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AGRONOMIC AND QUALITY EVALUATION OF RAINFED BARLEY (*HORDEUM VULGARE* L.) IN EASTERN MEDITERRANEAN CONDITION

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ABSTRACT

Using agronomic and quality characteristics, genotypic and phenotypic performance of barley lines were investigated in East Mediterranean condition in Turkey in three consecutive years from 2012 to 2014 based on randomized complete block design.

Growing seasons had dramatically different climatic conditions therefore, years were considered as different environments. 2014 was the best selection environment for drought tolerance. Agronomic traits such as heading date (HDD), maturity date (MTR), plant height (PHT), lodging rate (LRT), lodging angle (LAN), grain yield (YLD,) thousand kernel weight (TKW), hectoliter weight (HKW), barley leaf spot (SCALT) tolerance scoring, as well as quality traits such as fat, fiber, protein (PR) and starch (STR) contents of barley genotypes were measured in the three different environments.

Results showed that YLD was mostly correlated with PHT, MTR and FBR. All traits except PHT, HWT and PRT were significantly affected by genotype x environment interaction. Yield component traits such as TKW and HWT was moderately high in terms of heritability values while quality traits of FAT and PRT was contained highest heritability values. 13 lines and one cultivar of tested 25 genotypes were stable at yield over three environments. The highest yielding genotype was G16 in 2012. While G10 was the highest yielding genotype in drought conditions of 2014. All lines competed well with cultivars over three environments. In the present study, some barley lines appear to carry useful alleles for stable yield and quality traits. The results of this study will be helpful for barley breeders and farmers to improve and make use of barley cultivars adaptable for Mediterranean environments.

KEYWORDS:
Barley, agronomic, quality, correlations, principal component

INTRODUCTION

Barley (*Hordeum vulgare* L.) is considered as the fourth most important cereal crop in the world after wheat, maize and rice [1]. Barley can be grown on areas with low precipitation, and is known to have tolerance to salt, drought and frost. It has an advantage over other cereals in terms of early period of development. Therefore, barley is a suitable crop where rainfed agriculture is predominant. Water stress is the major abiotic stress causing yield reduction where yield loss in barley could be as much as 50% [2]. Turkey is one of the largest barley producer with about 3,7 % of the world production [3].

Future forecasts suggest that Mediterranean region will prone to climate change as it is a transition zone between temperate rainy climate of central Europe and arid climate of North Africa [4]. Therefore, rainfall in the Mediterranean environment is irregular [5] resulting in unpredictable environmental conditions for crop growth and significant genotype by environment interactions (GE). GE, described as the variation in relative performance of genotypes in different environments which is essential in plant breeding since it complicates testing and selection of superior genotypes thus decreasing genetic advance [6].

Acreages of barley cultivation is very limited in Cukurova Region. Wheat is more cultivated than barley which starts to be harvested in the beginning of June. Generally, second crop sowings (maize, soybean etc.) start in the middle of June after wheat. This brings some disadvantage for second crops like low grain yield, heat stress, problems related to autumn precipitation, disease and insect problems. If barley is preferred prior to second crop, harvest of it starts in beginning of May, approximately 1 month earlier than wheat. This may result with less injury of disease and insect compare to wheat and improvements of grain yield of second crop.

The objective of this study is to investigate adaptability and performance of the selected national barley cultivars and foreign barley genotypes provided by ICARDA, under varying Mediterranean climate conditions of three consecutive growing seasons by using agronomic, quality and scald tolerance characteristics. Using such resources in varying environmental conditions should be a better strategy for improving stable barley cultivars in unpredictable and drought prone Mediterranean environments. The results of this study are expected to be useful for barley breeders as well as farmers and local communities who seek profitable revenue.

MATERIALS AND METHODS

Plant Material. During 2012, 2013 and 2014, a total of 20 barley lines and 5 standard check cultivars (Table 1.), involving two and six rowed barleys, were planted on experimental fields of Eastern Mediterranean Agricultural Institution in Adana in Turkey. Previous crops were peanut, chickpea and maize in 2012, 2013 and 2014, respectively. Climate conditions were also depicted in Fig.1., Fig.2 and Fig. 3. The experiment was conducted in randomized complete block design with two replications in 2012 and four replications in 2013 and 2014. Years were analyzed as environments and named as E12 (2012), E13 (2013) and E14 (2014) for corresponding years. Phosphorus fertilizer (P_2O_5) was applied to the soil before planting as 60 kg ha^{-1}, and nitrogen (pure) was applied in 2 parts, the first part was given to the soil before planting and the other part was applied at tillering period. Total nitrogen amount was 120 kg ha^{-1}.

Trait measurements. 1) Heading date (HDD) was days from 75% emergence to 75% heading on plots, 2) maturity date (MTR) was days from heading date to yellowing of leaves and stems, 3) plant height (PHT) was average length of 10 plants at each plot from root crown to spikelet excluding awns [30], 4) lodging rate (LRT) was lodging resistance was assessed at the full maturity stage in a per cent scale where 100% lodging was the highest lodging rate, 5) lodging angle (LAN) was the angle between stems and ground in severe (5) to upright (0), 6) grain yield (YLD) was the amount of grain in 7 m^2 plots converted to kg ha^{-1}, 7) thousand kernel weight (TKW) was calculated by weighting one hundred kernels randomly selected from each plot four times [30], 8) hectoliter weight (HWT) was volume of weighed grains by using Loyka hectoliter measurement device for each plot, 9) barley leaf spot (*Rhynchosporium secalis*) disease AYL (SCALD) was tolerance scoring performed by using 2 digit scale in which first digit represent location of disease on plant while second digit represents the area covered by the disease [7]. Fat (FAT), fiber (FBR), protein (PRT) and starch (STR) contents of the grains were measured by the following the procedure: The samples were scanned by using NIR system model FOSS XDS Rapid Content™ Analyzer to obtain NIR spectra between 400-2500 nm. The spectral resolution was 2 nm. The ISI scan and Win ISI III 161 programs were used to collect the data for spectra. The calibration information of NIRS used to obtain the quality data of the barley samples is performed by the manufacturer procedure.

TABLE 1
Plant Materials and information of pedigree

Entry	Pedigree
G1	Avt/Attiki//M-Att-73-337-1/3/Aths/Lignee686/4/M-Att-73-337-1/3/Mari/Aths*2//Avt/Attiki
G2	Mzq/Gva//PI002917/3/WI2291/WI2269/4/WI3213
G3	Clipper//WI2291*2/WI2269
G4	Arizona5908/Aths//Avt/Attiki/3/S.T.Barley/4/Aths/Lignee686/5/Arbayan/Aths
G5	Weeah11//WI2291/Bgs/3/ER/Apm//AC253
G6	Carina/Moroc9-75
G7	Moroc9-75//WI2291/WI2269
G8	INRA55-86-2/Rabat1703/3/Hml-02/ArabiAbiad//ER/Apm
G9	Mr25-84/Attiki//Alanda-01/4/Arar/PI386540//Giza121/Pue/3/Lignee527/Chn-01
G10	Alanda/Hamra/4/Avt/Attiki//M-Att-73-337-1/3/Aths/Lignee686
G11	Alanda/5/Aths/4/Pro/TolI//Cer*2/TolI/3/5106/6/Baca'S'/3/AC253//CI08887/CI05761
G12	Avt/Attiki//M-Att-73-337-1/3/Aths/Lignee686/5/AwBlack/Aths//Arar/3/9Cr279-07/Roho/4/DD-14/Rhn-03
G13	Avt/Attiki//M-Att-73-337-1/3/Aths/Lignee686/5/AwBlack/Aths//Arar/3/9Cr279-07/Roho/4/DD-14/Rhn-03
G14	Arizona5908/Aths//Avt/Attiki/3/S.T.Barley/4/Aths/Lignee686/5/Aths/Lignee686/3/DeirAlla106/Lignee527//Asl
G15	Tipper//WI2291/WI2269/4/WI2198//ER/Apm/3/ER/Apm//AC253
G16	Moroc9-75//WI2291/CI01387/3/ER/Apm//Akrash
G17	Avt/Attiki//M-Att-73-337-1/3/Aths/Lignee686/5/AwBlack/Aths//Arar/3/9Cr279-07/Roho/4/DD-14/Rhn-03
G18	Nawair 1(Harmal-02/ArabiAbiad*2/4/Soufara-02/3/RM1508/Por//WI2269)
G19	Nawair 1(Harmal-02/ArabiAbiad*2/4/Soufara-02/3/RM1508/Por//WI2269)
G20	Nawair 1(Harmal-02/ArabiAbiad*2/4/Soufara-02/3/RM1508/Por//WI2269)
G21	Rihane-03 (standard)
G22	Harmal(standard)
G23	Beecher (standard)
G24	Moroc9-75 (standard)
G25	Hilal (standard)

Climatic conditions were given in Fig. 1, 2 and 3.

