
$>90^\circ$. Therefore, there is major contribution of trait to traits; because of they have opposite direction, so they can make up different genetic contribution [26], [5].

“which-won-where” pattern to identify the best genotypes for traits. The polygon view of a biplot is the best way to visualize the interaction patterns between genotypes and traits [27] to show the presence or absence of cross over GT interaction which is helpful in estimating the possible existence of different mega environments [28], [29]. Visualization of the “which won where” pattern of MET data is necessary for studying the possible existence of different more traits in the target traits [28].

Fig. 5, represents a polygon view of barley genotype MET data in this investigation. In this biplot, a polygon was formed by connecting the vertex genotypes with straight lines and the rest of the genotypes placed within the polygon. The partitioning of GT interaction divided into six sector. The traits (CC and CD) took place in sector 1 and related with G1; GY in sector 2 and related with G23; the three traits (HW, TGW and PC) in sector 3 and related with G3, G6, G7, G8, G13 and G21; SH and PH in sector 4 and related with G5, G10, G15, G19 and G24; HT in sector 5 and related with G12 and G25; LOD in sector 6 and related with more genotypes (G2, G9, G11, G14, G16, G17 and G22). On the other hand, there were correlation amongs sector 4 (PH), sector 5 (HT) and sector 6 (LOD), it means that the genotypes, have late heading time, are very tall and have lodging features as well as. The vertex genotypes in this study were G1, G7, G5 and G16. These genotypes were the best or the poorest genotypes in some or all of the traits, because they were farthest from the origin of the biplot [27]. From the polygon view of biplot analysis

of MET data, the genotypes fell in six sections and the traits fell in six sections. The first section contains G1 (resistance to cold damage), second section contains G23 (best yielding), third section contains 6 genotypes especially G7 (very quality), and other sections (4, 5 and 6) contains poor genotypes, which have tall plant height, late maturity and lodging and low yielding features. They were located far away from all of quality traits and GY, reflecting the fact that they yielded poorly. Also, those genotypes within the polygon (for example G5 and G16) were less responsive to quality and grain yield than the G23 and G7, have vertex genotypes [26], [10].

Comparison genotypes based on traits mean and instability. The genotype has both high traits mean and high stability is called a favorable genotype. It should have both high mean performance and high stability for all traits (Figure 5, Figure 6). The center of the concentric circles (ideal) is a point on the AEA (“absolutely stable”) in the positive direction and has a vector length equal to the longest vectors of the traits on the positive side of AEA (“highest mean performance”). Therefore, genotypes located closer to the stable line and has high mean values of traits are meaning that it is more favorable than others ([8]; [3]). Thus, any genotype was not located center of AEA (“absolutely stable”), but; G7, G13 and G24 took place of near center of AEA and high mean of traits. So these genotypes are favorable than others. According to Figure 6, the G20, G24 and G7 are high stable and moderate favorable, while G7 and G13 are moderate “stable” and more favorable, because these two genotypes have high mean value of traits. From this example, we can recommend G7 and G13 to study for more traits.



The relationship genotype by trait in seven environment

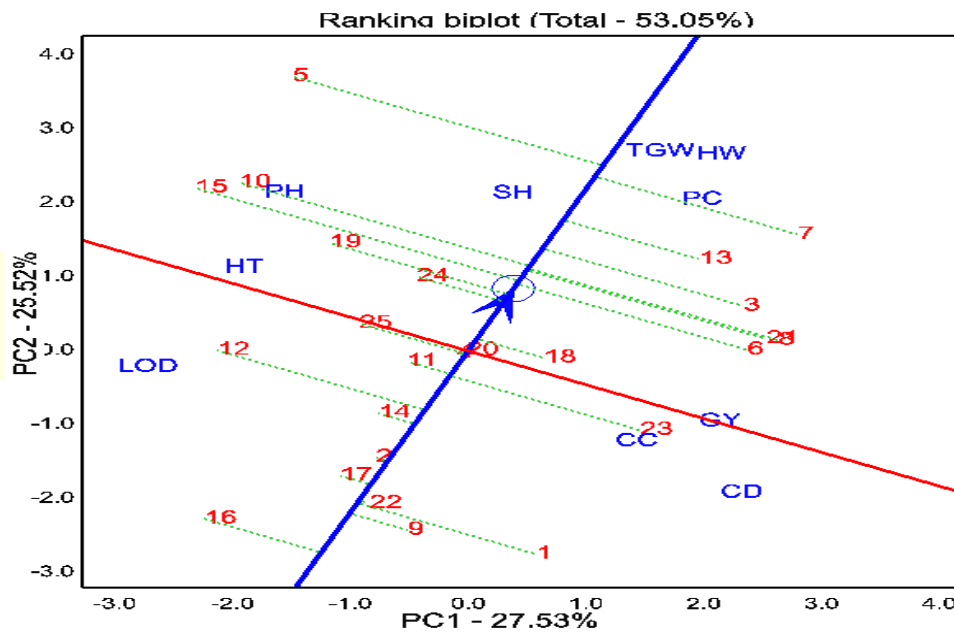


FIGURE 7

Ranking genotypes based on traits mean and instability

Ranking of genotypes based on traits. The genotype has both high traits mean and high stability is called an ideal genotype (Figure 7).

