Genetic variation in winter barley and selection of high yielding lines

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ABSTRACT

Barley (*Hordeum vulgare* L.) is an important crop with excellent nutritious feed and food grain. Winter barley, in particular, is predominantly grown in highland under rainfed systems due to its ability to tolerate cold. However, it has low productivity due to complex genetic mechanisms and limitations in determining an optimal environment for its selection and evaluation. This study evaluated the genetic variability, heritability and genetic gain for yield in barley, using preliminary un-replicated yield trials in 2011 at two locations and followed by replicated sets of yield trials in 2012, all in Syria. Significant genotypic variability was found at both stages of the evaluation/selection. During 2011, the best linear unbiased predictor means of test genotypes adjusted for spatial variability were found in the range of 1.75–3.75 t/ha at Tel Hadya and 0.03–1.58 t/ha at Breda. A set of 22 advanced yield trials comprising a total of 601 lines at Tel Hadya in 2012 yielded in the range of 1.85–3.13 t/ha. Based on the mean over these set of trials, the highest heritable trait was days to heading (broad-sense heritability on mean-basis= 0.64) followed by yield (the heritability = 0.30). The yield gain due to selection, at 20% intensity of selection, was 5.66% at Tel Hadya and 27.1% at Breda in 2011 using un-replicated genetic material, while it was 7.01 % for the replicated trials at Tel Hadya in 2012. We recommend use of the best lines selected in 2012 at Tel Hadya for further exploitation in genotype × environment interaction studies for high yield and specific and broad adaptation.

Key words: Barley (*Hordeum vulgare* L.), Genetic gain, Heritability, Selection, Yield trials.

INTRODUCTION

Barley (*Hordeum vulgare* L.) is an annual cereal crop grown in nearly all temperate regions of the world as well as in hotter and drier areas such as Asia Minor, North Africa and other Mediterranean countries. Worldwide, barley ranks fourth in terms of planting area after wheat, rice and maize (FAO, 2013). During 2011–2013, about 48 million hectares of barley was grown annually in a wide range of environments worldwide, of which 11 million hectares was winter barley (FAO, 2013). It is suited to areas with low precipitation, and has advantages in aspects such as tolerance to salt, drought and frost and the early period of development. However, abiotic stresses (water, heat, cold and salinity stresses) are the principal causes of crop failure worldwide. Among environmental stresses, water stress is the second contributor to yield reduction after disease (Nevo and Chen, 2010), reducing average yield for most major crops including barley by more than 50 % (see Table 3.7 in http://www.fao.org/docrep/010/a1075e/a1075e00.htm). The worldwide annual average barley production for 2011-2013 was about 136 million tonnes. Production of winter barley varieties is largely confined to cold and extremely cold highland regions where rainfed agriculture is predominant. While the worldwide productivity of barley slightly increased from 2.2 t/ha in 1996–2000 to about 2.79 t/ha in 2011–2013 (data not shown in tables), the long-term productivity (2001–2010) of barley in most Central and West Asia and North Africa (CWANA) countries is still low at 1.49 t/ha on average (Table 1).

Strategies of genetic improvement for winter barley yield under drought stress pose many practical problems including winter injury due to low temperature and soil heaving. The temperature changes during winter may be rapid and extreme with uncertain protective snow cover. Therefore, these factors deserve immediate attention in improving hardiness in winter barley and for increasing productivity. The most direct available procedure, long used by breeders, is to cross varieties to obtain genetic recombination with greater inherent hardiness (Rollins *et al.*, 2013). The complementary genes available in relatively non-hardy or even frost-resistant spring types should be considered in the breeding program, followed by field evaluations of these crosses in areas where winter injury is common. Regular evaluation and maintenance of genetic diversity is a key to germplasm improvement as described in major field crops such as maize, soybean, wheat and barley (Delannay *et al.*, 1983; Duvick, 1984; Murphy *et al.*, 1986; Horsley *et al.*, 1995). However, low genetic diversity in barley has been reported by most programs including the Minnesota and German breeding programs (Gutierrez *et al.*, 2009). It has been reported that advances in plant breeding together with improvement in plant production have led to an average

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TABLE 1: Long-term annual average (2001–2010) of barley growing areas, production, productivity, imports and exports in some Central and West Asia and North Africa countries.