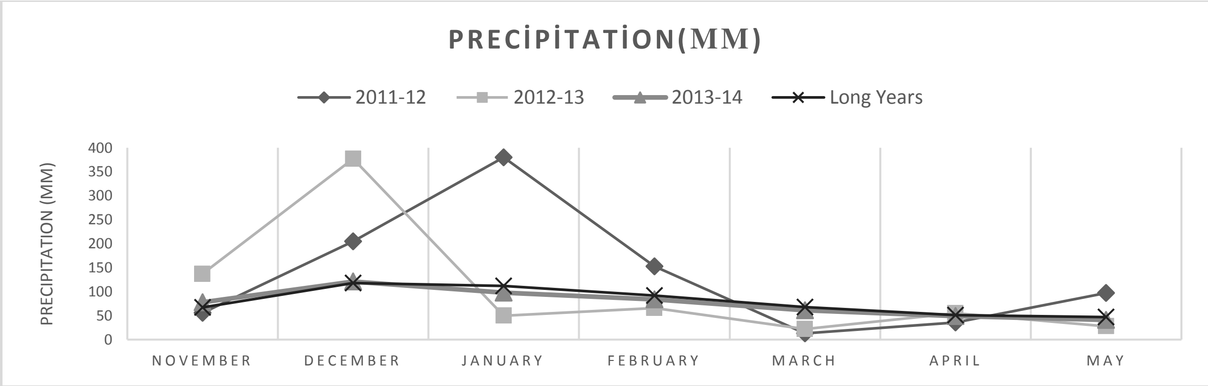

FIGURE 1
Precipitation for 2012, 2013, 2014 years.

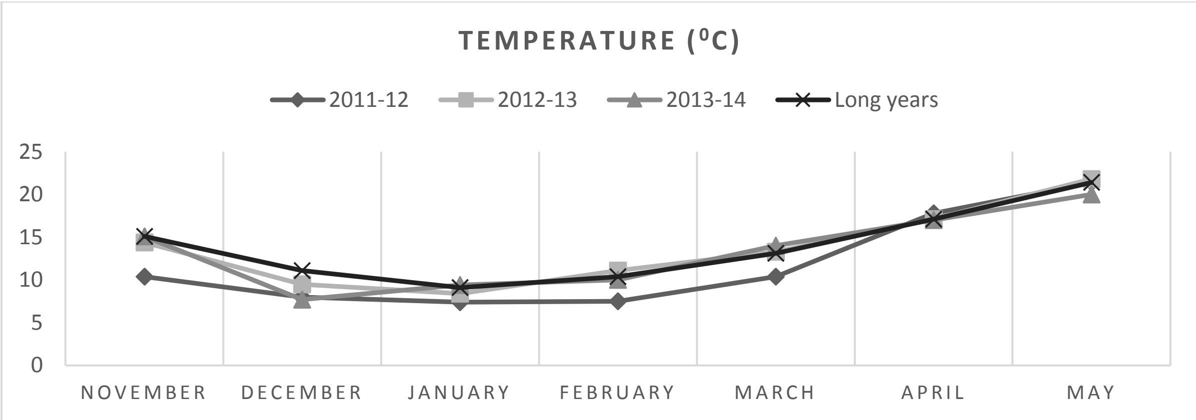

FIGURE 2
Temperature for 2012, 2013, 2014 years.

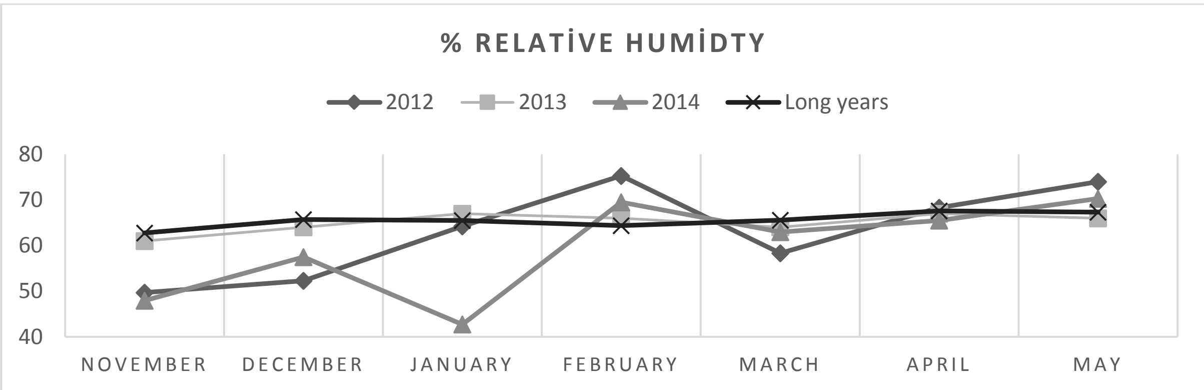

FIGURE 3
Relative humidity for 2012, 2013, 2014 years.

Precipitation was lower in 2014 compared to 2012 and 2013 years. In 2012, more rain was received in December compared to long year average and other two years of trial. In 2013, November, December and January received more rain, while March and April months were less rainy compared to long years. The driest year of trial period was 2014.

2012 year was lower temperature compared long year averages and other two years of the trial.

Relative humidity was lower than long year averages for November and December in 2012 and 2014. The least relative humidity was observed in January in 2014. Other months were near long year averages.

Statistical analysis. Data were analyzed using PROC MIXED in SAS 9.0 (SAS Institute Inc. 2011, Cary, NC). Locations (years) and genotypes were considered as fixed and blocks nested within the environments were random allowing for the detection of significant differences between means. Homogeneous error between the experimental sites allowed for data to be analyzed in a combined analysis. Broad sense heritability was estimated from the variance components using TYPE3 sum of squares with all effects including genotype treated as random, using the formula:

$$\mathbf{H=\sigma^2_G/[\sigma^2_G+\sigma^2_{GE}/r+\sigma^2_e/re]}$$

Where H, σ^2_G, σ^2_{GE}, σ^2_e represent broad sense heritability, genotypic variance, genotype by environmental variance and error variance, respectively, and e and r are the numbers of environments (n = 3) and replications (n = 4), respectively [8], [9]. Pearson's correlation using PROC CORR and principal component analysis (PCA) using the PRINCOM procedure in SAS were used to determine associations among the measured phenotypic traits. The contributions of each variable to the first two principal components with the highest loadings are depicted using biplots.

RESULTS

Weather data showed that there is dramatically less rain in E14 compared to other two years. In E12, it rained well during December, January and February. In E13, however, it rained well in November and December whereas in E14, it was below 50 mm of rain and was highly dry. Significant correlations existed between most of the variables (Table 2).

The magnitude of correlation coefficients was generally small but significant. The highest significant positive correlation was found between LRT and LAN (r=0.801) while the lowest one was between PHT and HWT (r=0.139). The negative correlation was the highest between MTR and AYL (SCALD) (r=-0.679) while it was the lowest between HWT and FAT (r=-0.168). The grain yield (YLD) was mostly correlated with PHT (r=0.457) while poorly but significantly correlated with FBR (r=0.163). However, there was a negative correlation between YLD and MTR (r=-0.312). A significant positive correlation existed between PHT and LAN (r=0.724) while the negative correlation was the highest between PHT and STR (r=-0.654). There was relatively high significant positive correlation between TKW and HWT (r=0.479), which are yield component traits. Scald damage was not correlated with yield, however, was significantly and positively correlated PHT, LRT, LAN and FBR while negatively correlated with HDD, MTR, HWT, and PRT. Although the magnitudes were small, there were significant correlations among quality traits in combined environment. FBR is negatively correlated with PRT (r= -0.420) and STR (R= -0.589) whereas FAT negatively correlated PRT (r= 0.268) and STR (r=0.194). Small correlation values were probably due to large environmental variation among environments.

