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IDENTIFYING OF RELATIONSHIP BETWEEN TRAITS AND GRAIN YIELD IN SPRING BARLEY BY GGE BIPLOT ANALYSIS

SUMMARY

Grain yield is very important and complicated trait in spring barley breeding and rely upon combination varied plant traits (agronomic and quality). For this reason, a real barley breeding program necessaries an appropriate mentality of the relationships between grain yield and traits. The aim of study was evaluate the relationship of grain yield and other traits of 25 spring barley genotypes in one location during two years by GGE Biplot analysis. The experiments were performed according to a complete randomized block design with three replications. Factors (G, GE, and GEI) were found to be highly significant (P < 0.01) for grain yield. GGE Biplot indicated that three group were occurred among traits, first group (thousand grain weight, protein content, crude cellulose and cold damage), second group (hectoliter weight, lodging, plant height and heading time), third group (grain yield and seed humidity). Moreover, the study showed that negative correlation was found between grain yield and traits without seed humidity. The results of AMMI model and GGE Biplot indicated that G12, G13, G16 and G18 is proper for grain yield, G2, G6, G19 and G1 desirable origin for quality and other agronomic traits to select for advance stage and use in barley breeding program.

Keywords: Spring Barley; GGE biplot; Yield; Traits, Correlation

INTRODUCTION

The considerable variation in crop circumstances, because of climatic conditions and different soil constituents, cause large annual variations in yield performance of crops. This is mainly because of low heritability of yield as a typical quantitative trait. Thus, grain yield could be affected by not only genotype, but also by environment as well by and genotype × environment interaction (Mortavazian et al 2014).

Barley (*Hordeum vulgare* L.) is the second important cereal crop of Turkey and accounts for about 25% of the total cereal production (SAP 2010). In South-Eastern Anatolia, barley has been cultivated for many years and has a significant role. It is also grown mainly on rainfall conditions, but genotype × environment interaction (GEI) restricts the progress in yield improvement under

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rainfed and unpredictable climatic conditions. Thus, experimental research needs to be carried out over multiple environment trials in order to identify and analyse the major factors that are responsible for genotype adaptation and final selection (Kilic 2014).

The yield 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) (Farshadfar et al 2013). Farmers need varieties that show high performance in terms of yield and other essential agronomic traits.

Modern barley breeding is largely directed towards the development of genotypes characterized with increased yield potential, wide adaptation and high responses to agronomic inputs (Przuli et al 2014). 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.

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. This methods; provide the correlative size and significant effects of GEI and its interaction (Asfaw et al 2009), This method enables better understanding of genotypes performance over several environments, and selection of stable and high yielding genotypes (Mirosavlievic et al 2014), Also it is important for testing promising lines under across environments to estimate stability and performance (Hagos and Abay, 2013), and thus, it is useful for breeders and supporting breeding program decisions. The cultivars which are used in South-eastern Anatolia Region are different depending on sub- regions, as three main sub-regions have different conditions to cultivate barley cultivars. So it is very important to identify cultivars for specific sub-region (Kendal 2016).

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.

MATERIAL AND METHODS

The experimental material comprising twenty lines, three national and two regional varieties (Table 1) were evaluated in different growing season (Fig. 1).

The experiment was conducted in a randomized block design with four replications at two rainfall-growing seasons (during 2004-05-2005-06). The seeding rate was used 450 seeds m-2. Plot size was 7.2 m-2 (1.2 × 6 m) consisting of 6 rows spaced 20 cm apart. Sowing was done by winter stagier 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. The climate data of growing seasons showed in Fig. 1.
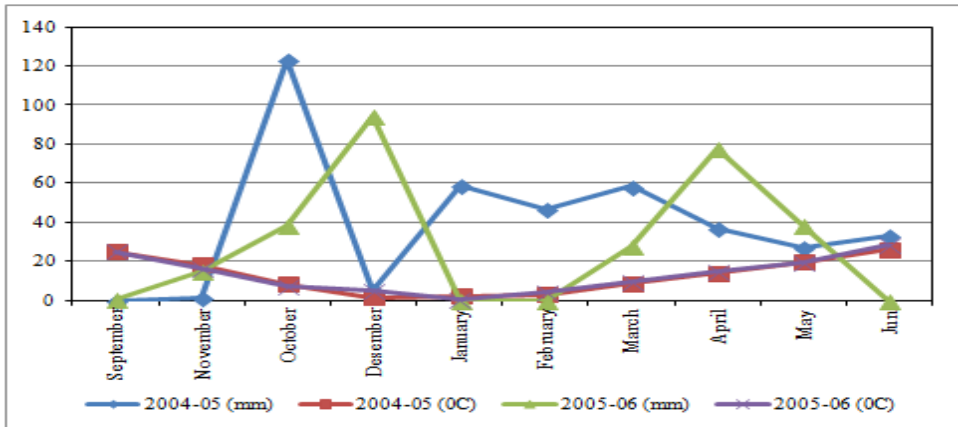
Fig.1. The average monthly rainfall(mm) and temperature(^{0}C).