Country	Population ('000,000)	Barley area ('000 ha)	Barley production ('000 t)	Barley productivity t/ha	Import barley ('000 t)	Export barley ('000 t)
Afghanistan	25.5	234	328.9	1.41	4.9	0.00
Algeria	37	777	1097.9	1.35	199.4	0.00
Armenia	3.3	64	115.2	1.78	6.7	0.00
Azerbaijan	9	190	430.2	2.26	15.1	0.13
Georgia	4.5	32	49.5	1.47	1.6	0.83
Iran	77	1547	2847.6	1.83	658.3	0.00
Kazakhstan	16.7	1698	1980.7	1.16	30.5	374.23
Kyrgyzstan	5.5	103	209.7	2.07	30.5	0.22
Morocco	33	2136	2029.4	0.95	410.4	0.01
Pakistan	180	97	90.8	0.94	1.7	2.10
Syria	22	1333	902.2	0.69	404.8	78.34
Tajikistan	8	44	63.9	1.44	3.6	0.00
Turkey	75	3356	7972.1	2.37	95.8	286.79
Turkmenistan	5.2	58	57.1	0.97	0.0	0.00
Uzbekistan	29	81	141.0	1.75	12.2	0.00
Total	**530.7**	**11750**	**18316**	**1.49**	**1876**	**743**

(Source: FAOSTAT, 2010)

annual increase of 80 kg/ha/year in winter barley yield in Germany during the last five decades (Ordon *et al*., 2005; Ahlemeyer *et al*., 2008).

While an improvement in winter barley occurs with the breeding cycle, the consequences associated with genetic gain has significant implications for the future, as favorable alleles are selected and fixed, resulting in reduced variability and presumably reducing the potential for future progress (Rasmusson and Phillips, 1997). It has been noted that in crops with a long history of improvement, the genetic gap between the improved and unimproved pools is growing larger with each breeding cycle (Holley and Goodman, 1988; Martin *et al*., 1991). While the selection strategy may determine the rate of gain, it is the genetic variation within the breeding population and the number of recombinants generated that determine the potential gain that can be realized with optimal selection (Condon *et al*., 2009). Genetic gains are used to compare different breeding strategies in terms of changes in traits among released cultivars and associated economic impact in a given region. The objectives of this study were to (1) evaluate genetic variation in the material at a preliminary stage, (2) estimate genetic variation contained in the material selected and advanced and (3) estimate the gain due to selection and identify lines for further exploitation.

MATERIALS AND METHODS
Preliminary yield trials (PYTs): During the 2010-2011 season, 908 lines from F6 generation of winter barley and six check genotypes were evaluated at two locations, Tel Hadya (a relatively wetter location) and Breda (a drier location) in northern Syria, in augmented designs with a block of size 40 on 24 × 40 rectangular layouts. Six check-

genotypes (Pamir-009, Radical, Bulbul, Lignee131, Himalaya-12 and Atahualpa) were replicated on the layout, and permitted fitting various models to capture spatial variability in the field. The PYTs were planted on 1 December 2010 at Tel Hadya and 10 December 2010 at Breda. Seeds were sown at a density of 250 plants/m² in six-row plots of 6.25 m long and spaced 0.2 m apart using a plot seeder. On maturity, all six rows were harvested in 2011 at both locations. Agronomic data were recorded on growth habit (GH), growth vigor (GV), plant height (PH), days to heading (DH) and grain yield (GY).

Yield trials (YTs): A number of genotypes from PYTs were advanced for inclusion in replicated barley YTs in 2012 when a total of 601 entries were evaluated in 22 sets of 30 genotypes each including two common checks: Pamir-009 and Radical. These trials were conducted in alpha designs with six blocks of five plots each and in three replications at the two research stations: Tel Hadya and Breda. The last set had 15 genotypes and three blocks. The YTs were planted on 1 November 2011 at Tel Hadya and 1 December 2011 at Breda. Seeds were sown at a density of approximately 250 plants/m² in eight-row plots of 7.5 m long and spaced 0.2 m apart. All six rows were harvested in 2012 at Tel Hadya and only 1.0 m² harvested from the central rows of plots at Breda.