The first two principal components explained 58% of the total variation. The PC1 explained 37% of the variation and positively correlated with PHT, LRT and LAN while it was negatively correlated with MTR and STR. The PC2 explained 21% of the variation and positively correlated with HDD, TKW, HWT and PRT while it was negatively correlated with AYL (SCALD) and STR. The PCA biplot clearly discriminated the three environments where YLD, TKW and HDD formed a cluster on E12, AYL (SCALD) was on E13, and MTR, FAT, STR and PRT formed a cluster on E14 (Fig. 4).

The other variables such as FBR, LRT, LAN and PHT formed a cluster between E12 and E13 while HWT was between E12 and E14. Except for STR, most of the traits with high G x E interaction values were higher in E12 and E13 (Fig. 4). There was also significant variation among quality parameters such as STR, FBR and FAT with respect to environments.

TABLE 2
Correlation among variables in combined 3 years

	YLD	HDD	MTR	PHT	LRT	LAN	TKW	HWT	AYL (Scald)	FAT	FBR	PRT	STR
YLD	1	0.42	-0.32	0.46	0.24	0.39	0.35	0.26	0.04	-0.26	0.16	-0.19	-0.34
HDD	**	1	-0.26	0.60	0.27	0.47	0.39	0.54	-0.40	-0.30	0.15	0.05	-0.68
MTR	**	**	1	-0.61	-0.58	-0.66	-0.09	0.17	-0.68	0.33	-0.45	0.45	0.35
PHT	**	**	**	1	0.58	0.72	0.37	0.14	0.21	-0.26	0.48	-0.30	-0.65
LRT	**	**	**	**	1	0.80	0.09	-0.09	0.32	-0.23	0.26	-0.28	-0.28
LAN	**	**	**	**	**	1	0.27	0.04	0.26	-0.28	0.39	-0.30	-0.51
TKW	**	**	ns	**	ns	**	1	0.48	-0.10	-0.17	0.07	0.03	-0.35
HWT	**	**	**	*	ns	ns	**	1	-0.46	-0.25	-0.24	0.24	-0.31
AYL (SCALD)	ns	**	**	**	**	**	ns	**	1	-0.11	0.35	-0.46	0.07
FAT	**	**	**	**	**	**	**	**	ns	1	0.02	0.27	0.19
FBR	**	*	**	**	**	**	ns	**	**	ns	1	-0.42	-0.59
PRT	**	ns	**	**	**	**	ns	**	**	**	**	1	-0.02
STR	**	**	**	**	**	**	**	**	0.29	**	**	ns	1

Upper right are correlation coefficients and lower left are significance values between variables.
*, and ** denote significant correlation at $p<0.05$ and 0.01, respectively. ns: not significant.

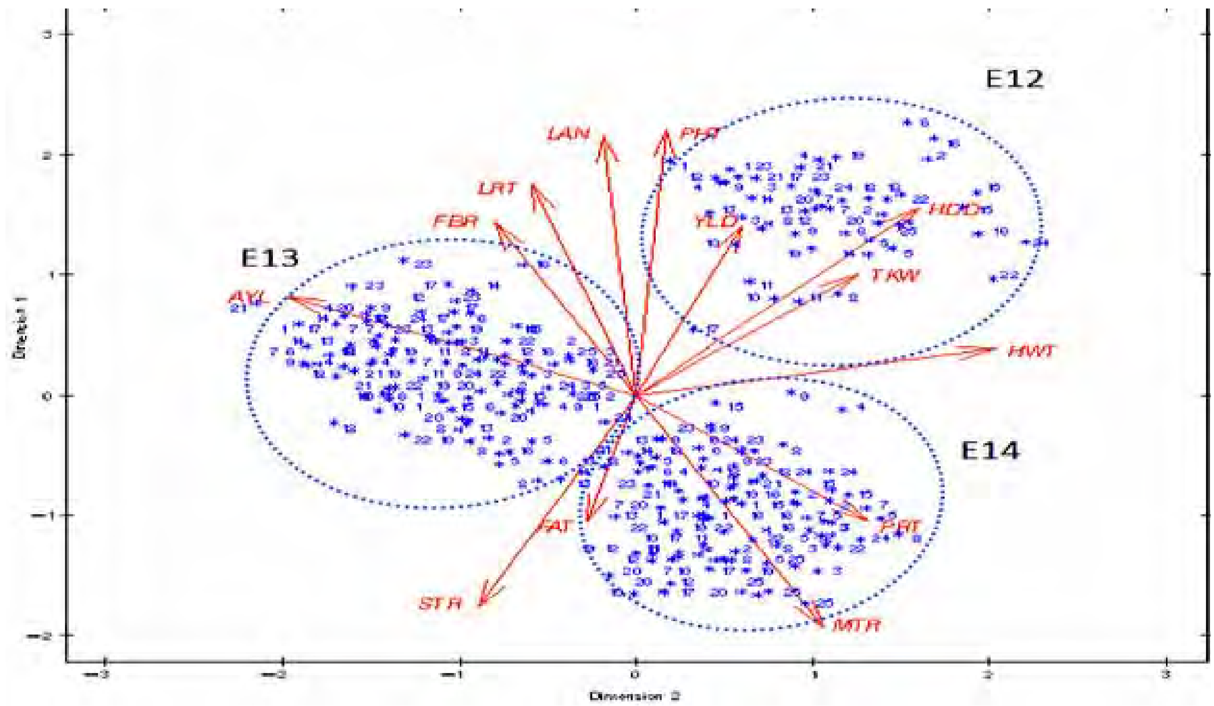

FIGURE 4
PCA biplot of agronomic and quality traits measured over three environments.

TABLE 3
Analysis of variance results

	Rep	E	Error1	G	GxE	Error2	H^2
YLD (kg ha^{-1})	801819	33630862**	523769	1548822**	1415298**	497894	0.089
PHT (cm)	55.55	19189**	224	278**	59.73	54.19	0.785
HDD (d)	9.033	10214**	9.13	83.29**	35.31**	3.222	0.576
MTR (d)	22.91	10488**	26.66	84.25**	40.31**	4.479	0.522
TKW (g)	24.04	1660**	17.37	217**	57.68**	26.023	0.734
HWT (kg hl^{-1})	1.835	1171**	9.938	61.54**	10.235	8.214	0.834
LRT (%)	584	42731*	2497	1710**	623**	419	0.635
LAN (0-5)	0.01	117**	0.434	1.533**	0.697**	0.38	0.546
AYL (%)	4.131	152020**	2.96	800**	628.153**	66.741	0.215
FAT (%)	0.097	2.641**	0.06	0.579**	0.111**	0.052	0.809
FBR (%)	0.957	39.15**	0.284	2.864**	1.101*	0.686	0.616
PRT (%)	4.8	59.98**	5.735	3.338**	0.745	0.893	0.777
STR (%)	4.165	1480**	14.69	19.56**	9.463*	6.415	0.516

All traits were significantly affected by genotypes or environment. There were also significant G x E interactions regarding all 13 traits studied except PHT, HWT and PRT. Using genotypic and environmental variances, broad sense heritability values were also calculated and moderately high heritability values were observed for most of the traits (Table 3).

Although YLD contained the lowest heritability value, as expected, yield component traits such as TKW and HWT was moderately high in terms of heritability values. Regarding quality traits FAT and PRT was including the highest heritability values. The insignificant G x E interaction values showed that PHT, HWT and PRT were not influenced by the environments, however, significant variations were observed on main effects of genotypes.

Mean comparison for heading days of genotypes in combined environments given Fig. 5.

In general, HDD period was longest in E12 while shortest in E13 (Fig 3). The longest HDD period belonged to G21 (131 d) while shortest to G12 (92.3 d).

Mean comparison for maturity days of genotypes in combined environments were given in Fig. 6.

