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IDENTIFYING BARLEY GENOTYPES FOR OPTIMUM INPUT CONDITIONS IN THE WANA REGIONS

ABSTRACT

Barley (*Hordeum vulgare* L.) is an important cereal crop for its high demand for grain feed and forage/ grazing for the animals as well as for human food in the WANA region under the low rainfall situations and thus creating an urgent need for developing high yielding barley genotypes. A total of 542 hulled and hulless genotypes with seven checks were evaluated at three locations with diverse agro-ecological conditions, Terbol in Lebanon and Marchouch and Allal Tazi in Morocco. The aim of this study was to understand the nature of genotype × environment interaction (GEI), quantify the genotypic variability and identify high yielding genotypes. The mixed models were fitted to evaluate heritability and predicted means to identify genotypes with specific adaptation to the locations using GGE -biplot. GEI across locations was significant for days to heading, days to maturity, plant height, spike length and grain yield. On a trial-wise analysis, days to maturity was most heritable (49 – 50% broad sense heritability on mean basis) while the grain yield was the least (5 – 13%). The genotype G427 (4812 kg/ha) at Marchouch, the check VMorales (4889 kg/ha) at Allal Tazi and G528 (6995 kg/ha) at Terbol were the highest yielding genotypes. Several hulled and hulless genotypes with higher grain yield and early flowering time in the three environments were identified for utilization by the national programs globally. The test locations, Marchouch and Allal Tazi, were found comprising one mega environment while Terbol showed maximum discrimination of genotypes for grain yield.

Keywords: Barley (*Hordeum vulgare* L.), GGE-biplot, grain yield, optimum input conditions

INTRODUCTION

Barley (*Hordeum vulgare* L.) is the fourth important cereal crop after maize, wheat and rice globally cultivated in an area of 49.8 m ha producing 144.8 m tones barley with 2.91 t × ha $^{-1}$ productivity (FAOSTAT 2014). The gain in productivity of barley has not been quite visible despite the continuous efforts from breeders especially in the West Asia and North Africa regions, primarily because of the rainfed cultivation being practiced in these

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two regions with less input management. (FAOSTAT 2014). There is an increase in demand of barley for higher yields with better grain/ straw quality for feed, forage food and malting in the regions with optimum rainfall or limited irrigation conditions (Verma *et. al.* 2005). Similar situation has been observed in other ICARDA mandate regions of East Africa and South Asia, where barley grain for feed, food and industrial raw material is be-coming increasingly important. There is a need for barley genotypes with better performance under different management conditions of water and nutrients to increase grain yield with better grain quality as well as the in-come of smallholder farmers across. This has become much more important under the current situation of the reduction in barley area in developing countries (FAOSTAT 2014) because of limited gain in productivity (as basically it has been treated as low input crop for marginal /problematic soils) and lack of government support for pricing and procurement policies.

Genotype (G) by environment (E) interaction (GEI), defined as the differential genotypic expression across environments, reduces genetic progress in breeding programs by minimizing associations between phenotypes and genotypes and complicates testing and selection of superior genotypes (Voltas *et al.* 2002; Comstock and Mall, 1963) . De Kroon and van der Laan (1981) defined two types of GEI: quantitative or non -crossover interaction and qualitative or crossover interaction. Quantitative interaction represents a change in magnitude of differences among the genotypes in different testing locations without any rank changes. Change in rank orders or crossover interaction (or qualitative interaction) is the most important in plant breeding, because it prevents the prediction of genotypes performance in different locations. In presence of this last type of GEI, the way to increase genetic gains is the identification of specifically adapted genotypes. Consequently, the type of GEI plays an important role in identifying the genotypes suitable either for specific or broad adaptation.

The development of barley genotypes for specific regions as well as across a wide range of regions/ environments is the primary objective of the ICARDA barley breeding program. There is a need of both kind of genotypes to obtain more yield in specific environments as well as to have genotypes with wide adaptation for yield and other traits. The barley breeding program at ICARDA was developing genetic materials, with increased grain yield, suitable for its mandate regions of north and east Africa, west, central, west and south Asia, in Syria utilizing the well classified locations available there. However, the recent conflicts in Syria has made it essential to evaluate the genotypes in other agro-ecological environments, such as Morocco, and Lebanon to address its primary requirements of sharing of improved barley germplasm with national barley programs in the different regions.