The environments: Tel Hadya had more days below 0°C than Breda in both 2010/11 and 2011/12 seasons. The 2011/12 season had more days below 0°C compared to the 2010/11 season at both the locations. During 2010/11 there were 19 days below 0°C at Tel Hadya, with an absolute minimum temperature of -5.1°C; Breda had 14 days below 0°C and an absolute minimum temperature of -4.0 °C. During 2011/12, Tel Hadya had 44 days below 0°C compared to 32 days

in Breda, and the absolute minimum temperatures were -5.6 °C and -4.0 °C, respectively. The highest frequency of days below 0 °C and the absolute minimum temperatures were during December – February for both locations. During 2011, annual rainfall was 259.1 mm at Tel Hadya and 259.3 mm at Breda with the respective values for 2012 of 456.0 and 298.3 mm. Monthly rainfall distributions at the two locations are shown in Fig 1 covering the crop growing season of November–May, which indicates that 2011/12 was wetter than 2010/11 at each location.

Statistical analysis: The data from the un-replicated trials in 2011 were analyzed using a screening of nine spatial models comprising combinations of three ways of accounting for the linear trend in column direction – with or without a linear trend and random cubic smoothing spline in column number – and three structures for plot errors – first-order autoregressive (AR) errors along rows, first-order AR errors along rows as well as AR along columns, and independent errors, using methods given in Rollins *et al*. (2013) for augmented designs. For the replicated trials, conducted in incomplete block designs in 2012, data were analyzed according to Singh *et al*. (2003) where a set of 18 models were fitted to select the best model which captures the spatial variability. Fitting of the nine models was carried out using the REML (restricted maximum likelihood, also residual maximum likelihood) method of Genstat software (Payne, 2013). The best model was selected using Akaike Information Criterion (AIC). Using the best model, BLUPs (best linear unbiased prediction) estimates were obtained for the genotypes along with estimated standard errors. Comparison of the test genotypes with best check was done using least significant difference (LSD) values for a pair of test and check genotypes.

Since the set of same genotypes in the PYT were evaluated at the two locations, the genotype × environment interaction was obtained using weighted analysis of variance on the BLUEs (best linear unbiased estimates) and BLUP means. The test genotypes of individual YTs differed across the trials except for the set of common check genotypes. To compare any two test genotypes, i.e. those between any two trials, an adjustment to the BLUPs was made for the difference in the trials (i.e. difference in the fields where trials were conducted in 2012).

Computation of heritability and gain due to selection was done in terms of σ_g^2 and σ_e^2, which are estimates of genotypic variance and experimental error (environmental variance) components, respectively. Broad-sense heritability (h^2) on a mean basis is given by $h^2 = \sigma_g^2 / (\sigma_g^2 + \sigma_e^2 / r)$ ($i = 1, 2, ..., k$), where r is the number of replications each genotype mean is based on. Genetic gain (GG) at selection intensity p, based on normal distribution of the trait, is given by $GG(p)\,(\%) = 100C(\sigma_g^2 / \overline{Y}) / (\sigma_g^2 + \sigma_e^2 / r)^{1/2}$, where C is a constant determined in terms of ordinate of the standard normal distribution corresponding to abscissa at proportion p, $0 < p < 1$, and $\overline{Y}$ is the trial or location mean. For $p = 0.20$, $C = 1.4$ (Kempthorne, 1983; Singh *et al*., 2012). The genotypic coefficient of variation (GCV) was obtained as $GCV(\%) = 100\sigma_g / \overline{Y}$. Realized gain (RG) was computed from the BLUPs adjusted for trial differences in terms of the common checks using the formula, RG(p) (%) =100 ((mean of BLUPs for top 100p% of lines)/(mean of BLUPs of all lines) - 1) .