The center of the concentric circles is a point on the AEA (“absolutely ideal”) in the positive direction and has a vector length equal to the longest vectors of the traits on the positive side of AEA (“highest mean performance”). Therefore, genotypes located closer to the ideal circle are meaning that it is ideal genotype than others [8]. In the study, any genotype was not located center of AEA (“absolutely stable”), but; G5, G7, G3 and G13 took place of near center of AEA. So these genotypes are ideal than other genotypes. Consequently, G7 and G13 are close to ideal genotype, so, these genotypes can be recommended for release in terms of all traits. The researchers reported that the biplot show excellent discriminating to select genotypes for all traits and to recommendation for release [29].

CONCLUSION

The AMMI results indicated that yield performance of barley genotypes were highly influenced by environment followed G effect and GE interaction with the least effects. The genotype G8 and G23 showed best performance among genotypes tested across environments, while the oldest cultivar (Tokak) had least grain yield and adaptability. Therefore, the G8 was desirable in terms of high mean yield and stability; this means that the study provided an indication of the genetic progress. According to the results, the specific genotypes were appropriate for specific traits (G7 for quality, G8 for GY). The AMMI method and GGE biplot analysis allowed a meaningful and useful

summary of GE interaction data and assisted in examining the natural relationships and variations in genotype performance across test environments. As a result indicated that G8 and G23 are suitable to recommend for release and G7 valuable source for quality to use in barley breeding program.

ABBREVIATIONS

Abbreviations and Symbols. AMMI, Additive main effects and multiplicative interaction; AEA, average-environment axis; AEC, average-environment coordination; GE, genotype by environment interaction; GGE, G + GE; MET, multi-environment trials; PC, principal component; PCA, principal component analysis; E, environment; G, genotype; TGW, thousand grain yield; HW, hectoliter weight; PC, protein content; SA, sieving above; LS, lower sieving.

REFERENCES

- [1] Kilic, H. (2014) Additive main effect and multiplicative interactions (AMMI) Analysis of grain yield in barley genotypes across environments. *J Agr Sc.* 20, 337-344.
- [2] Przuli, N., Momeilović, V., Simić, J., Miroslavljević, M. (2014) Effect of growing season and variety on quality of spring two-rowed barley. *Genetika.* 46, 59-73.
- [3] Farshadfar, E., Rashidi, M., Jowkar, M.M., Zali, H. (2013) GGE Biplot analysis of genotype × environment interaction in chickpea genotypes. *Euro J Exp Bio.* 3(1), 417-423.