Grain yield (GY) is a combined effect of G, E and GEI but in genotypes evaluation only G and GEI are relevant and thus taken into account. The GGE-biplot methodology, proposed by Yan (1999), graphically displays genotypic main effects (G), main effect plus GEI of multi environment trials and facilitates visual cultivar evaluation. In this work we used this

methodology to investigate G and GEI across the three new ICARDA's testing locations. Flowering time is one of the most important adaptive traits in plants and its genetic regulation acts to ensure that it occurs at seasonal optima for pollination and seed development. It also determines the duration of other crop developmental phases (vegetative, reproductive and grain filling) and, indirectly, the number of tillers/effective spikes and spikelets/grains that contribute to final yield. In those environments characterized by low erratic rainfall during spring and early summer flowering time often became one of the main determinants of GY because the duration of crop cycle affects the timing and intensity of the stress experienced by plants. Maturity also plays an important role on GY determination in those environments, where drought stress often occur from the beginning of the anthesis to maturity, therefore a combination of early heading and maturity is desirable in semi-arid conditions. Both plant height (PLH) and spike length (SL) are significantly correlated with GY as reported by Singh *et al.* (1987), furthermore SL is related with direct yield components such as grain numbers per spike and grain weight. To identify high yielding barley genotypes adapted to optimum inputs, eight sets of high input barley geno-types (six sets comprising of hulled and two sets of hulless grain), were evaluated at three locations ie. Marchouch (MCH) and Allal Tazi (ALT) in Morocco and Terbol (TRL) in Lebanon. Understanding the presence and nature of genotype × location interaction, quantify the genotypic variability, and heritability, identify high yielding genotypes with broad or specific adaptation to the locations, and identify high yielding genotypes were the other objectives in addition to identify the locations with ability to discriminate the barley genotypes.

MATERIALS AND METHODS

Experimental sites

The genetic materials (barley genotypes) were evaluated during 2013 -14 at three locations MCH (33°56' N, 6°63' W), 255 m above sea level (ASL) with 350 mm average annual precipitation and, situated in the central region of Morocco and is characterized by a mid-season length and by final heat and drought stress; ALT (34° 52' N, 6.32 W), is situated in the same region of Morocco at 11 m ASL with 450 mm average annual precipitation and is characterized as high disease pressure site for the main barley diseases; TRL, (33^{o}49' N, 35^{o} 59' E), 950 m ASL, with 519 mm average annual precipitation in Lebanon. TRL is warm -temperate location and is characterized by dry and cool summers. Thus, there were three locations used for evaluation of the same set of genetic material. However, the genetic materials were grouped in hulled and hulless barley to cover the evaluation of a much larger number of genotypes.

Experimental designs

Six trials (Trial 1 -6) of hulled barley, each comprised of 75 genotypes and 5 checks (Assi, Harmal, Rihane-03, VMorales and WI 2291) and one trial (Trial 7) of hulless barley materials comprised 73 genotypes and seven checks (Atahualpa and Himalaya 12 in addition to the above five hulled checks) were evaluated in alpha design with blocks of size 10 and two replications. The other trial of hulless barley (Trial 8) comprised 19 genotypes and six checks, was conducted in 5 × 5 simple lattice design. The set of test materials (i.e. other than checks) differed over the trials, but the five checks were common across all the sets of hulled type, while in hulless bar-ley Trials 7 and 8, six checks were common. Every set of material was evaluated at each of the three locations. Further details on the genotypes are available on request. Each genotype was planted in 2.5 m long six -row plots with a distance of 30 cm between rows. The sowing was done between 25 November and 15 December 2013, and harvested between10–25 June 2014 depending upon location. Grain yields (GY) were recorded on the net plot harvested and converted to kg × ha^{-1} for statistical analyses. Other traits recorded were days to heading (DH, days; from sowing date), days to maturity (DM, days; from sowing date), plant height (PLH, in cm on five plants per replication) and spike length (SL, in cm on five plants per replication).

Statistical methods

Individual trials, for each trait, were analyzed using plot -wise data from all the three locations and the variance components for genotypes (σ^2_g) and genotype × location interactions (σ^2_{gl}) were estimated using the restricted maximum likelihood (REML) method after accounting for the assumed random effects of the replications within locations and incomplete blocks with-in replications within locations. The locations effects were assumed fixed. Furthermore, the genotypic variation was partitioned into the variation due to test entries (σ^2), check entries (with effects assumed fixed) and a factor *test* test vs. check (assumed as fixed effects, due to large number of test entries). The interactions with locations were assumed random. Assessment of genotypic and interaction variances was carried out for significance using normal approximation of their estimates divided by the respective standard errors. The computational codes were written using Genstat statistical software (Payne, 2014) and are available on request. The function code, VFUNCTION of the Genstat software was used to estimate broad - sense heritability:

$$h^2 = \frac{\sigma_g^2}{\sigma_g^2 + \frac{\sigma_{gl}^2}{L} + \frac{\sigma_e^2}{rL}}$$

on mean basis, where,

σ_e^2 is plot-wise error variance,

r stands for number of replications (2) and

L for the number of locations (3) (Kempthorne, 1983).