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

Genotype	Cultivar and /Pedigree of Province line
G1	GOB/HUMAI10/3/MPYT169.1Y/LAUREL//… CBSS95M00804T-F-1M-2Y-3M-0Y
G2	GOB/HUMAI10/3/MPYT169.1Y/LAUREL//... CBSS95M00804T-F-1M-5Y-1M-0Y
G3	FRESA CMB94A.917-D-4M-1Y-2M-2Y-1M-0Y
G4	FRESA CMB94A.917-D-4M-1Y-2M-2Y-2M-0Y
G5	1.1.1.ŞAHİN-91
G6	CEN-B/2*CALI92//ROBUST/3/LIGNEE640/DS/… ICBSS95M00871T-A-4M-1Y-1M-0Y
G7	GOB/HUMAI10/3/MPYT169.1Y/LAUREL//OLM… CBSS95M00804T-F-1M-10Y-1M-0Y
G8	CARDO/QUIBENRAS/3/ROBUST//GLORIA-B… ICBSS96WM00273T-C-1M-1Y-2M-0Y
G9	LBIRAN/UNA80//LIGNEE640/3/BBSC/4/CH… ICBSS97Y00828T-D-4Y-1M-0Y
G10	1.1.2.SUR-93
G11	LENT/BLLU//PINON ICBSS97M00698T-C-2M-1Y-0M
G12	CEN-B/2*CALI92//MINN DESC1/3/CABUYA ICBSS96M00727T-L-1M-1Y-1M-0Y
G13	TOCTE/QUINA/3/RHODES/CI14100//LIGNEE5…CBSS96M00842T-U-3M-2Y-1M-0Y
G14	GLORIA-BAR/COPAL//SEN/3/BBSC/… CBSS97Y00874T-D-3Y-1M-0Y
G15	1.1.3.TOKAK-157
G16	CABUYA/4/GLORIABAR/COPAL//BEN.4D/3/S… CBSS97Y00819T-D-2Y-1M-0Y
G17	WI2269/Espe/3/WI2291/Bgs//Hml-02 ICB97-0152-0AP-13AP-0AP
G18	Kv//Alger/Ceres.362-1-1/3/WI2269/4/Sara ICB93-0727-F7SSD-92AP-0AP
G19	Kv//Alger/Ceres.362-1-1/3/WI2269/4/Sara ICB93-0727-F7SSD-98AP-0AP
G20	1.1.4.VAMIKHOCA
G21	Sara/4/H.spont.96-3/3/Roho//Alger/Ceres362-1-1 ICB93-0698-F7SSD-43AP-0AP
G22	Hashma/4/Baca's'/3/Ac253//CI08887/CI05761 ICB97-0238-0AP-5AP-0AP
G23	Hashma/Kataf-01 ICB97-0239-0AP-7AP-0AP
G24	Line3229C26/3/Moroc975//WI2291/CI01387/6/Aths/… ICB97-1345-0AP-5AP-0AP
G25	1.1.5.AKHİSAR

Statistical analysis: The data grain yields of twelve (25) genotypes in two growing seasons were evaluated by AMMI analysis (Gauch 1988). 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 (Yan and Thinker, 2006). GGE biplot methodology is composed of the biplot concept (Gabriel 1971) and GGE concept (Yan et al 2000). The graphs generated based on (1) The AMMI 1 model showing genotype x environment means, (2) Mega environments "which-won-where" pattern to identify the best genotypes in each season, (3) The relationship genotype by trait, (4) "which-won-where" pattern to identify the best genotypes for traits, (5) Ranking genotypes based on traits by mean and stability, (6) Comparison of genotypes based on traits by ideal genotype.