- [4] Asfaw, A., Alemayehu, F., Gurum, F., Atnaf, M. (2009) AMMI and SREG GGE biplot analysis for matching varieties onto soybean production environments in Ethiopia. *Scientific Research and Essay*. 4(11), 1322-1330.
- [5] Mirosavljevic, M.N., Przulj, D., Bocanski, B., Stanisavljevic, M. (2014) The application of AMMI model for barley cultivars evaluation in multi-year trials. *Genetika*. 46(2), 445-454.
- [6] Hagos, G.H. and Abay, F. (2013) AMMI and GGE Biplot analysis of bread wheat genotypes in the northern part of Ethiopia. *J Plant Breed and Genet*. 01, 12-18.
- [7] Gauch, H.G. (1988) Model selection and validation for yield trials with interaction. *Biometrics*. 44, 705-715.
- [8] Yan, W. and Tinker, N.A. (2006) AMMI Biplot analysis of multi-environment trial data; Principles and applications. *Can J Plant Science*. 86, 623-645.
- [9] Gabriel, K.R. (1971) The biplot graphic display of matrices with application to principal component analysis. *Biometrika*. 58, 453-467.
- [10] Mortazavian, S.M.M., Nikkha, H.R., Hassani, F.A., Sharif-al-Hosseini, M., Taheri, M., Mahlooji, M. (2014) GGE Biplot and AMMI Analysis of yield performance of barley genotypes across different environments in Iran. *J Agr Sci Tech*. 16, 609-622.
- [11] Kendal, E. and Dogan, Y. (2015) Stability of a Candidate and Cultivars (*Hordeum vulgare* L.) by GGE Biplot analysis of Multi-environment Yield Trials in Spring Barley. *Agriculture and Forestry*. 61(4), 307-318.
- [12] Kendal, E. and Sener, O. (2015) Examination of genotype \times environment interactions by GGE biplot analysis in spring durum wheat. *Indian J Genet Pl Br*. 75(3), 341-348.
- [13] Gauch, H.G. and Zobel, R.W. (1997) Identifying mega-environments and targeting genotypes. *Crop Sci*. 37, 311-326.
- [14] Mirosavljević, M.N., Pržulj, N., Čanak, P. (2014) Analysis of new experimental barley genotype performance for grain yield using AMMI Biplot. *Selekcija I Semearstvo*. 1, 38.
- [15] Mirosavljević, M.N., Pržulj, N., Čanak, P., Momčilović, V., Aćin, V., Jocković, B., Hristov, N., Mladenov, N. (2015) Relationship between Grain Yield and Agronomic Traits in Winter Barley. *Ratar Povrt*. 52(2), 74-79.
- [16] Rezene, Y. (2014) GGE and Ammi biplot analysis for field PEA yield stability in Snnpr state, Ethiopia. *International Journal of Sustainable Agricultural Research*. 1(1), 28-38.
- [17] Yan, W. and Holland, J.B. (2010) A heritability adjusted GGE biplot for test environment evaluation. *Euphytica*. 171(3), 355-369.
- [18] Yan, W. and Rajcanw, I. (2002) Biplot analysis of test sites and trait relations of soybean in Ontario. *Crop Science*. 42, 11-20.
- [19] Oral, E., Kendal, E., Dogan, Y. (2018) Selection the best barley genotypes to multi and special environments by AMMI and GGE biplot models. *Fresen. Environ. Bull*. 27, 5179-5187.
- [20] Jalata, Z. (2011) GGE-biplot Analysis of Multi-environment yield trials of barley (*Hordeum vulgare* L.) genotypes in Southeastern Ethiopia Highlands. *Int J Plant Breed Genet*. 5(1), 59-75.
- [21] Tarakanovas, P. and Ruzgas, V. (2006) Additive main effect and multiplicative interaction analysis of grain yield of wheat varieties in Lithuania. *Agr Research*. 4(1), 91-98.
- [22] Becker, H.C. and Leon, J. (1988) Stability analysis in plant breeding. *Plant Breed*. 101, 1-23.
- [23] Mohammadi, M., Karimizadeh, R., Noorinia, A.A., Ghojogh, H., Hosseinpour, T., Khalilzadeh, G.R., Mehraban, A., Roustaii, M., Hasanpor Hosni, M. (2013) Analysis of yield stability in multi-environment trials of barley (*Hordeum vulgare* L.) genotypes using AMMI model. *Curr Opin Agric*. 2(1), 20-24.
- [24] Solonechnyi, P., Vasko, N., Naumov, A., Solonechnaya, O., Vazhenina, O., Bondareva, O., Lovnivenko, Y. (2015) GGE biplot analysis of genotype by environment interaction of spring barley varieties. *Zemdirbyste-Agriculture*. 102 (4), 431-436.
- [25] Sarkar, B., Sharma, R.C., Verma, R.P.S., Sarkar, A., Sharma, I. (2014) Identifying superior feed barley genotypes using GGE biplot for diverse environments in India. *Indian J Genet*. 74(1), 26-33.
- [26] Karimizadeh, R., Mohammadi, M., Sabaghni, N., Mohamoodi, A.A., Roustami, B., Seyyedi, F., Akbari, F. (2013) GGE Biplot Analysis of Yield Stability in Multi-environment Trials of Lentil Genotypes under Rainfed Condition. *Not Sci Biol*. 5(2), 256-262.
- [27] Yan, W. and Kang, M.S. (2003) GGE Biplot Analysis: A graphical tool for breeders, geneticists, and agronomists. CRC Press. Boca Raton. 213p.
- [28] Yan, W.L., Hunt, A., Sheng, Q., Szlavnic, Z. (2000) Cultivar evaluation and mega-environment investigation based on the GGE biplot. *Crop Sci*. 40, 597-605.
- [29] Sayar, M.S. and Han, Y. (2015) Determination of forage yield performance of some promising Narbon Vetch (*Vicia narbonensis* L.) lines under rain-fed conditions in Southeastern Turkey. *Journal of Agricultural Sciences*. 20, 376-386.

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