For genotype selection, we are interested in assessing the performance of genotypes across all the trials, rather than individual trials, the availability of common checks provided that adjustment when the plot-wise data, of a given type say hulled -barley, were analyzed. The estimation procedure accounted for the trials differences, blocks and replication differences within trials within locations, genotypes within trials and their interactions with locations. The heritability, using the above expression, was estimated for the genotypes and location data over all the trials combined. The mean performances of the genotypes, at different locations or over all the locations, were estimated as the best linear unbiased predictor (BLUPs), and were used for selecting the genotypes for specific or broad adaptation.

Specific adaptation of genotypes to locations was assessed in terms of the genotypes performance overall the locations and adding the specific environment effect as GEI, denoted as GGE and presented as GGE-biplot. In this study there is a large number (542) of genotypes, their representation in GGE biplot would crowd the plot. Furthermore, since poorly performing genotypes in all the locations are not of interest, we removed them from the plot, setting an option for cutting at 50 percentiles in the Genstat software.

RESULTS

Genotypic variability and genotype × location interaction in individual trials

As can be expected slightly lower variability and hence higher P-value were be found in Table 1 for genotypic differences and G × L interaction arising from only the test materials, i.e. without including the common checks. Out of the 6 trials in hulled barley, G × L interactions were found significant in all the 6 tri-als for DH, DM and PLH, in 4 trials for GY (with or without checks), 5 trials for SL (including checks) and in 3 trials with only test entries. The variability in the genotypic material, with or without checks, was found significant ($P<0.05$) in all the trials for SL, 5 trials for DH and DM, 2 trials in PLH, while for GY in 1 trial with tests only and 2 trials with all the genotypes. Thus in some traits, genotypic variability was affected by inclusion of the checks.

In case of hulless materials, G × L interaction was found significant in both the trials for DH, PLH and SL, and in 1 trial for DM and GY. Genotypic variation was significant in only one of the two trials for DH, DM, SL and GY, while non-significant for PLH in both the trials. This indicates that the significance of the response of different sets of genotypes to the locations varied with the trials and type of the material (hulled vs. hulless).

Table 1

P-values indicating significance of variation due to genotypes and G × L interactions in individual trials for the five traits

Trait	Genetic material	Source	Hulled Trials						Hulless Trials	
			1	2	3	4	5	6	7	8
DH	All	σ^2_g	0.0004	0.0018	0.0057	0.0018	0.0336	0.0003	0.0014	0.1220
		σ^2_{gl}	0.0053	0.0000	0.0000	0.0000	0.0000	0.0000	0.0004	0.0032
	Tests only	σ^2_{test}	0.0003	0.0021	0.0088	0.0031	0.0601	0.0010	0.0011	0.3126
		σ^2_{tl}	0.0085	0.0000	0.0000	0.0000	0.0000	0.0000	0.0008	0.0139
DM	All	σ^2_g	0.0231	0.0066	0.0535	0.0122	0.0237	0.0101	0.0200	0.0925
		σ^2_{gl}	0.0051	0.0002	0.0036	0.0000	0.0000	0.0000	0.0000	0.1663
	Tests only	σ^2_{test}	0.0264	0.0076	0.0583	0.0174	0.0206	0.0116	0.0243	0.2791
		σ^2_{tl}	0.0039	0.0013	0.0028	0.0000	0.0000	0.0000	0.0000	0.1020
PLH	All	σ^2_g	0.0974	0.3296	0.1280	0.3533	0.0146	0.0002	0.0668	0.2391
		σ^2_{gl}	0.0063	0.0135	0.0031	0.0011	0.0000	0.0003	0.0265	0.0000
	Tests only	σ^2_{test}	0.1551	0.2449	0.1104	0.3248	0.0398	0.0003	0.1609	0.3195
		σ^2_{tl}	0.0059	0.0326	0.0028	0.0010	0.0000	0.0003	0.0137	0.0000
SL	All	σ^2_g	0.0031	0.0014	0.0151	0.0024	0.0037	0.0006	0.0287	0.3311
		σ^2_{gl}	0.0013	0.0128	0.0006	0.0331	0.2158	0.0097	0.0001	0.0000
	Tests only	σ^2_{test}	0.0051	0.0005	0.0184	0.0017	0.0047	0.0018	0.0890	0.0000
		σ^2_{tl}	0.0093	0.1166	0.0017	0.1651	0.3754	0.0077	0.0002	0.0000
GY	All	σ^2_g	0.1834	0.0000	0.3452	0.3103	0.1183	0.0000	0.2054	0.0000
		σ^2_{gl}	0.3386	0.0175	0.0010	0.0000	0.0104	0.1940	0.1246	0.0000
	Tests only	σ^2_{test}	0.3091	0.0000	0.4359	0.2444	0.1418	0.4945	0.3837	0.0000
		σ^2_{tl}	0.3290	0.0124	0.0014	0.0000	0.0082	0.2003	0.1644	0.0000