RESULTS AND DISCUSSION

The results of AMMI Analyses in grain yield: The variance of AMMI analysis showed that as $p<0.01$, the factors (genotype and environment) had significant effect on barley grain yield of twenty five genotypes tested in two growing seasons, while GEI was not significant (Table 2 and 3).

Table 2 The variance of AMMI analysis on grain yield of barley

Source of Variance	DF	Sum of square	Mean of squares	F Ratio	F_prob
Total	149	120248993	807040	*	*
Treatments	49	79415660	1620728	3.97	0.00000
Genotypes	24	52259398	2177475	5.34	0.00000
Environments	1	12103134	12103134	28.73	0.00000
Block	4	1685176	421294	1.03	0.39426
Interactions	24	15053128	627214	1.54	0.07387
IPCA	24	15053128	627214	1.54	0.07387
Residuals	0	0	*	*	*
Error	96	39148157	407793	*	*

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

The high addition of environment effects showed that there were important differences between growing season for grain yield. The results of AMMI analysis showed similar results of Kendal and Dogan(2015) and Yan and Rajcan (2002), 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 2). 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. (Kendal 2015, Kilic 2014). Results of GGE biplot analysis also indicated that the PCA 1 axis accounted 78.58%, PCA2 accounted for 21.42% (Fig. 3). 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 and Fig 1. Gauch & Zobel (1997), Kendal and Dogan(2015), 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 are 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 (Carbonell et al 2004). 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.

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 (Tarakanovas and Ruzgas 2006).

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 (Fig. 2). The environment and genotypes indicated much more variability in both main effect and interaction. According to AMMI, majority of genotypes (G4, G9, G10, G12, G13, G14, G16, G18, G24, G25) showed good performance, because of they took place above on axis (mean yield). It is believed that these genotypes were high yielding and desirable.

On the other hand, G1, G2, G3, G15, G6, G7, G21 demonstrated low performance, due to they located under on axis (mean yield). So, these cultivars and environments, which located under on axis (mean yield) were low yielding and undesirable. Moreover, 2005-06 growing season had both high yield potential and positive IPCA1 scores; it means that this growing season is desirable, because of high rainfall. While G16 and G25 had highest grain yield amongst genotypes, G12, G16 was very stable with low and positive IPCA scores (Table 4). According to Mirosavlievic et al (2014), the genotypes have small IPCA1 values are more stable, Becker & Leon (1988) 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 Mohammadi et al (2013), in barley.

Table 3. The average yield performance of genotypes at two growing seasons (kg ha^{-1})

Genotype	2004-05		2005-06		Mean		IPCAg[1]
1	4417	aj	6283	cg	5350	HK	-1.940.078
2	5172	aj	4914	Ij	5043	IK	1.234.731
3	5731	af	5544	Ej	5638	DI	1.126.829
4	5608	ag	5972	Cı	5790	DH	305.114
5	5517	ah	5603	Ej	5475	EJ	973.276
6	4942	aj	5433	Fj	5272	HK	-138.945
7	4661	aj	5817	Cı	5239	HK	-877.658
8	6081	ad	7667	A	6874	AB	-1.520.920
9	5336	aj	6225	cg	5781	DH	-479.251
10	6017	ae	5664	Dj	5840	DH	1.375.833
11	6297	ac	7792	A	7044	A	-1.383.968
12	5747	af	6506	Cf	6126	CG	-284.197
13	5689	af	6636	Be	6163	BF	-566.402
14	5525	ah	6217	cg	5871	DH	-184.595
15	4608	aj	4686	J	4647	K	732.572
16	5672	af	6919	Ac	6296	BD	-1.014.611
17	5106	aj	6228	cg	5667	DI	-827.857
18	6094	ad	6267	cg	6181	BE	591.469
19	4517	aj	5064	Hj	4790	JK	0.31209
20	6647	a	6733	Ad	6690	AC	720.121
21	5053	aj	5483	Fj	5268	HK	205.512
22	5369	aj	5514	Fj	5442	FJ	632.970
23	5433	aı	5378	Gj	5406	GJ	931.775
24	5300	aj	6531	Cf	5915	DH	-989.710
25	6381	ab	6047	Ch	6214	BD	1.346.783
Mean	5477	B	6044	A			
CV(%)	10.0		11.2				
LSD	97.0**		111.9**				

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 (Yan et al 2000).