RESULTS AND DISCUSSION
Genotypic variability
PYTs (2011): The spatial model found best for GY was first-order auto-correlation along rows and along columns of the rectangular layout at both locations. The genotypic variability was significant ($p<0.001$). The genotype × environment interaction was not significant when BLUPs were used but was significant when BLUEs were used. This appears to be because the standard errors of estimates were relatively higher for the BLUPs. For each trait recorded in 2011, Table 2 gives mean and genotypic variation in terms of GCV and broad-sense heritability, h^2, estimates for un-replicated trials on a mean basis. The mean yields were 2.79 t/ha and 0.85 at Tel Hadya and Breda, respectively.
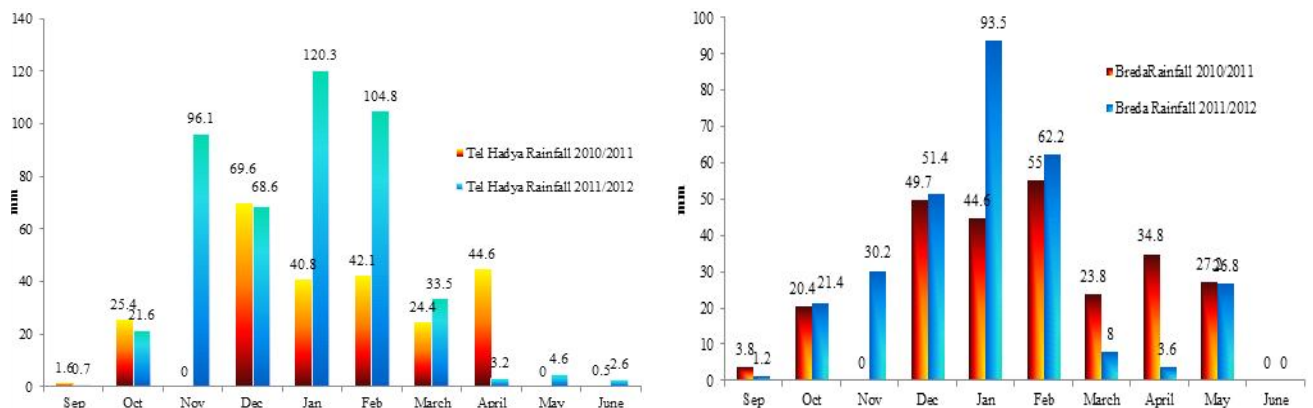

FIG. 1: Monthly rainfall (mm) distributions at Tel Hadya and Breda, Syria during 2010–2012

Checks differed in rank for GY in 2011 at both the locations, indicating the presence of genotype $\times$ environment interaction. However, all means of checks for GY were lower in Breda. Bulbul and Pamir-009 were the highest yielding genotypes in Tel Hadya, and were also used as common checks in the YTs in 2012 in both locations. While Himalaya-12 was the lowest yielding check at both locations, the genotype $\times$environment interaction was of the cross-over type between Atahualpa, Radical and Lignee-131 (Fig. 2).
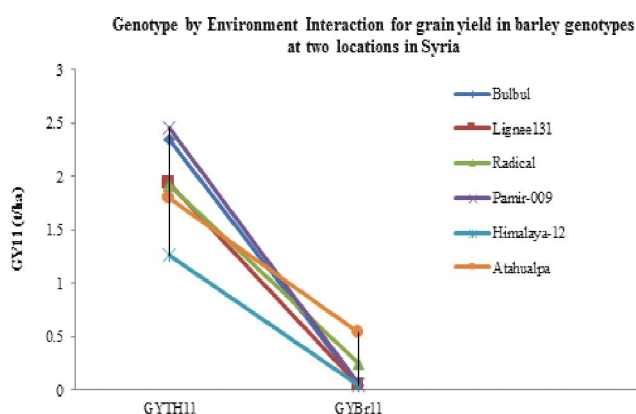

FIG. 2: The genotype by environment interaction for grain yield in six barley check varieties tested at two locations in Syria in 2011.

YTs at Tel Hadya (2012): Out of the total 601 barley genotypes evaluated in PYTs (2011), we promoted a total of 350 winter barley genotypes that were evaluated in a set of 22 YTs (2012) at Tel Hadya and Breda, but the data from the latter location could not be available. For these 22 YTs at Tel Hadya, average h^2 was the highest for DH where the GCV was the maximum (9.27 %) (Table 2). The BLUP means for GY were in the range of 1.85–3.13 t/ha (overall mean, 2.27 t/ha). The heritability estimates of GY at Tel Hadya differed substantially between the two years: h^2= 0.14 in 2011 (un-replicated) and 0.30 in 2012 (three replications). The h^2 was strongly correlated with GCV at Tel Hadya (r=0.82; $p < 0.001$ correlations not shown in tables). However, the GCV was higher in 2011 (1.58) than in 2012 (1.03) (Table 2).