GY= grain yield, DH= days to heading, DM= Days to maturity, PLH= Plant height (cm), SL=Spike length. σ^2_g, σ^2_{gl}, σ^2_{test}, and σ^2_{tl}, respectively, are variance components due to genotypes, genotype × location interaction, test genotypes only and test genotype × location interaction.

Table 2

Estimates of variance components, and heritability in the six (hulled) and two (hulless) yield trials across the three test locations.

Test / All genotypes	Traits	DH		DM		PLH	
		H	HL	H	HL	H	HL
	Trial mean	93.0	93.8	134.9	134,0	96.2	96.0
	CV (%)	3.6	4.9	2.2	2.7	7.6	7.5
All genotypes	σ^2_g	4.15	5.79	2.19	2.22	5.99	3.29
	SE(σ^2_g)	0.612	1.717	0.416	0.964	1.386	2.255
	P-value(σ^2_g)	6.2E-12	0.000371	7.23E-08	0.010526	7.76E-06	0.072407
	σ^2_{gl}	7.08	6.39	5.65	5.21	9.99	5.34
	SE(σ^2_{gl})	0.674	1.882	0.529	1.300	2.054	3.836
	P-value(σ^2_{gl})	0	0.345×10^{-5}	0	3.05E-05	5.73E-07	0.08195
	σ^2_e	11.25	21.33	8.97	12.82	53.26	51.91
	SE(σ^2_e)	0.480	1.853	0.379	1.142	2.163	4.474
	σ^2_p	22.48	33.51	16.81	20.26	69.24	60.54
Tests only	σ^2_{test}	4.10	5.86	2.18	2.27	6.02	3.06
	SE(σ^2_{test})	0.617	1.828	0.421	1.036	1.415	2.387
	P-value(σ^2_{test})	1.56E-11	0.000671	1.08E-07	0.014257	1.05E-05	0.100005
	σ^2_{tl}	7.16	7.49	5.78	6.01	10.62	7.06
	SE(σ^2_{tl})	0.685	1.972	0.536	1.366	2.119	3.970
	P-value(σ^2_{tl})	0	7.27E-05	0	5.49E-06	2.7E-07	0.037736
	σ^2_e	11.25	20.05	8.84	12.03	52.49	50.48
	SE(σ^2_e)	0.480	1.787	0.379	1.061	2.167	4.310
	σ^2_p	22.51	33.4	16.80	20.30	69.13	60.59
All genotypes	h^2	0.49	0.50	0.39	0.36	0.33	0.24
	SE(h^2)	0.043	0.086	0.051	0.112	0.057	0.135
Tests only	h^2	0.49	0.50	0.39	0.36	0.33	0.22
	SE(h^2)	0.044	0.090	0.052	0.118	0.058	0.144