A mega-environment is defined as a group of environments that consistently share the same best cultivar(s) (Yan and Rajcan 2002). 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 (G12, G14), it is still possible, and beneficial, to divide the target environments into meaningful mega-environments (Fig. 3).
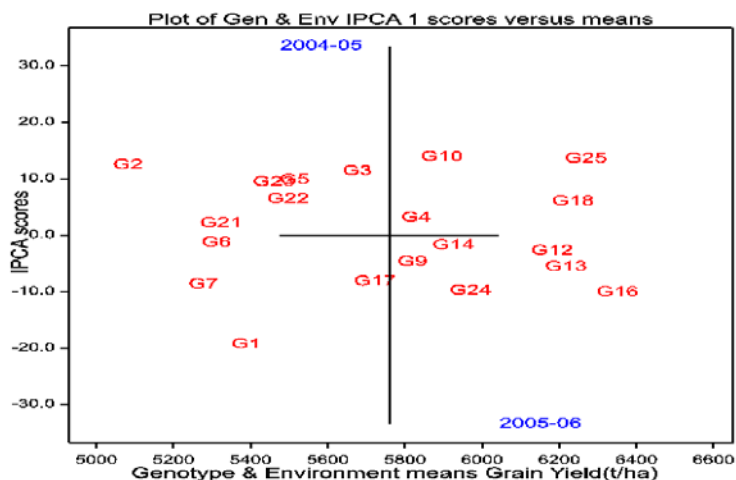

Fig. 2. The AMMI 1 model showing grain yield (kg/ha-1) of genotypes and growing seasons.
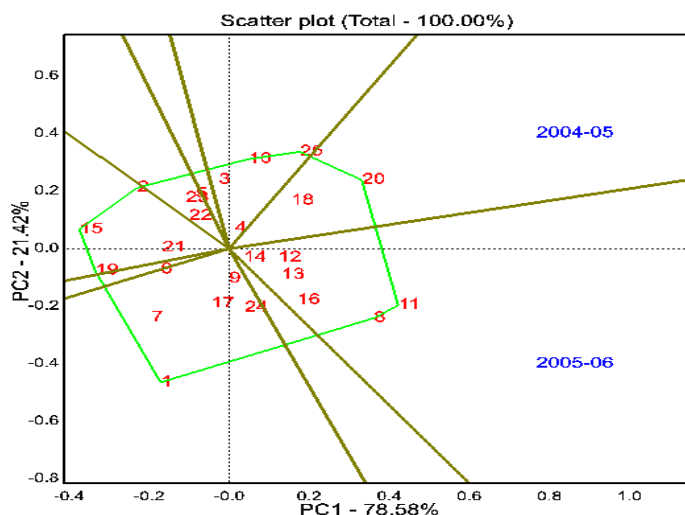

Fig. 3. Which genotype performed better in which environment for grain yield of barley

Mainly, these eight lines divide the biplot into eight sectors. The growing seasons located in different sectors; this means that the growing seasons had different ecological conditions. On the other hand, first sector consist of G11, G6 G23, G25 and G23 was high yielding and represented of vertex the 2005-06 growing season. The second sector consists of 2004-05 season with G18, G20, took places of vertex of this sector. The other sector just consists of some