In terms of MTR, E14 was longer than both E12 and E13 which these two were similar in MTR. The longest period of MTR was observed on G11 and G12 (64.75 d) in E14 while G19 (30 d) was the shortest MTR in E13.

Averages of 3 year barley genotypes of plant height given Fig. 7.

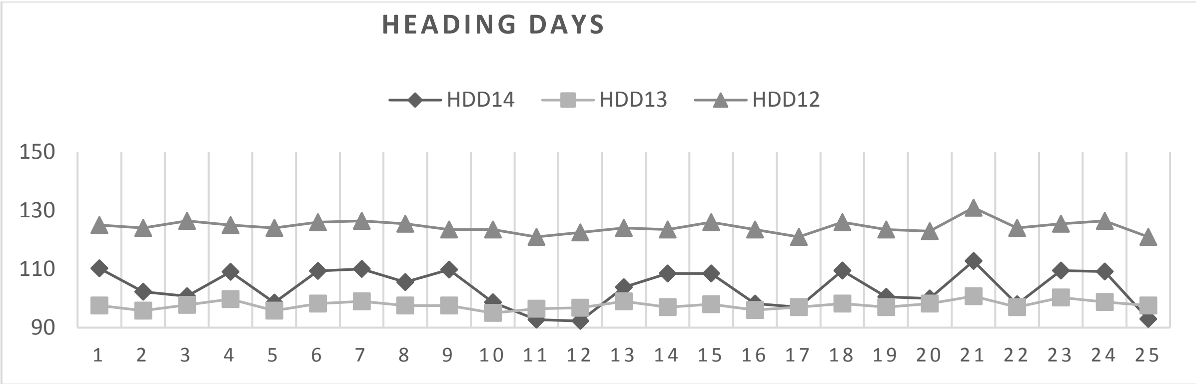

FIGURE 5
Mean comparison for heading days of genotypes in combined environments.
Tukey's HSD of HDD for HSD_{GxE}= 4.934 d

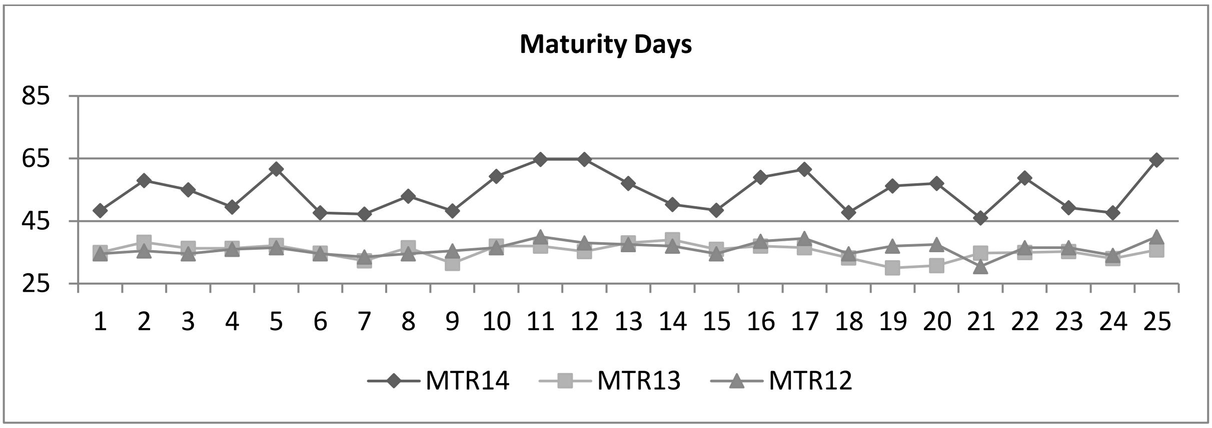

FIGURE 6
Mean comparison for maturity days of genotypes in combined environments.
Tukey's HSD of MTR for HSD_{GxE}= 5.818 d

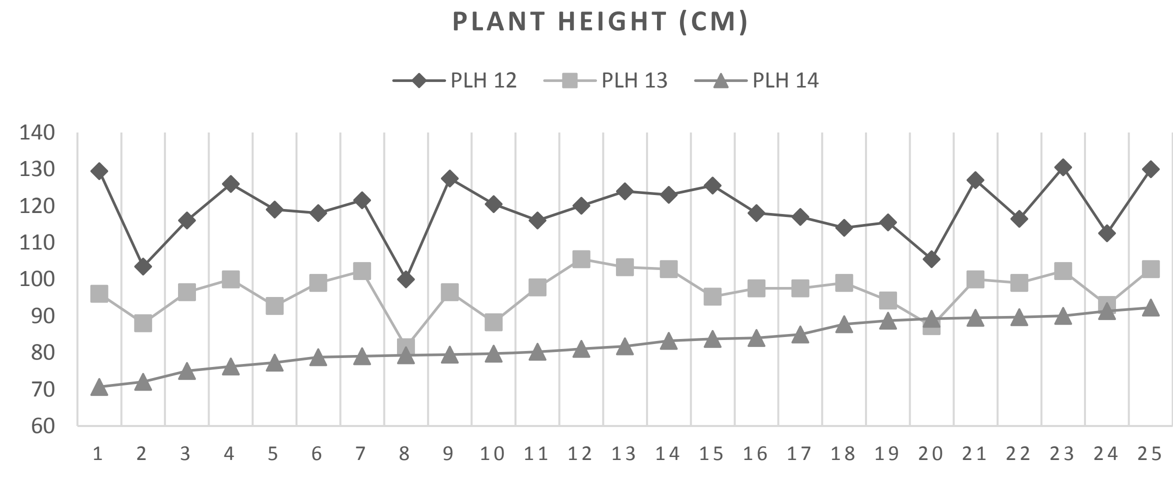

FIGURE 7
Mean comparison for plant height of barley genotypes in combined environments.
Tukey's HSD of PLH for HSD_{GxE}= 4.25 cm

The three environments were significantly differed in terms of PHT values and the E12 was higher in PHT (119.06) than E13 (96.71) and E14 (82.60) (Duncan's critical range <2.5, $p<0.05$). Regarding the genotypes, there seemed significant variations within standard cultivars and lines as well as between standard cultivars and lines. The highest PHT (130.5 cm) was obtained from G23 in 2012, which is a standard cultivar, while the lowest was observed on G1 (70.7 cm) in 2014.

In E13, barley genotypes' Scald is given in Fig. 8.

Outbreak of Scald was mainly detected in E13 and few Scald scores were obtained in E12 and it was not detected at all in E14. Therefore, only E13 data were used in the variance analysis. In general, none of the genotypes were found to be resistant (i.e. higher disease score than 75) but some genotypes such as G2, G5, G11, G14, G24, and G25 were scored equal to or less than 75 in E13.

Lodging rate of barley genotypes for 3 years are given Fig. 9.

As expected, LRT values were lowest in E14. The highest LRT values were obtained from G16 and G23 in E12. In E14, the genotypes G3, G5, G7, G8, G11, G12, G15, G16 and G25 were not lodged at all. Lodging rate values of G5, G8, G11 and G15 were similar since differences were insignificant in three environments (Tukey HSD GxE= 56.26, p>0.05). The GxE interaction also showed that G2, G7, G12, G16, G17, G19 G20 and G23 had significantly higher LRT values in E12 than in E14. Additionally, G3, G7 and G17 had significantly higher LRT values in E13 than in E12.

Plant lodging angles of barley genotypes are given in Fig. 10.

Similar to LRT, the LAN values were also the lowest in E14 but distinctively the highest in E12. Only G5 was similarly low in LAN values in three environments while others were significantly different in LAN values at least in two environments.

Yield of barley genotypes are given in Fig. 11.