Genetic gains

The estimated genetic gain (GG (p)) and realized gain (RG(p)) due to selection for grain yields are given in Table 3. Furthermore, both the genetic gains in PYTs (2011) were higher in Breda compared to Tel Hadya. When the intensity of selection was increased from 5 to 20% at Breda, the GG decreased from 39.94 down to 27.1, respectively (Table 3). Similarly, when the intensity of selection at Tel Hadya increased from 5 to 20%, the GG was reduced from 8.34 to 5.66%, respectively. The RG values were much higher than the GG values which arises from theoretical consideration of normality assumption for the trait. Furthermore, the RGs at Tel Hadya were very close for the two cycles, although numerically slightly higher for 2012 compared to 2011. The higher values of RG could be sensitive due to the predicted means arising from only a single selected set of lines. The GG, although resulting in lower estimates, may be preferred. The gains were higher at Breda, a drier site than Tel Hadya.

TABLE 2. Mean, minimum, maximum, genotypic coefficient of variation and broad-sense heritability of traits in the yield trials using best linear unbiased predictor means

Location		PHT	PHB	SPL	DH	GY
a) Preliminary yield trials in 2010/11						
Tel Hadya	Mean	62.59	54.21	7.88	106.24	2.79
	Minimum	51.32	37.71	6.20	90.59	1.75
	Maximum	81.99	82.04	9.53	115.25	3.75
	GCV(%)	17.30	50.42	3.64	2.09	1.58
	h^2 (%)	0.26	0.75	0.32	0.34	0.14
Breda	Mean	45.03	39.12	6.18	NA	0.85
	Minimum	33.59	24.68	3.92	NA	0.03
	Maximum	53.29	55.73	8.24	NA	1.58
	GCV(%)	17.20	61.13	8.12	NA	4.60
	h^2 (%)	0.27	0.80	0.54	NA	0.35
b) Advanced yield trials in 2011/12 at Tel Hadya						
GY (t/ha)	Mean	72.23	63.25	8.98	110.9	2.27
	Minimum	68.16	59.38	8.41	102.4	1.85
	Maximum	80.38	71.54	9.47	116.2	3.13
GCV(%)	Mean	2.42	3.14	0.51	9.27	1.03
	Minimum	0	0	0	0.23	0
	Maximum	10.96	17.92	7.32	49.85	4.34
h^2 (%)	Mean	0.09	0.09	0.06	0.64	0.30
	Minimum	0	0	0	0.12	0
	Maximum	0.34	0.41	0.57	0.94	0.71

PHT= Plant height to the top of the spike (cm). PHB= plant height to the bottom of the spike (cm). SPL= spike length (cm). DH= days to heading. GY= grain yield (t/ha). GCV(%)= genotypic coefficient of variation. h^2(%)= broad-sense heritability from un-replicated trial. NA= not recorded at Breda

TABLE 3. The genetic gain due to selection for barley grain yield at three selection intensities.

Intensity of selection (%) (100 p)	Tel Hadya, 2011		Breda, 2011		Tel Hadya, 2012	
	RG(p)	GG(p)	RG(p)	GG(p)	RG(p)	GG(p)
			----%----			
5	17.73	8.34	57.18	39.94	18.4	10.33
10	14.83	7.09	49.08	33.98	15.3	8.78
20	11.68	5.66	38.89	27.1	11.3	7.01

RG (p)= Realized gain due to selection (%), GG= Estimated genetic gain due to selection (%), both at intensity of selection (p).

Therefore, a drier site, such as Breda, may be preferred for selection of the genetic material.

Genotypic selection: The top-ten winter barley lines in PYTs (2011) and YTs (2012) are listed Table 4. These lines were also significantly superior to their respective best check. We have labeled PYTs lines g1, g2…g914 and YTs lines as G1, G2…G601.