genotypes, which are not related with study growing season. Consequently, G11 had high yielding at 2005-06 growing season; while G20 for 2004-05. The result of this study showed that G11 is suitable to recommend to high potential growing season, while G20 for low potential growing season. Solonechnyi et al (2015), reported that there is a strong correlations between growing seasons, which located in same sector. Sarkar et al (2014), 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. Mortazavian et al (2014), 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(Table 4) 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 29.85% of total variation, while second PCA explained 22.29%. Together, both axes accounted for 52.14% 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.
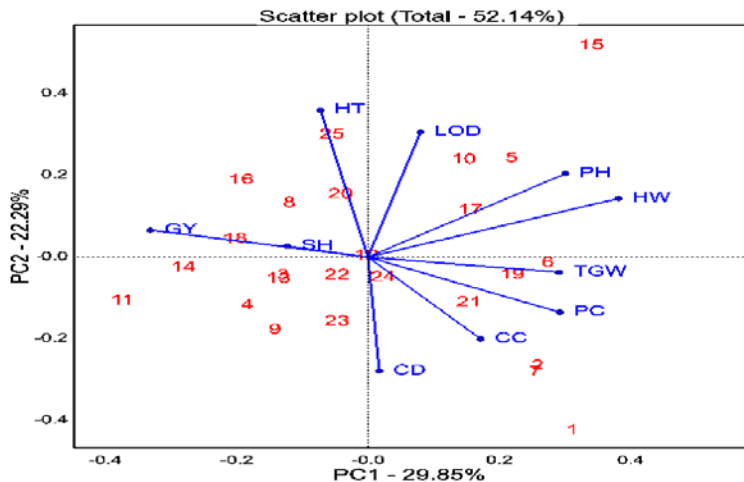

Fig. 4. The relationship genotype by trait in five environments

Therefore, the results of traits showed that there is high variation among genotypes. According to results, G11, G14 and G18 are desirable for GY, G6 and G19 are desirable for quality, so they can be recommended for release. On the other hands, all standarts(G5, G10, G15, G20 and G25) and G8 ,G16 had been late maturity time, very tall and lodging scores, so these genotypes is not

recommend for growing season. The genotypes which located near to the biplot center(G20) have less contribution to G or GE, while genotypes having longer vectors show the most contribution of G and/or GE (Yan and Tinker 2006). When the angle between two genotypes is >90°, then this two genotype are different as genetic. So, G11 with the longest vectors is the best genotypes for grain yield, while G6 for TGW and PC. The genotypes are far from center of Biplot graphs, are specific genotypes(G1, G15 and G11) for specific trait.

Table 4. The traits value of average of 25 genotypes across 5 environment.

Genot ypes	Grain yield (kg/ha⁻¹)	Heading time (date)	Plant height (cm)	Thousand grain weigh (g)	Hectoliter weight (g/l)	Protein content (%)	Crude cellulose (%)	Seed humidity (%)	Lodging (%)	Cold damage (Scor.1-9)
1	5350	104	98	47.5	73	12.3	6.05	8.4	0	6
2	5043	103	95	49.6	72	12.7	6.10	8.5	20	7
3	5638	110	88	43.1	65	11.1	5.45	8.6	30	5
4	5790	110	85	41.0	63	11.6	5.55	8.6	30	6
5	5560	118	103	47.6	75	12.4	5.95	8.7	30	3
6	5188	113	105	40.3	73	12.7	5.35	2.8	20	7
7	5239	104	95	50.6	73	12.9	5.85	8.3	0	6
8	6874	118	100	39.9	70	11.6	5.45	8.6	20	7
9	5781	120	95	34.5	65	12.1	5.60	8.4	0	7
10	5840	118	105	44.5	75	11.9	5.55	8.5	20	4
11	7044	112	88	35.0	61	11.6	5.55	8.5	0	5
12	6126	113	98	42.8	70	12.2	5.00	8.6	2	5
13	6163	110	95	40.0	68	11.0	5.60	8.5	0	5
14	5871	120	88	39.3	63	10.2	5.70	8.7	0	2
15	4647	117	110	42.3	76	12.5	5.60	8.6	80	0
16	6296	112	95	36.1	66	11.1	5.45	8.7	60	4
17	5667	110	103	43.8	73	12.2	5.75	8.8	30	3
18	6181	113	95	37.8	66	11.1	4.75	8.6	0	4
19	4790	105	110	38.4	74	11.8	6.05	8.8	0	4
20	6690	111	105	42.1	74	10.7	5.15	8.8	0	3
21	5268	108	103	40.1	71	12.6	6.15	8.5	0	5
22	5442	110	93	38.1	65	12.8	5.35	8.5	0	1
23	5406	107	93	38.1	65	12.4	6.10	8.9	0	3
24	5915	109	103	38.8	71	12.0	5.60	8.8	0	5
25	6214	113	98	44.0	71	10.3	6.10	8.6	50	1
Mean	5457	111	96	39.7	63.2	12.3	4.9	10.7	28.5	3.9

There are negative correlation between two traits, are opposite to each other(GY-TGW, HT-CD) on graph and the angles of vector is >90°. Therefore, there is major contribution of trait to traits; because of they have opposite direction, so they can make up different genetic contribution (Jalata 2011).