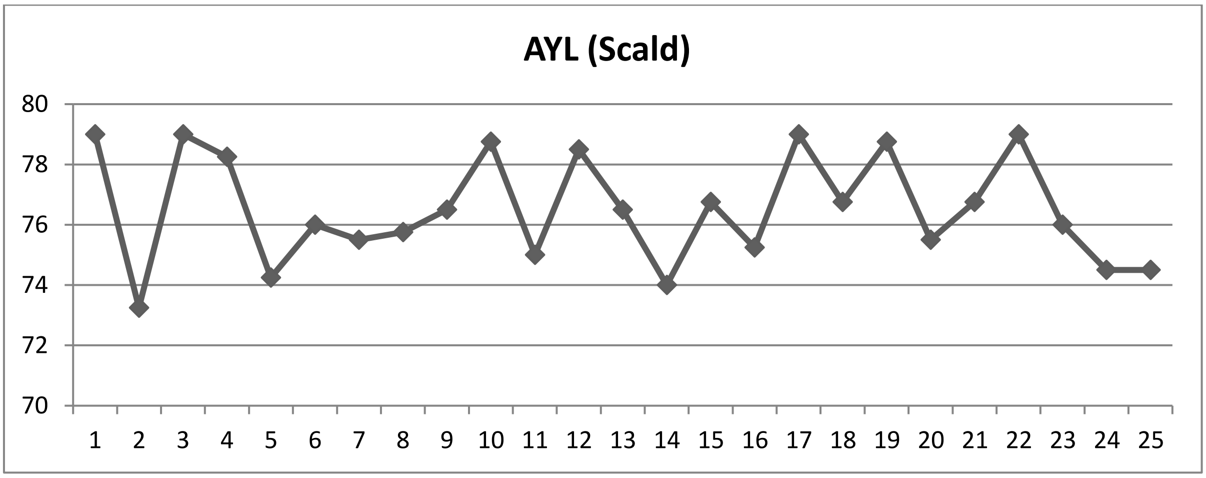

FIGURE 8
Mean comparison for Scald of barley genotypes in E13.
Tukey's HSD of Scald for E13= 4.088

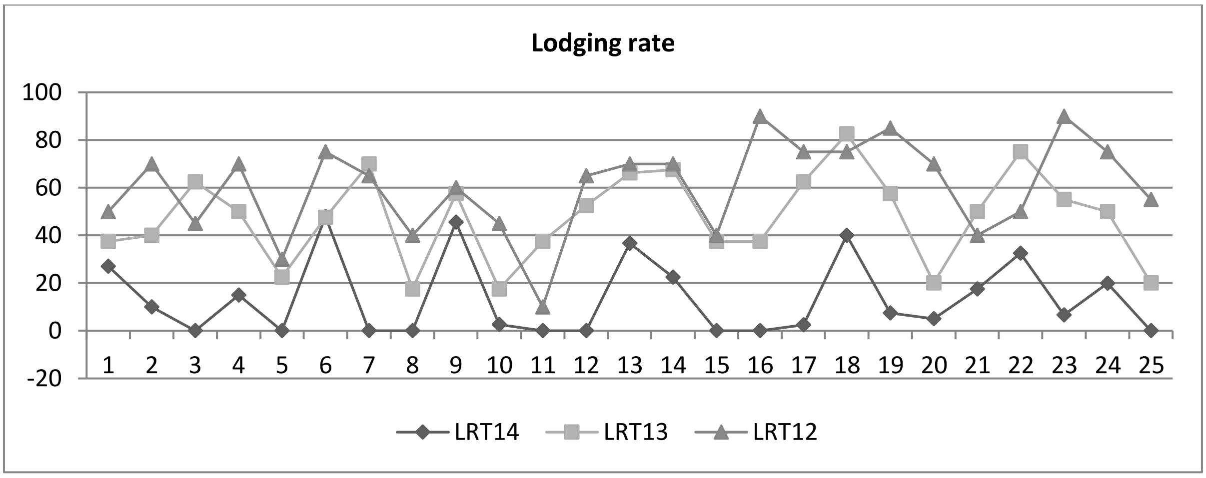

FIGURE 9
Mean comparison for lodging rate of barley genotypes in combined environments.
Tukey's HSD of LRT for HSD_{GxE}= 56.26 %

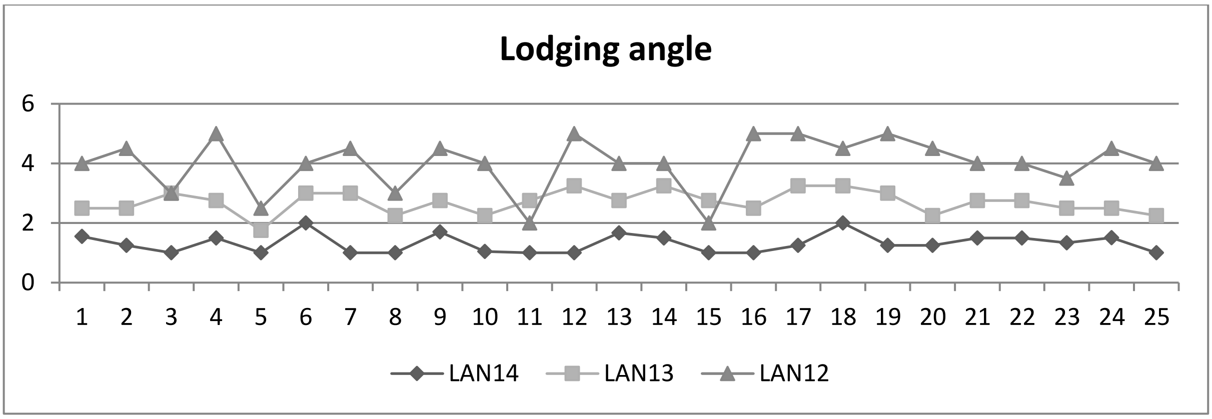

FIGURE 10

Mean comparison for lodging angle of barley genotypes in combined environments.

Tukey's HSD of LAN for HSD_{GxE}= 1.694

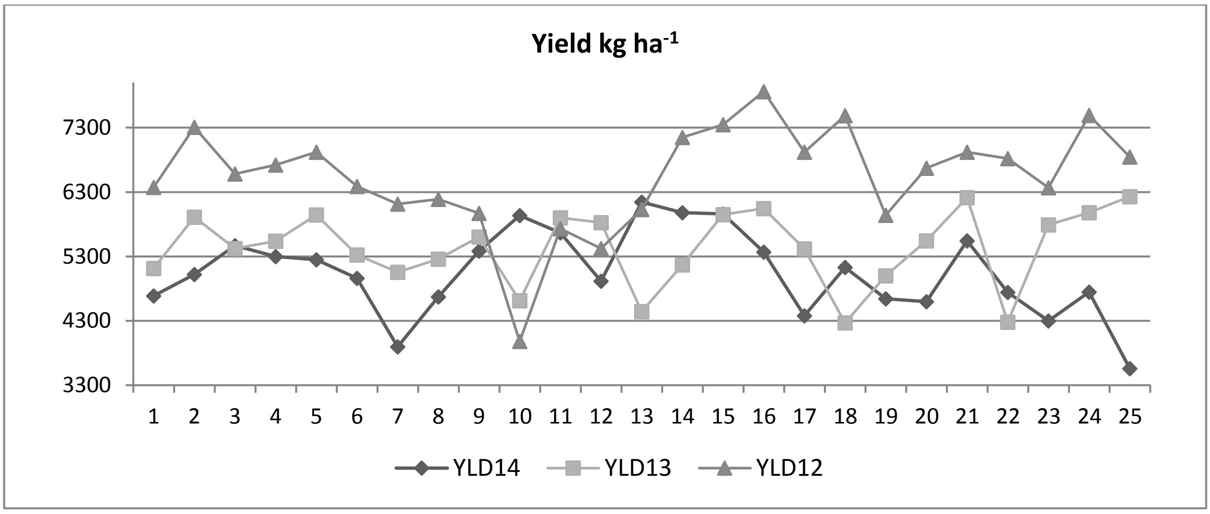

FIGURE 11

Mean comparison for yield of barley genotypes in combined environments.