For the best ten lines from the PYTs (2011), the adjusted BLUP means of GY at Tel Hadya in 2011 ranged from 3.34 t/ha (g815) to 3.75 t/ha (genotype g857). Although the BLUP means of GY in 2011 at Breda were lower compared to that at Tel Hadya, yet the top-ten yielding varieties yielded between 1.40 t/ha for genotype g287 to 1.58 t/ha for g191. Genotype g857 was among those that out-yielded the best check in each location. Among the check genotypes, the top yielding at Tel Hadya in 2011 were Pamir-009 (yield 2.40 t/ha) and Bulbul (2.30 t/ha), which did not differ significantly ($p > 0.05$). When test genotypes were compared with checks for GY, 509 genotypes yielded significantly ($p < 0.05$) higher than the best check using LSD5% (value = 0.718) and their predicted mean values were in the range of 1.09–4.59 t/ha (data not shown in tables). The lines which yielded higher than the best check at a given location were selected to enhance the genetic advance in the forthcoming breeding cycle.

The results of YTs (2012) at Tel Hadya showed significant differences among winter barley genotypes for GY. The top ten lines yielded in the range 2.75 t/ha (for genotype G327) - 2.92 t/ha (for G502) while the overall mean for all the lines was 2.27 t/ha (Table 4).

The genetic diversity in a breeding program is essential to insure against unforeseeable changes in the environment, and to maintain genetic progress (Gepts, 2006). In addition, genetic diversity should be maintained in barley to decrease vulnerability to abiotic stresses and pests, and to assure continued genetic improvement (Martin *et al.*, 1991). The results of PYTs showed a wide genetic diversity for all traits under study at both locations (Table 2). An ideal population for a breeding program should have a high frequency of favorable alleles and as few detrimental alleles as possible. As a plant breeding program matures, it is expected that the frequency of favorable alleles will increase while detrimental alleles will tend to disappear. Genetic gain

studies within breeding programs can be used to assess the success of plant breeding strategies and their effects on the variation within breeding populations as a response to selection (Condon *et al.*, 2009).

The diversity in the ICARDA winter barley breeding program was associated with breeding efforts, and there was reasonable diversity for all traits in the present study. These results are interesting compared to the low diversity documented in some breeding programs – including that of Minnesota, using pedigree information and observation of phenotypic traits (Rasmusson and Phillips, 1997), and of Germany (Gutierrez *et al.*, 2009). In contrast, Sweden and Denmark have the most diverse reported breeding programs (Malysheva-Otto *et al.*, 2007).

Several strategies can be used to maintain genetic gain, including the use of elite crosses known as advanced cycle breeding (Gutierrez *et al.*, 2009) which leads to significant genetic gain in quantitative traits due to the accumulation of favorable alleles (Rasmusson and Phillips, 1997). The present study used a data-driven method to identify compatible genotypes and to compare their performance outside the targeted environment. The evaluation of winter barley genotypes under drought stress conditions appeared to preserve genotypes possessing alleles for drought tolerance that might be lost by selection under only optimum conditions (Calhoun *et al.*, 1994). The presented selection strategy took advantage of the high heritability in the stressed environment ($h^2 = 0.35$ at Breda) in 2011, and consequently resulted in higher genetic gain (GG(0.2) = 27.1%). Thus, results of the present study showed that progress in yield and drought tolerance was mainly achieved by phenotypic detection and combination of the genetic diversity present within the primary winter barley materials.

The choice to promote the best barley genotypes to YTs in 2012 was made on selection criteria based primarily on yield performance at each location, and resulted in promoting 350 barley genotypes to YTs in 2012 (Table 4). Tel Hadya received more rainfall (456.0 mm) than Breda (298.3 mm) in 2012. We also compared means of the breeding program at the two locations in the first year, while in the second year, lack of data from Breda did not allow comparison with the results.