Table 2

Continued

	Traits	SL		GY	
		H	HL	H	HL
Test / All genotypes	Trial mean	8.52	8.71	5005	4243
	CV (%)	15.0	16.6	19.9	24.4
All genotypes	σ_g^2	0.34	0.18	10105	26932
	SE(σ_g^2)	0.053	0.104	18041	33239
	P-value(σ_g^2)	6.79E-11	0.03865	0.287701	0.208897
	σ_{gl}^2	0.36	0.37	127264	1989
	SE(σ_{gl}^2)	0.060	0.161	34984	65447
	P-value(σ_{gl}^2)	1.07E-09	0.010388	0.000138	0.487878
	σ_e^2	1.63	2.08	995278	1075840
	SE(σ_e^2)	0.065	0.177	39768	89346
	σ_p^2	2.33	2.64	1132646	1104761
Tests only	σ_{test}^2	0.35	0.15	14409	5140
	SE(σ_{test}^2)	0.052	0.106	18844	30091
	P-value(σ_{test}^2	2.02E-11	0.078764	0.222241	0.432185
	σ_{tl}^2	0.26	0.49	134487	0.09521
	SE(σ_{tl}^2)	0.063	0.168	36732	0.006601
	P-value(σ_{tl}^2)	1.53E-05	0.001655	0.000125	0
	σ_e^2	1.66	1.91	984098	1072118
	SE(σ_e^2)	0.068	0.149	40005	74323
	σ_p^2	2.27	2.55	1132993	1077257
All genotypes	h^2	0.46	0.28	0.05	0.13
	SE(h^2)	0.044	0.125	0.080	0.146
Tests only	h^2	0.49	0.24	0.06	0.03
	SE(h^2)	0.044	0.138	0.081	0.160

H= hulled, HL= hulless. SE= Standard error, P-value computed as Prob [variable> variance component estimate/its standard error]. σ^2_{gl} σ^2_{test}, σ^2_{tl}, σ^2_e and h^2 is heritability in broad-sense and on mean basis

Standard normal $\sigma^2_p = \sigma^2_g + \sigma^2_{gl} + \sigma^2_e$.

Genotypic variability and genotype x location interaction from all the trials

The datasets from all the trials of each type were combined and genotypic and G × L estimates of variances components and heritability were calculated for six hulled trials and for the two hulless trials separately are shown in Table 2. Thus, two analyses were carried out one using Trials 1 – 6 and the other using Trials 7 and 8. Genotypic variance was significant for all traits except PLH in hulless trials and GY for both hulled and hulless trials. There were significant ($P<0.05$) G × L interactions for all the traits except for PLH and GY for hulless genotypes including checks. The G × L for these two types were significant when based on tests only, with relatively very small G × L interaction variance component for GY. There were substantial differences for the heritability for hulled and hulless materials for PLH, SL and GY. The heritability estimates in general were close whether only test materials were used or all. Considering all the genotypes, DH was most heritable with h^2=49 – 50% and GY was least heritable with h^2= 5 – 13%, for hulled and hulless material respectively.

Selection of best performing lines to specific location

Considering the number of genotypes evaluated as large, we have restricted to 10 most desirable genotypes for GY and five for DH and DM from hulled materials (Table 3) and 5 most desirable for the hulless in Ta-ble 4, nearly 5% intensity of selection. Tables 3 - 4 show the rankings of genotypes for GY, DH and DM in each specific testing location. Denoting the test genotypes as n, using a prefix G (i.e. genotype 101 is denoted as G101), the highest yielding accessions for GY were G427 (yield: 4812 kg × ha^{-1} at MCH), the check VMorales (4888 kg × ha^{-1} at ALT) and G528 (6995 kg × ha^{-1} at TRL). Genotypes with earliest heading were G470 (69.7 days at MCH and 85.0 days at ALT) and G305 (93.8 days at TRL), spreading over 24 days between MCH and TRL. Earliest maturing genotypes were G234 in 121.6 days at MCH, G547 in 125.8 days at ALT and G305 in 140.8 days at TRL, with a spread of 19 days between two extreme locations.

In the hulless genotype group, there was no significant GxL location interactions for GY and PH. Based on means over the three locations as well as at each location, the four hulless test entries G769 (4487 kg × ha^{-1}), G817 (4472 kg × ha^{-1}), G721 (4469 kg × ha^{-1}) and G709 (4465 kg × ha^{-1}) stayed within top five entries in overall basis as well as on each of the three locations. Himalaya12 was the best hulless check. The three hulled checks, Harmal (4546 kg × ha^{-1}), VMorales (4507 kg × ha^{-1}) and WI2292 (4490 kg × ha^{-1}) were slightly higher yielding then the better hulless entries. Geno-types with early heading were the check Himalaya12 (77.3 days at MCH), G704, G705 and G724 across the three locations on mean basis. Himala-ya12 was also earliest maturing (120.6 days) followed by G730, G775 and G704 on mean basis at three locations.