Tukey's HSD of YLD for HSD_{GxE}= 1.940 kg ha^{-1}

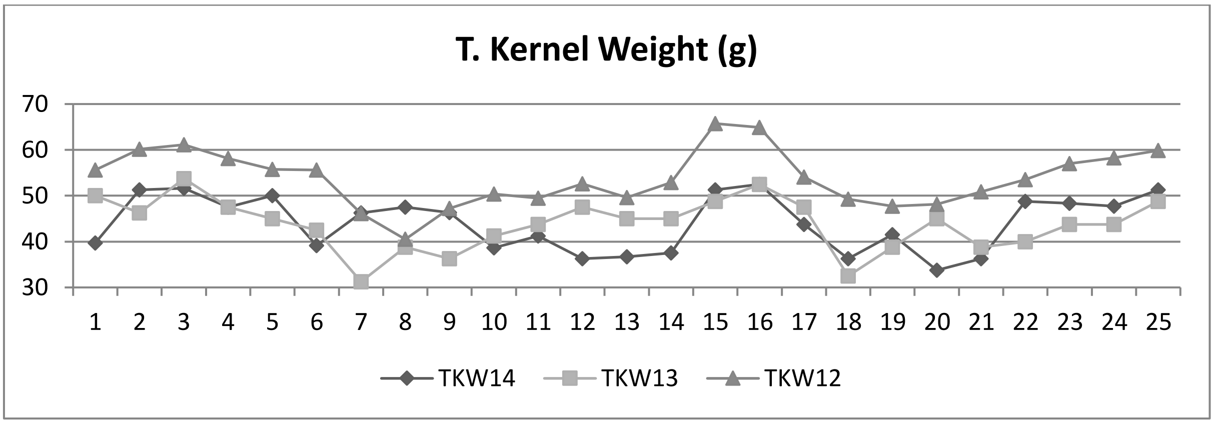

FIGURE 12

Mean comparison for TKW of barley genotypes in combined environments.

Tukey's HSD of TKW for HSD_{GxE}= 14.02 g

Most of the lines including G1-7, G8-9, G11-13, G15, and G19 were stable in YLD. However, except for G21, all cultivars were sensitive to different environments. The highest and the least yield values were obtained in E12 and E14, respectively. The highest YLD was obtained from G16 (7861 kg/ha) in E12 while the lowest was from G25 (3557 kg/ha) in E14. Interestingly, G10 was significantly higher in YLD in E14 (5934 kg/ha), which is the driest environment, than in E12 (3979 kg/ha), which was the high yielding environment.

TKW values for barley genotypes are given in Fig. 12.

The higher TKW mean was measured during E12 while E13 and E14 resulted in similar TKW. The highest TKW was obtained from G15 (65.75 g) in E12 and the least was from G7 in E13. However, G7 (46.25 g) had significantly higher TKW in E14, the driest environment, than in E13.

Averages of 3-year barley genotypes of hectoliter weight given in Fig. 13.

Significantly higher HWT mean was found in E12 (68.53) compared to E14 (64.07) and E13 (59.78) (Duncan's critical range <1.0, p<0.05). The HWT values of lines were also comparable to standard cultivars in combined environments. The highest HWT was obtained from genotype 5 (68.92) in 2012 and the lowest was from genotype 4 (55.2).

PR of barley genotypes are given in Fig. 14.

Protein values were significantly higher in E14 (15.87) than in E12 (15.11) and in E13 (14.31) (Duncan's critical range <0.32, p<0.05). The PRT values also varied among genotypes and the highest was 19.41 from G12 in 2012 and the lowest was 13.21 from G21 (standard cultivar) in 2013.

STR values of barley genotypes are given in Fig. 15.

In general, STR values were found to be the lower in E12 compared to E13 and E14 which appeared to be similar (Fig. 15). The highest STR value was obtained from G5 (64.43 g) in E13 while the lowest was from G11 (48.68 g) in E12. In three environments G17, G23, G24 and G25 appeared to be similar while other genotypes significantly differed at least in two environments.

FBR values for barley genotypes are given in Fig. 16.

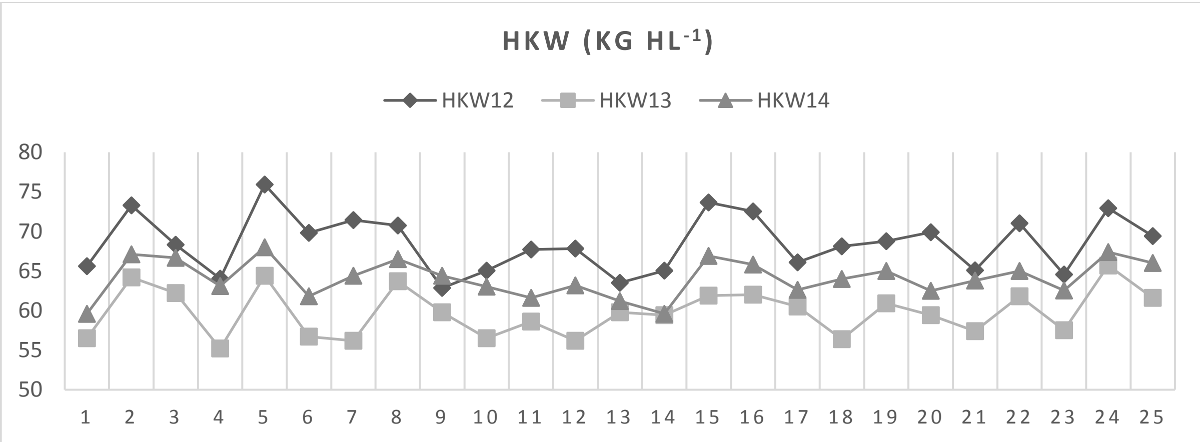

FIGURE 13

Mean comparison for hectoliter weight of barley genotypes in combined environments.

Tukey's HSD= 4.25 gr

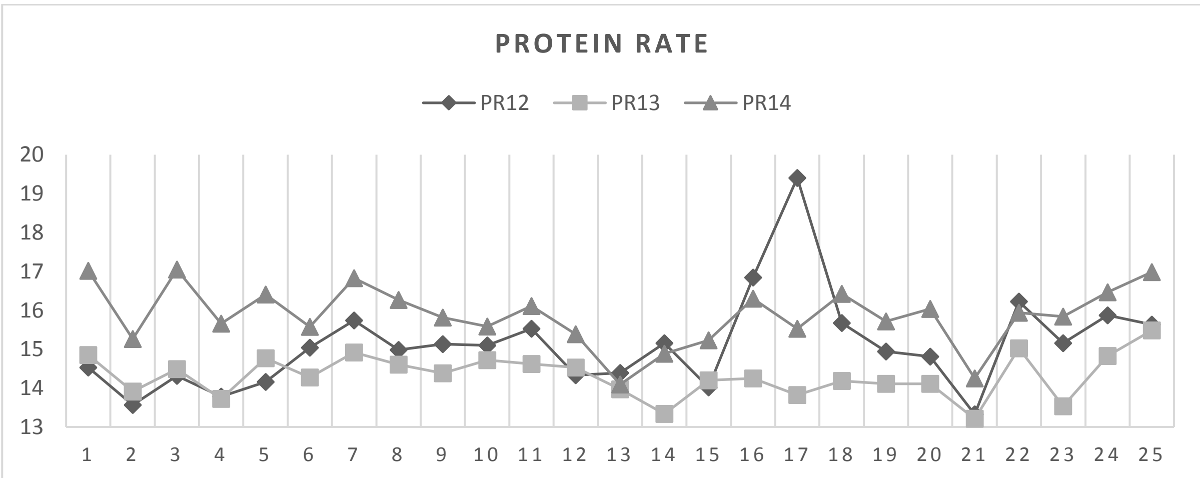

FIGURE 14

Mean comparison for PR of barley genotypes in combined environments.