"Which-won-where" pattern to identify the best genotypes for traits:The GGE biplot visualize the correlation amongs tratits and grouping them also to visualize the interaction patterns between genotypes and traits (Yan and Tinker 2006). 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 (Yan et al. 2000). 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 three group. The traits(TGW,PC, CC and CD)took place in first group and related with G6, G19, G21, G2 and G7; HT, LOD, PH and HW in second group and related with G5, G10 and G25; GY and SH in thirth group and related with G13 and G14.Other genotypes did not related with any group of tratis. On the other hand, there were correlation amongs tratis which took places in same group. 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, G15 and G11. These genotypes were the best for special traits or the poorest genotypes some for all of traits because they were farthest from the origin of the biplot(Yan and Kang 2003).
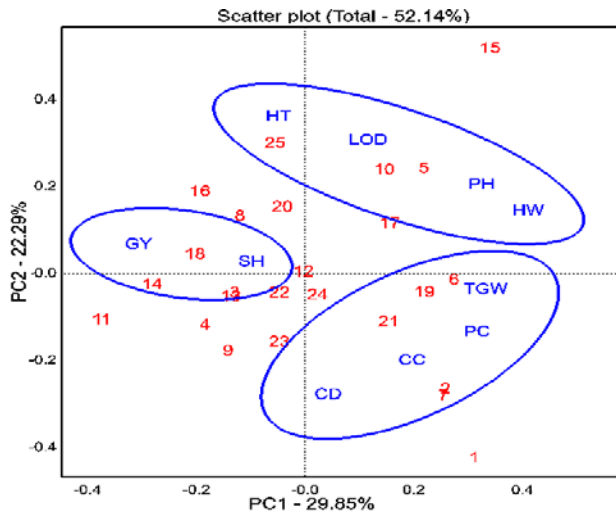

Fig. 5. Gge biplot showing the performance of each cultivar at each environment.

Ranking 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 (fig. 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 stabile line and has high mean values of traits are meaning that it is more favorable than others (yan and tinker, 2006; farshadfar et al 2013.thus, g17 is located center of aea ("absolutely stable"), but; g5, g6 and g15 took place of near center of aea and high mean of traits. So these genotypes are favorable than others. According to fig.5, the g15, g5 and g6 are low stable and more favorable, while g17 are "stable" and favorable, because this genotype has high mean value of traits. From this example, we can recommend g17 and g5 to study for more traits. On the other hand, some genotypes (g11, g14, g4, g9, g18, g13, g16, g23, g8 and g22) were unfavorable, because these genotypes had low mean values of traits.
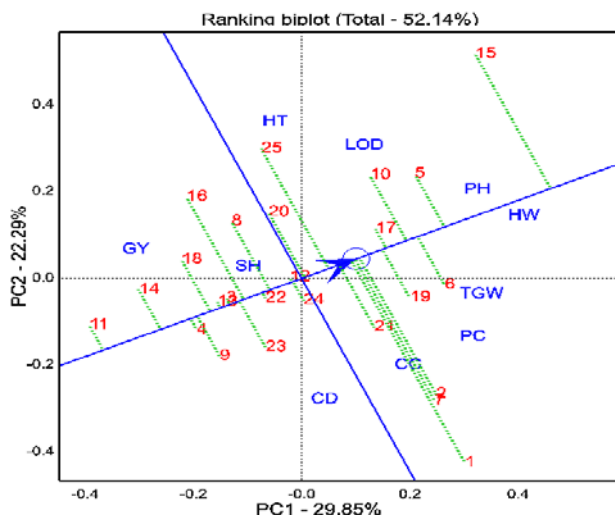
Fig. 6. Ranking genotypes based on traits mean and instability