Table 3

Top hulled-type test genotypes and the best check on predicted means for grain yield, heading days and maturity at different locations from combined analysis over location

Location	Marchouch		Allal Tazi		Terbol		All locations	
	Genotype	Mean	Genotype	Mean	Genotype	Mean	Genotype	Mean
Grain yield (GY) (Top 10)								
1	G427	4812	G619	4869	G528	6995	G427	5314
2	G124	4806	G555	4785	G459	6796	G652	5275
3	G415	4770	G527	4734	G127	6765	G127	5268
4	G315	4767	G423	4733	G610	6713	G535	5260
5	G215	4752	G650	4701	G660	6695	G527	5259
6	G365	4735	G542	4687	G521	6678	G247	5257
7	G535	4730	G624	4675	G607	6678	G315	5231
8	G230	4718	G344	4662	G517	6677	G538	5223
9	G330	4701	G615	4648	G226	6668	G415	5222
10	G433	4699	G427	4646	G259	6664	G117	5218
Best check	Harmal	4609	VMorales	4888	Rihane03	6677	VMorales	5181
Av. SE				340				232
Av.LSD (5%)				916				557
Days to heading (top 5)								
1	G470	69.7	G470	85.0	G305	93.8	G470	85.3
2	G469	70.2	G475	85.3	G633	93.9	G475	85.5
3	G472	70.7	G474	86.0	G312	94.7	G472	85.5
4	G475	73.4	G472	86.1	G647	95.2	G466	86.2
5	G466	74.4	G473	86.2	G204	95.6	G469	86.4
Best check	Assi	75.6	Assi	88.2	Assi	99.3	Assi	87.7
Av. SE				2.06				1.42
Av.LSD (5%)				5.48				3.56
Days to maturity (top 5)								
1	G234	121.6	G547	125.8	G305	140.8	G547	130.7
2	G504	121.6	G546	126.2	G633	141.1	G546	130.9
3	G635	121.6	G348	127.6	G668	141.2	G475	131
4	G204	121.6	G470	127.7	G537	141.2	G524	131.1
5	G561	121.7	G524	128.0	G667	141.3	G668	131.1
Best check	Assi	121.8	Assi	131.2	Assi	143.9	Assi	132.3
Av.SE				1.78				1.19
LSD (5%)				4.77				3.03

Av. SE= Average standard error of predicted mean. Av. LSD (5%) = Least significant difference at 5% level of significance

Table 4

Top five hulless test genotypes and the best check based on predicted means for grain yield, heading days and maturity at different locations from combined analysis over locations

Trial	Marchouch		Allal Tazi		Terbol		All locations	
	Genotype	Mean	Genotype	Mean	Genotype	Mean	Genotype	Mean
				Grain yield				
1	G769	3833	G769	4139	G769	5490	G769	4487
2	G817	3818	G721	4128	G817	5477	G817	4472
3	G709	3812	G817	4122	G721	5469	G721	4469
4	G721	3811	G702	4120	G709	5467	G709	4465
5	G803	3806	G709	4117	G702	5463	G702	4462
Best check	Himalaya12	3796	Himalaya12	4100	Himalaya12	5454	Himalaya12	4450
Av. SE		275		275		275		320
Av. LSD(5%)		482		482		482		430
				Days to heading				
1	G724	77.36	G718	90.78	G711	96.11	G704	88.75
2	G704	77.41	G704	90.79	G735	96.52	G705	88.89
3	G743	77.65	G724	90.94	G809	97.06	G724	89.01
4	G705	77.67	G743	91.59	G705	97.21	G730	89.69
5	G725	78.03	G762	91.69	G747	97.66	G743	89.6
Best check	Himalaya12	77.31	Himalaya12	90.83	Himalaya12	99.63	Himalaya12	89.25
Av. SE		2.3		2.3		2.3		1.6
Av. LSD(5%)		6.3		6.3		6.3		4.3
				Days to maturity				
1	G730	120.7	G730	128.7	G705	140.9	G730	128.7
2	G775	120.7	G743	130	G802	141.1	G743	130
3	G704	120.9	G704	130.1	G775	141.4	G704	130.1
4	G705	121	G775	130.3	G762	141.5	G775	130.3
5	G762	121	G725	130.5	G805	141.5	G725	130.5
Best check	Himalaya12	120.6	Himalaya12	132.3	Atahualpa	141.4	Himalaya12	131.8
Av. SE		1.9		1.9		1.9		1.2
Av. LSD(5%)		5.1		5.1		5.1		3.3

Av. SE= average standard error of means, Av. LSD (5%)= average least significant difference at 5% level of significance