Tukey's HSD GxE= 4.25%

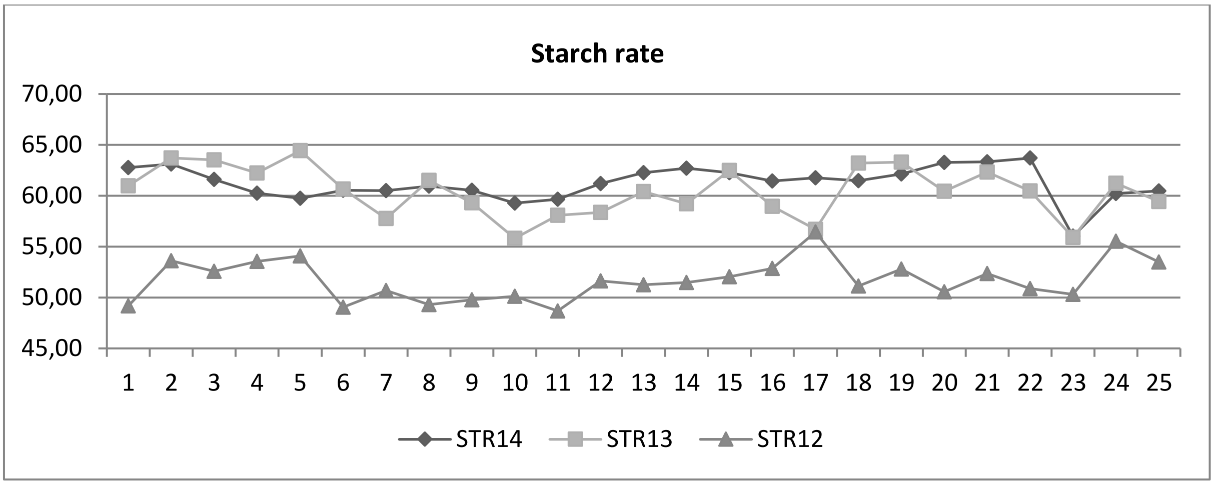

FIGURE 15
Mean comparison for % STR values of barley genotypes in combined environments.
Tukey's HSD of STR for HSD_{GxE}= 6.963 %

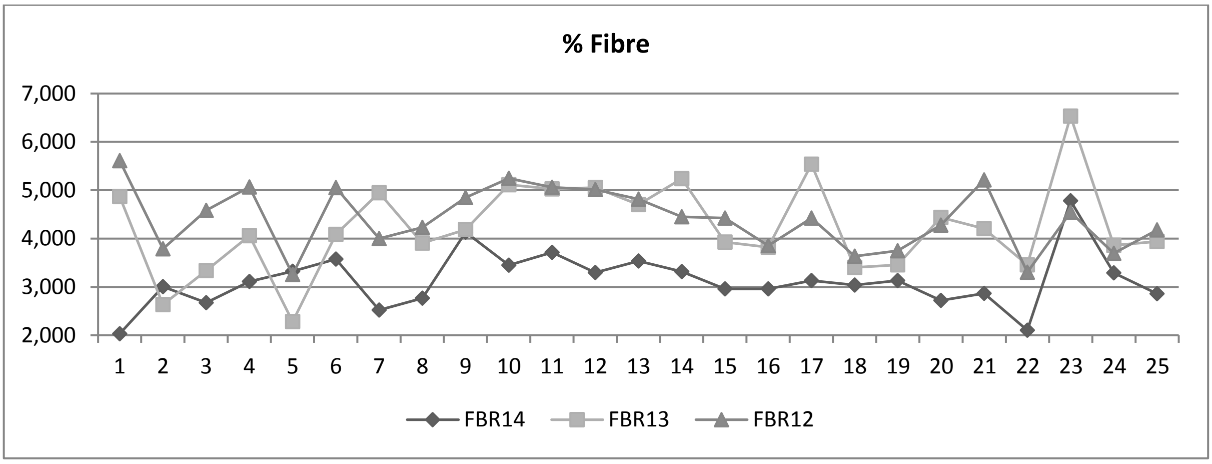

FIGURE 16
Mean comparison for % FBR values of barley genotypes in combined environments.
Tukey's HSD of FBR for HSD_{GxE}= 2.277%

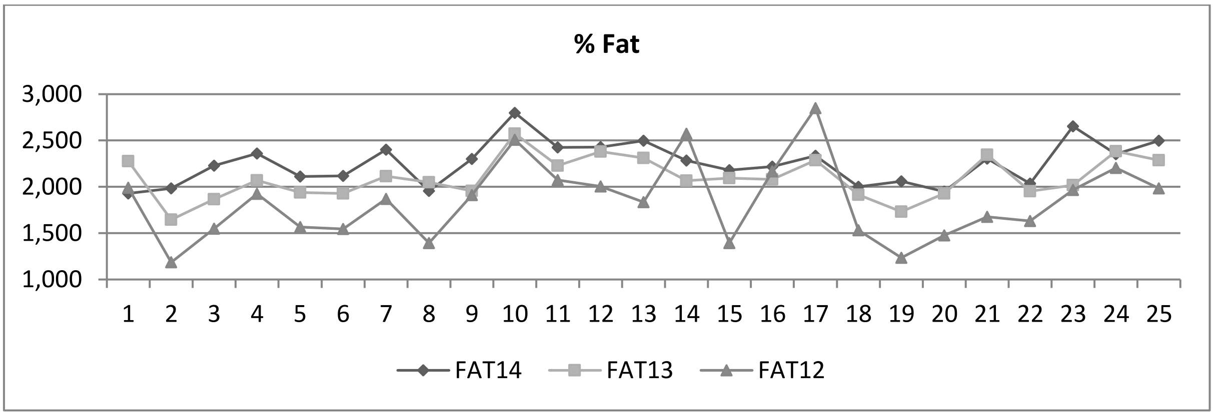

FIGURE 17
Mean comparison for % FAT values of barley genotypes in combined environments.
Tukey's HSD of FAT for HSD_{GxE}= 0.629%

The values of FBR were generally lower in E14 and the lowest FBR was obtained from G1 (2.03 g) while the highest was from G23 (6.53 g) which also was higher in three environments (Fig.16). Although, the FBR values in E14 were low in general, all the genotypes were similar in FBR values except

G1 in E12, G7 in E13, G17 in E13 and G21 in E12, which was significantly higher than E14.

FAT values of barley genotypes were given in Fig. 17.

Similar to STR, FAT values were the lowest in E12 (Fig. 17). Across environments, significant differences were observed in G2, G8, G13, G15, and G19. G15 was significantly lower in E12 (1.395 g) compared to E13 (2.100 g) and E14 (2.180 g). On the contrary, FAT values of G23 was significantly higher in E14 (2.653 g) than in E12 (1.965) and E13 (2.020 g).

DISCUSSION

The study was conducted at a typical Eastern Mediterranean climate. The major limitation to have higher yield in Mediterranean environment is water availability [10] and therefore, any superior germplasm under these conditions may carry some positive drought tolerance traits. Many studies on drought tolerance of crops indicate that different mechanisms may be relevant at different productivity levels [11]. Mediterranean region usually receives rain during December and January and is expected to have higher temperature trend which makes the region vulnerable to global warming [4]. Indeed, there existed dramatic climate change as E12 and E13 had the higher rainfall than E14, therefore, E14 was considered as a better selection environment for drought tolerance of barley genotypes used in this study. Selection environment is vital for breeders who even develop new strategies such as distributing early segregating populations to other breeders or farmers [12]. This strategy seemed to be useful when the number of different target environments are large to select suitable genes in each specific target environment [13].

Almost all traits were significantly different in E14 due to dramatic reduction of rain. However, water is not the only factor affecting yield and there are several other environmental influences since optimum response to water limited yield potential was found to be 20 kg ha^{-1} [14]. In our study, preceding crop before barley was maize in E14 which was dramatically reduced yield. Relatively high yield and yield component traits were observed when preceding crops in E12 and E13 were peanut and chickpea, respectively, which are known to boost growth and development of cereals by fixing nitrogen to soil [15]. When preceding crops were a cereal before barley, yield and component traits were reduced compared to legume rotation [16]. Therefore, E14 was the poor and driest environment compared to other two, and appeared to be the best selection environment for drought stress. Average of standard cultivars out yielded those of foreign genotypes by %6 in E12 and E13 while foreign genotypes out yielded standard cultivars by %11 in E14. Average yield of standard cultivars was less than those of 18 genotypes. Similar findings were reported for local landraces which were superior over modern cultivars in stressed environments [17]. While other most modern cultivars were superior to landraces in non-stressed environments [18]. Interestingly, G10 and G13 had the highest YLD on lowest yielding environment in E14. On the other hand, G25 appeared to be sensitive to water stress since it was the lowest yielding genotype in E14, it was relatively high yielding in other two environments. In terms of stable yield, G11 had similar YLD in three environments.