TABLE 4. Best linear unbiased predictor means of grain yield for the best ten lines yielding significantly better than the respective best check and their unadjusted values

Trial	Genotype	Name	Pedigree	BLUP (t/ha)	Unadjusted values (t/ha)
a) Preliminary yield trials, 2010-11, Tel Hadya					
Test entries	g857	CWB117-77-9-7/4/Belt67-1608/Slr/3/Dicktoo/Cascade//Hip/5/Kc/MullersHeydla//Sls/3/GkOmega/4/Sararood*2	ICB05-1441-0AP-7AP-0AP	3.75	3.2
	g623	Excelle//CWB117-77-9-7/Sls/3/Antares/Ky63-1294//CWB117-77-9-7	ICB05-1233-0AP-3AP-0AP	3.57	4.59
	g767	Roho//Alger/Ceres362-1-1/3/Tipper/4/Alpha/Durra//Slr/5/Tipper/Arda	ICB05-1334-0AP-3AP-0AP	3.56	4.4
	g799	Tipper/ICB-102854//Tokak/3/Tipper/Arda	ICB05-1359-0AP-7AP-0AP	3.49	4.16
	g774	ICB-103351/Arta//K-88M1/4/Coss/OWB71080-44-1H/3/Alpha//Sul/Nacta	ICB05-1347-0AP-4AP-0AP	3.46	3.82
	g714	CWB117-77-9-7/Roho/Masurka/3/Supie/5/Roho//Alger/Ceres362-1-1/3/Tipper/4/Roho/Masurka	ICB05-1294-0AP-10AP-0AP	3.45	3.17
	g80	Courlis//Alanda/Hamra-01/3/Regina	ICB06-1770-25AP-0AP	3.41	4.13
	g404	Modeibeia; SE of Shoubak/Sararood	ICB06-2090-1AP-0AP	3.41	2.53
	g822	ChiCm/An57//Albert/3/ICB-102379/4/GkOmega/5/Sararood*2	ICB05-1428-0AP-9AP-0AP	3.38	3.95
	g815	ChiCm/An57//Albert/3/ICB-102379/4/GkOmega/5/Excelle//CWB117-77-9-7/Sls/6/GaraArpa	ICB05-1426-0AP-2AP-0AP	3.34	3.53
Av. SE$				0.315	0.516
Checks	g912	Pamir-009		2.40	2.35
	g914	Atahualpa		2.39	2.17
	g909	Bulbul		2.30	2.5
	g911	Radical		2.07	1.97
	g910	Lignee131		1.85	1.53
	g913	Himalaya-12		1.78	1.47
Av.SE$				0.216	0.73
b) Preliminary yield trials, 2010-11, Breda					
Test entries	g191	PRATO/Regina	ICB06-1838-31AP-0AP	1.58	1.95
	g855	CWB117-77-9-7/4/Belt67-1608/Slr3/Dicktoo/Cascade//Hip/5/Kc/MullersHeydla//Sls/3/GkOmega/4/Sararood*2	ICB05-1441-0AP-5AP-0AP	1.56	1.58
	g857	CWB117-77-9-7/4/Belt67-1608/Slr3/Dicktoo/Cascade//Hip/5/Kc/MullersHeydla//Sls/3/GkOmega/4/Sararood*2	ICB05-1441-0AP-7AP-0AP	1.56	1.56
	g71	Couris//Alanda/Hamra-0l/3/Regina	ICB06-1770-16AP-0AP	1.54	1.67
	g822	ChiCm/An57//Albert/3/ICB-102379/4/GkOmega/5/Sararood*2	ICB05-1428-0AP-9AP-0AP	1.52	2.06
	g817	ChiCm/An57//Albert/3/ICB-102379/4/GkOmega/5/Ste/Lignee640//Hml-02/ArabiAbiad*2/3/Sararood*2	ICB05-1427-0AP-3AP-0AP	1.46	1.82
	g121	Skorohod/Regina	ICB06-1797-41AP-0AP	1.45	1.72
	g836	Scio/3/Igri/MOB2639//P13161/Igri/4/YEA168.4/YEA605.5//Lignee131//ArabiAbiad/5/GaraArpa	ICB05-1433-0AP-7AP-0AP	1.44	1.51
	g168	PRATO/Regina	ICB06-1838-4AP-0AP	1.41	1.83
	g287	Pamir-147/Sonata/8/Alpha/Durra/7/P101/5/3896/28//584/28/4/5050/6/Tipper	ICB06-2011-5AP-0AP	1.40	1.92
Av. SE$				0.159	0.094
Checks	g909	Bulbul		0.00	0.07
	g910	Lignee131		0.00	0.07
	g911	Radical		0.23	0.24
	g912	Pamir-009		0.09	0.06
	g913	Himalaya-12		0.22	0.02
	g914	Atahualpa		0.75	0.45
Av. SE$				0.212	0.133

contd.........