Specific adaptation of lines to the locations

The graphical representation of genotype and genotype × environment interaction, known as GGE biplots, is presented in Fig. 1 for hulled material. In order to bring clarity to the figure and also to retain only high yielding ones, we

culled those genotypes from the bi-plot if their yield was less than 50 percentiles of the yields in each locations. The two dimensional singular value decomposition of GGE gave 79% explanation of total sum of squares and both the principle components were very close (43% vs 36%). Of the three locations, TRL showed maximum discrimination between the genotypes while ALT the least. The top yielding lines based on overall means in Table 3 are seen in Fig 1 at the vertices, e.g. G427, G127 and G315, or near them such as G652. Based on the total phenotypic value minus the location mean, i.e. GGE interaction, value, genotype G127 is specifically adapted to TRL, G427, G535 and G652 to MCH, and G315 to ALT. No such plot was prepared for hulless genotypes due to non-significant interactions for GY.

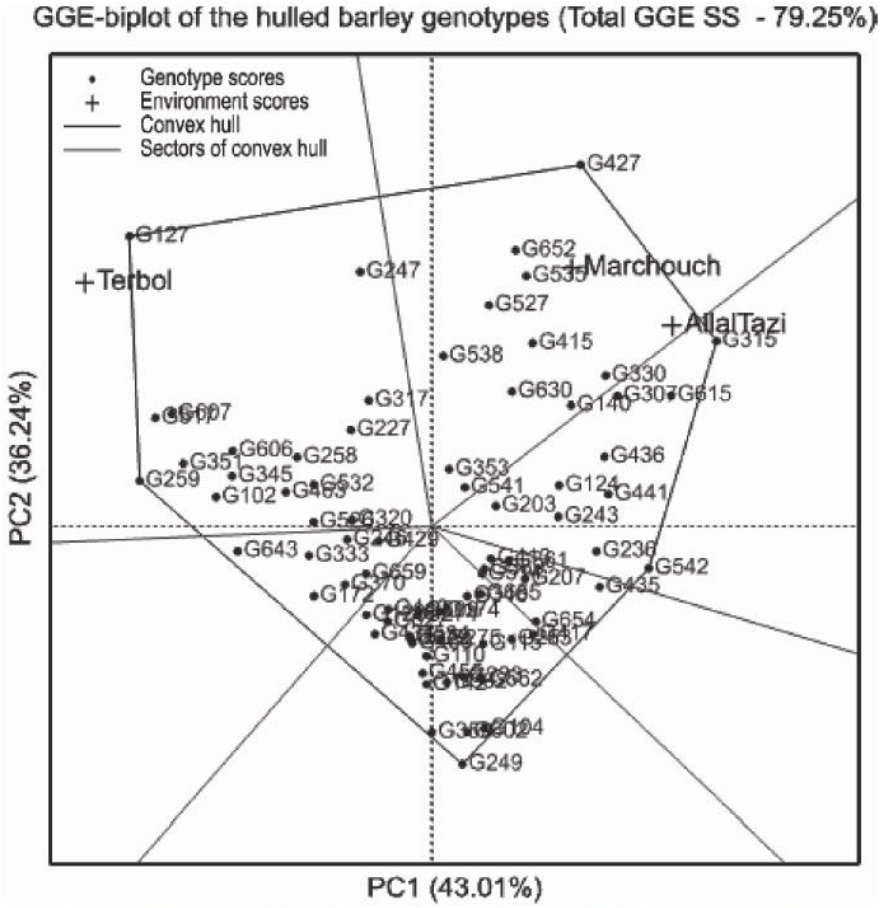

Fig 1. GGE biplots of hulled barley genotypes (from Trials 1-6) and three locations, when 50% of poorly performing genotypes were culled from the three environments

DISCUSSION

Multi-environment trials are important for testing general and specific adaptation of germplasm, due to frequent fluctuation in yield performances across different testing locations, which arise from different environmental locations and are referred to as GEI (Dias *et al.* 2003). GEI was significant for most of the traits in most of the trials, as expected due to the nature of the traits investigated (Table 1). GEI for GY in barley has been reported in numerous studies, such as those performed by Ceccarelli and co-workers under Mediterranean conditions (1991, 1994, 1996, 1998 among others), in which they consistently reported the presence of crossover-type of GEI. As already mentioned in the premises this type of interaction produces changes in rank order of genotypes across environments. For GY we observed that the best yielding genotypes in each location were different. No common high yielding genotypes were found within top ten between yield trials performed in Morocco and TRL. This means there were crossover interactions of variable degrees. The Spearman rank correlations were found as 0.094 (P=0.044) between genotype yields at the two Morocco location, and the rank correlations between genotype yields at Terbol was 0.231 (P<0.001) with that at Marchouch and 0.070 (P=0.137) at Allal Tazi. Genotype effect for GY was significant only in 3 field trials (2 hulled and 1 hulless) while GEI for GY was significant in 5 locations (4 hulled and 1 hulless), this support our hypothesis of the presence of differentially adapted genotypes in different locations.