In addition to genetic variability, correlation analysis between quantitative traits of any crop is of major significance for successful selection, since selecting for a certain trait may negatively influence the expression of other traits. We found significant phenotypic correlation among quality traits. Yield and its component traits are mostly positively inter-correlated. However, YLD was negatively correlated with most quality traits except PRT and a negative correlation between YLD and PRT was reported earlier [19]. A negative significant correlation between grain yield and maturity was expected since long maturity periods increase the plant growth and might reduce the productivity [20]. However, a positive correlation between PHT and HDD indicates that enhanced plant growth requires more time for heading. A positive correlation was also expected between PHT and LAN, and LRT since as the plant gets taller it may not hold the spike and lodging will be inevitable. The positive correlation of PHT with YLD, TKW and HWT suggests that plant stature increases the productivity [21, 22]. A positive correlation among YLD, LRT and LAN may be because of large spike size rather than plant height. Contrary to earlier findings [22, 23], a negative correlation between MTR and HDD may be attributed to strong genotype by environmental interaction or as the weather gets hot plants, which are headed earlier, tend to go maturity faster. Lodging appeared to be higher in rainy and legume preceded environments. A significant positive correlation between lodging variables and YLD indicates that lodging did not reduce the yield [24]. In general, higher grain size in barley is expected to result in higher starch content [25]. In the present study, however, TKW and HWT are negatively correlated with STR probably because large numbers of six-rowed barley genotypes, which are assumed to have high protein content. Scald disease damage was higher as the plant height and lodging values increased. This indicates that taller plants are vulnerable to the disease.

Principal component analysis well characterized the environments in which genotypes showed significant variation. It seems that dramatic climate and soil changes in environments clearly separated the genotypes and affected their variation differently in each environment. The two principal components accounting about 60% of the total variation to separate the barley genotypes with respect to environments. The first principal component differentiated the barley genotypes with respect to PHT, LRT and LAN. Excessive plant height is not desired since plant height positively correlated with LRT and LAN and is widely used as an indirect selection criterion where E12 seemed to be a better environment for such selections. The first principal component was negatively correlated with MTR and STR in suitable environment of E14. Maturity period is significant since barley is grown during winter months [26]. Starch content negatively correlates with protein content [25]. The second principal component differentiated barley cultivars on HDD, TKW HWT, PRT, AYL (SCALD) and STR. The E14 is suitable selection environment for HDD and TKW whereas E13 is suitable for AYL (SCALD), which was mainly observed and scored in E13. Although no genotype was found to be resistant against AYL (SCALD), the genotypes which was longer MTR, higher HWT and PRT seemed to have reduced disease intensity. Therefore, E13 was the best selection environment for AYL (SCALD) resistance of barley.

The variance analysis showed that there were large differences among genotypes and a strong genotype x environment interaction existed for most of the traits. Our results showed that the lines used in the present study can compete with standard cultivars in terms of these three traits suggesting a possible use for breeding. Variation on PHT and HWT was independent of environments, and the shortest lines were G8 and G20 which were significantly shorter than the tallest cultivars G21, G23, and G25. [23], also found no genotype x environment interaction for PHT. It is interesting that G18, G19 and G20 are sister lines, however, G18 and G19 was similar in plant height with G21, G23 and G25 while G20 was not. It may be possible that G20 contains some dwarfing genes. Similarly, there were lines which was as high in HWT values as standard cultivars. The lines G2, G5, G8, G15 and G16 was significantly higher in HWT than cultivar G23. The lines and cultivars, which was extreme in values, may be used for mapping population related to PHT and HWT traits.

Significant G x E caused some genotypes responded to differently in different environments. Significant GxE findings reported for barley genotypes grown in drought stressed and non-stressed conditions [27], [28]. In terms of YLD, G10 had the highest YLD in the poorest E14 compared to E12 and E14 indicating that this line is promising for drought tolerance as well as planting after maize. It was also appeared that G25 is the most sensitive cultivar to drought and out yielded majority of the genotypes. [29], also identified G25 as high yielding cultivar for Mediterranean climate. Yield was the lowest heritability value (about %10). In varying 28 Mediterranean environments heritability values ranged from 0.00- 0.83% with an average of 46% [18]. Therefore, indirect selection criteria should be the best strategy for breeding programs.

The longest HDD values were obtained in E12 which received rainfall from November to March indicating that long term rain extended the heading time. Although less HDD variation was observed in E12 and E14, variation among genotypes was larger in E14. Conversely, E14 had the largest MTR values and variation among genotypes. Large variation among environments resulted in higher residual effect and lower heritability value for HDD and MTR. Therefore, selecting the genotypes, in the present study, for these two traits in poor environments may be useful.

The genotypes used in this study showed great variation in terms of TKW in each environment and were affected by environment greatly. Significant GXE interaction was found on barley cultivars in line G7 in E14 as high TKW value as in E12 and significantly higher TKW than in E13 was observed. Although there was no significant difference, G8 out performed in E14 compared to E12 and E13. Thousand kernel weight is a significant component of yield and could be used as an indirect selection criterion due to its higher heritability value than that of yield. Interestingly, except G1, all cultivars were higher in TKW values in E14 than in E1 and E13 suggesting that these cultivars can be used to improve TKW in breeding programs for drought tolerance.

As expected, LRT and LAN values were significantly positively correlated and great variation existed among genotypes. As expected, both traits generally were higher in values in rainy environments i.e. E12 and E13. Large difference in environments probably resulted with larger standard error and also variation among genotypes in LRT seems lower than in LAN. It also caused moderate level of heritability values. Considering three environments, G6, G9, G13 and G18 seemed more sensitive to lodging while G5, G11 and G15 appeared more tolerant.

Scald disease only observed in E13 probably due to rainy conditions in this year between November and January followed by hot and dry period which may fit well for disease emergence. Even though data were obtained in E13, no completely resistant source was observed; there was great variation among genotypes in terms of scald tolerance. Due to lower disease scores (=<75), G2, G5, G11, and G14 seemed to be more tolerant than other lines while G24 and G25 was more tolerant than other cultivars.

Variation on PRT was independent of environments. PRT was big for most of the lines, except line G21 had significantly lower PRT than the cultivars G22, G24 and G25. Barley cultivars generally shows no genotype by year interaction in terms of PRT and other quality traits such as FAT, FBR and STR in

Mediterranean environment [29]. Contrary to the results of [29], in our study, quality traits such as FAT, FBR and STR were also strongly affected by genotype by environment interaction. FAT and STR showed similar pattern in that they had generally higher values in E14. Variation for FAT seemed larger than that for STR. There is significant positive correlation between two, and heritability of FAT was higher than STR suggesting that FAT is useful for selecting for yield. G15 and G19 seemed to have lower fat in rainy environments and can be promising in selecting for yield as well. Conversely, FBR had lower values in E14 than in E12 and E13, however, large variation existed among and within environments.

Lodging rate values of G5, G8, G11 and G15 were similar and they seemed to tolerate lodging since difference was insignificant in the three environments (Tukey HSD GxE= 56.26, p>0.05).

G18 was found to have decreasing STR in E12 (51.13 g) while it tended to increase in E13 (63.21 g).

G5 had similar FBR values and was found to have the higher FBR (3.32 g) value in the dry environment of E14 than in E12 (3.23 g) and E13 (2.28 g).

In the present study, some barley lines appeared to carry useful alleles for stable yield and quality traits. The results of this study will be helpful for barley breeders and farmers to improve and make use of barley cultivars adaptable for Mediterranean environments.

CONCLUSION

If barley is preferred prior to second crop, harvest of it starts in beginning of May, approximately 1 month earlier than wheat. This may result with less injury of disease and insect compare to wheat and improvements of grain yield of second crop. Varying environmental conditions should be a better strategy for improving stable barley cultivars in unpredictable and drought prone Mediterranean environments.

13 lines and one cultivar of tested 25 genotypes were stable at yield over three environments. Results showed that YLD was mostly correlated with PHT, MTR and FBR. All traits except PHT, HWT and PRT were significantly affected by genotype x environment interaction. The highest yielding genotype was G16 in 2012. While G10 was the highest yielding genotype in drought conditions of 2014. All lines competed well with cultivars over three environments. In the present study, some barley lines appear to carry useful alleles for stable yield and quality traits. The results of this study will be helpful for barley breeders and farmers to improve and make use of barley cultivars adaptable for Mediterranean environments.

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