Comparison of genotypes based on traits by ideal genotype: the genotype has both high traits mean and high stability is called a ideal genotype (fig. 7).
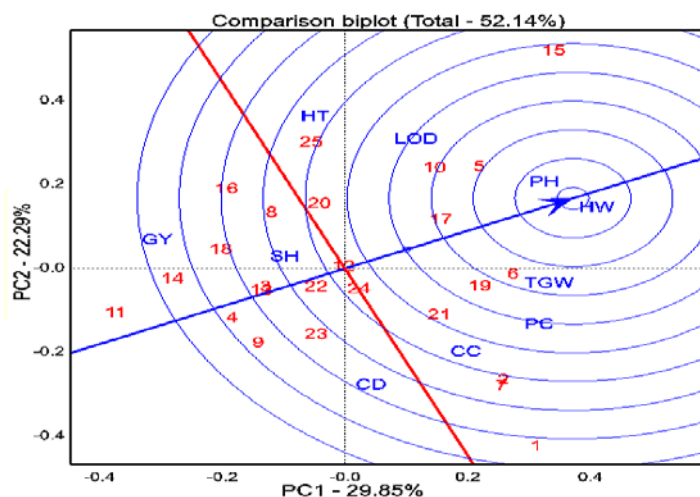

Fig. 7. The relationship genotype by trait in two seasons

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"). So, genotypes located closer to the ideal circle are meaning that it is ideal genotype than others (Yan and Tinker, 2006). In the study, any genotype was not located center of AEA ("absolutely stable"), but; G5, G6 and G17 took place of near center of AEA. So these genotypes are ideal than other genotypes.

Consequently, G6 and G17 are close to ideal genotype, so, these genotypes can be recommended for release in terms of all traits.

On the other hand, more genotypes located far from ideal genotype and, these genotypes (g11, g14, g4, g9, g18, g13, g16, g23, g8 and g22) are not ideal genotypes to study and release. The researchers reported that the biplot show excellent discriminating to select genotypes for all traits and to recommendation for release (sayar and han, 2015).

CONCLUSIONS

The GGE Biplot and AMMI results indicated that yield performance of barley genotypes were highly influenced by growing season conditions (rainfall, hot stress). The genotype G12, G13, G16 and G18 demonstrated best performance among genotypes tested growing seasons, while G2 had least grain yield and adaptability. Therefore, the G16 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 (G6, G19 and G21 for quality, G14 and G18 for GY, G2 and G7 resistance to cold damage). The AMMI method and GGE Biplot analysis permitted a meaningful and useful summary of GE interaction data and assisted in examining the natural relationships and variations in genotype performance across test growing seasons. As a result indicated that that G12 and G16 are suitable to recommend for release and G6, G19 and G21 valuable source for quality to use in barley breeding program.

ABBREVITATIONS

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

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 Vol. 4(11) pp. 1322-1330.

Becker, H.C. and Leon, J.(1998). Stability analysis in plant breeding, Plant Breed, 101:1-23.

Carbonell, S. A., Filho, J.A., Dias, L.A., Garcia, A.A and Morais L.K.(2004) Common bean cultivars and lines interactions with environments. Sci. Agric (Pracicaba Braz) 61(2):169-177.

Farshadfar, E., Rashidi, M, Jowkar M.M. and Zali, H. (1971).GGE Biplot analysis of genotype × environment interaction in chickpea genotypes, European J. of Exper. Biology, 3(1):417-423.

Gabriel, K.R. (1971. The biplot graphic display of matrices with application to principal component analysis, Biometrika 58: 453-467.

Gauch, H.G. and Zobel, R.W (1997). Identifying mega-environments and targeting genotypes. Crop. 37:311-326.

Gauch, H.G. (2013). Model selection and validation for yield trials with interaction", Biometrics 44,705-715, 1988.

Hagos, G. H. and Abay, F. (2013). AMMI and GGE Biplot analysis of bread wheat genotypes in the northern part of Ethiopia. Journal Plant Breeding and Genetic. 01:12.18,

Jalata, Z. (2011).GGE-biplot Analysis of Multi-environment yield trials of barley(Hordeum vulgare L.) genotypes in Southeastern Ethiopia Highlands. International J.of P. Breeding and Gen. 5(1):59-75.

Kendal, E. (2015). Determination of relationship between chlorophyll and other features in durum Wheat (Triticum turgidum L. var. durum) using SPAD and biplot analyses. Journal of Agricultural and Technology, Vol. 17(supplementary Issue)-1873-1886.