DH has been reported as one of the main contributors to GEI in cereals (Cuesta-Marcos *et al.* 2009). Phenology in spring barley is driven mainly by growth habit, photoperiod responsive genes (*PPD*) and by the earliness per se or early maturity genes (*EPS/EAM*). These classes of genes have a direct interaction with the environmental cues and they determine the duration of crop developmental phases. Furthermore those traits have a direct influence on crop adaptation and the geographic distribution of cultivars (Boyd *et al.* 1996). In the case of DH, genotypes ranking was different, firstly G470 was the one with earlier heading in both MCH and ALT stations, and furthermore within the top 20 early genotypes in both MCH and ALT, 12 genotypes and 1 check were common between the two locations.

Furthermore the variance associated to the G × L interaction for GY in hulled trials explains the 11.2% of the phenotypic variance while G explains only 0.9%. This confirms that in the case of GY genotypes are specifically adapted to different environments. Surprisingly for DH the variance associated to G × L interaction was higher than variance associated to G (31.5% against 18.46%), this may be explained by temperature differences between Morocco (MCH and AT) and Lebanon, in fact TRL is characterized by lower temperatures during the winter. It is well know that temperature have effects on duration of developmental phases in cereals, especially in the transition from vegetative to reproductive phase. G × L effect is probably due to the differential genotypic response to low temperature at different locations. Plant material used in this study has spring growth habit, but some genotypes may retain some minor ver-

nalization alleles (facultative types) that, in autumn sowing, may affects plant behavior under low temperatures with consequent effects on flowering time.

As expected lowest heritability was found for GY (5%, hulled genotypes), while for others traits was ranging from 24% to 50%. GGE-biplot on genotype-focused scaling (Fig. 1) shows the graphical representation of G and GEI for hulled material, top yielding genotypes based on the overall means are located at the vertices of the polygon G427, G127 and G315. G127 is the most adapted to TRL, is the 3rd top yielding genotype at TRL and as well as in the top ten across all locations. G427, is the best adapted genotype to MCH and is also the best yielding genotype over all locations. G315 is the best adapted to ALT and the 7th in the yield ranking over all locations. Furthermore in the plot there are several high yielding genotypes (over all locations) that show good adaptation to both MCH and ALT: G427, G652, G415, G535, G315, G330 and G538. This apparently contradicts our hypothesis regarding the specific adaptation of different genotypes to different environments. The explanation can be find in the comparison biplot (Fig,. 1), that shows how both MCH and ALT are in the same sector of the polygon; this mean that these two location are part of the same mega environment and, this may explain the presence of common high yielding genotypes between the two environments for both GY and DH. Fig. 1 also shows that MCH and TRL are better representative locations for our breeding program since GGE-biplot shows that both locations are just opposite to the polygon sectors. The ICARDA spring barley breeding program at Morocco is addressing mainly for North Africa and West Asia regions, (while another location in India is being used for South Asia), thus the selection of locations that are representative of these two macro-environments is of primary importance to develop adapted high yielding germplasm; that will be further tested for specific adaptation by National Agricultural Research Programs (NARS) across the WANA. These two environments (MCH ad TRL) are potentially suitable for testing materials from international research projects, where MCH also give the additional benefit of having higher incidence of biotic stresses in addition to the evaluation of grain yield, while Terbol is exclusively for testing the yield potential as there is no significant incidence of any biotic stresses.

CONCLUSIONS

The present study summarized the data from eight trials comprising of hulled and hulless barley genotypes evaluated in alpha designs at three locations in two in Morocco and one in Lebanon during 2013-14 cropping season. Combined analysis of data indicated significant GxE interactions in all the traits except grain yield for hulless genotypes. The study enabled us to identify the two better representative locations (MCH and TRL) for evaluation of genotypes in the breeding program representing wider agro-climatic range. The best specific adapted high yielding genotypes for both macro-environments, respectively G427 for MCH and G127 for TRL as also showed in the GGE-biplot. Several higher yielding hulled and hulless genotypes have been found on over all mean as well as location specific as compared to the respective best checks.

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