Kendal, E. (2016). GGE Biplot analysis of Multi-environment Yield Trials in Barley (Hordeum vulgare L) Cultivars. Ekin J. of Crop Breeding and Genetics, (2016) 2-3:90-99.

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 & Forestry, Vol. 61, Issue 4: 307-318, 2015, Podgorica, DOI: 10.17707/Agricult Forest. 61.4.37.

Kendal, E and Sener, O. (2015). Examination of genotype × environment interactions by GGE biplot analysis in spring durum wheat. Indian Journal of Genetics and Plant Breeding, 75(3): 341-348 (2015), DOI: 10.5958/0975-6906.2015.00054.1.

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.

Mirosavlievic, M., Przulj, N., Bocanski, N., Stanisavlievic, D., Mitrovic, B. (2014). The application of AMMI model for barley cultivars evaluation in multi-year trials. Genetika, Vol: 46, No. 2, 445-454.

Mirosavlievic, M. N., Przuli, N. and Canak, P. (2014). Analysis of new experimental barley genotype performance for grain yield using AMMI Biplot. Selekcıja I Semenarstvo, Vol: broj 1..

Mirosavlievic, M. N. Przuli, N. and Canak, P. Momcilovic, V. Aćin V., Jocković, B. Hristov, N. Mladenov, N. (2015). Relationship between Grain Yield and Agronomic Traits in Winter Barley. IFVC, doi:10.5937/ratpov52-7860.

Mohammadi, M., Karimizadeh, R., Noorinia, A A., Ghojogh, H. Hosseinpour, T., Khalilzadeh, GR., 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. Current Opinion in Agriculture Curr. Opin. Agric. 2(1), 20-24.

Mortazavian, S. M. M., Nikkhah, H. R., Hassani F. A., Sharif-al-Hosseini M. Taheri, M. and Mahlooji, M. (2014).GGE Biplot and AMMI Analysis of yield performance of barley genotypes across different environments in Iran. J. Agr. Sci. Tech. Vol. 16: 609-622.

Przuli, N., Momcilović, V., Simić, J. and Mirosavljević, M. (2014). Effect of growing season and variety on quality of spring two-rowed barley. Genetika, 46: 59-73,

Rahmatollah, K., Mohtasham, M., Naser, S., Ali, A.M., Barzo, R., Faramarz, S., Fariba, A. (2013).GGE Biplot analysis of yield stability in multi-nvironment trials of lentil genotypes under rainfed Condition. Not Sci Biol, 5(2):256-262.

Sarkar, B., Sharma, R.. C. R, Verma Ananta Sarkar P. S. and Sharma, I. (2014). Identifying superior feed barley genotypes using GGE biplot for diverse environments in India. Indian J. Genet., 74(1): 26-33 (2014) DOI: 10.5958/j.0975-6906.74.1.004.

Solonechnyi, P., Vasko, N., Naumov, A., Solonechnaya, O., Vazhenına, O., Bondareva, O., Lovnivenko, Y. 2015. GGE biplot analysis of genotype by environment interaction of spring barley varieties. Zemdirbyste-Agri., vol. 102, 431–436.

Sayar, M.S. and Han, Y. (2015).Determination of seed yield and yield components of grasspea (Lathyrus sativus L.) lines and evaluations using GGE Biplot analysis method. Tarim Bilimleri Dergisi- J. Agric. Sci,, 21(1): 78-92.

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.

Yan, W. L., Hunt, A. Sheng, Q. and Szlavnics, Z. (2000). Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop Sci. 40: 597-605.

Yan, W. and Rajcanw, I. (2002). Biplot analysis of test sites and trait relations of soybean in Ontario. Crop Science 42. 11-20.

Yan, W., Kang MS. (2003). GGE Biplot Analysis: A graphical tool for breeders, geneticists, and agronomists. CRC Press, Boca Raton, p 213..

Yan, W. and Tinker, N.A. (2006). Biplot analysis of multi-environment trial data; Principles and applications", Canadian Journal of Plant Science 86, 623-645.

Yan, W and Holland, J.B. (2010). A heritability adjusted GGE biplot for test environment evaluation Euphytica, 171(3): 355−369.