c)   Advanced yield trial, 2011-12, Tel Hadya

	No. 2012@	Source 2011&	No. 2011@			
Test entries	G502	PYT	g736	CWB117-77-9-7//Roho/Masurka/3/132TH/Tokak//Malta1-4-3094-2/4/K-88M1//GkOmega/Tokak	2.92	3.29
	G329	AZ	g39	CWB117-77-9-7//Alpha/Durra(TH)/4/YEA168-4/YEA605.5//Lignee131/ArabiAbiad/3/Sararood	2.91	3.35
	G324	AZ	g34	GkOmega/CWB117-5-9-5/5/Excelle/4/Alpha/Durra/3/4679/105//YEA132TH	2.85	3.29
	G309	AZ	g8	Sadik-02*2/3/Pamir-154//ICB-100709/WB156	2.84	3.28
	G131	CAC	g9	Baishishek/3/YEA168-4/YEA605.5//Lignee131/ArabiAbiad	2.83	2.35
	G310	PY	g539	Pamir-010/Sahara-3768/3/YEA168.4/YEA605.5//Lignee131/ArabiAbiad	2.81	3.25
	G363	PYT	g537	Robur/WA2196-68//DZ40-66/8/Harma-02//11012-2/CM67/7/Mola/4/Brea'S'/DL70//Mozdosky/3/Nopal'S'/5/CI10622/CI05824/6//Lignee640-0AP	2.80	2.85
	G361	CAC	g3	Robur/WA2196-68//DZ40-66/8/Harma-02//11012-2/CM67/7/Mola/4/Brea'S'/DL70//Mozdosky/3/Nopal'S'/5/CI10622/CI05824/6//Lignee640	2.78	2.83
	G126	AZ	g37	Pamir-168/4/Roho//Alger/Ceres362-1-1/3/CWB117-77-9-7	2.75	2.27
	G327	PYT	g893	CWB117-77-9-7//Alpha/Durra(TH)/4/YEA168-4/YEA605.5//Lignee131/ArabiAbiad/3/Sararood	2.75	3.19
Checks	G700	-	-	Pamir-009	2.26	2.27
	G800	-	-	Radical	2.24	2.24
Av. SE$					0.23	0.34

$Av.SE= average standard error. @ Genotypes labeled g1… g914 evaluated in 2010/11 and G1..G601 evaluated in 2011/12. & PYT = Preliminary Yield Trial for winter barley, AZ = Winter barley nursery for Azerbaijan in 2010-11, CAC= Winter barley nursery in for CAC (Central Asia and Caucasus) region in 2010-11.

Within top ten lines, two genotypes were common at Tel Hadya and Breda during 2011, which is logical considering the environmental conditions in these locations, but these two genotypes showed broader adaptation for yield and may serve as important resources in the future. None of the top-ten selected in 2011 was top ranked in 2012. This is probably due to the differential response of genotypes to the amount and distribution of rainfall in 2011 and 2012. Considering the terminal drought (April 2012 has 3.2 mm of rainfall) in 2012, genotypes identified as tolerant to drought were more realistic than those identified in 2011 in Tel Hadya. Although the total amount of rainfall was much lower in Tel Hadya in 2011, it was well distributed across the growing season and there was good rainfall in March and April (Fig. 1).

Despite both locations received nearly the same amount of rainfall in 2011, the genotypes reacted differently to drought stress conditions. Tel Hadya was the higher yielding environment (2.79 t/ha with 259.1 mm, Table 2), while Breda was drought stressed (0.85 t/ha with 259.3 mm). Nevertheless, heritability (h^2) of GY was found not significantly associated with its mean in either location. However, there was positive correlation between h^2 and GCV, suggesting that selection of genotypes from the environment with higher h^2 would result in higher genetic gain regardless of the mean of GY in the testing environment.

To further enhance the genetic gains, the winter barley breeding program at ICARDA is faced with the dilemma of identifying and introgression of new germplasm into new varieties, without disturbing the existing favorable gene complexes that contribute to numerous favorable traits. It was reported (Martin et al., 1991; Condon et al., 2009) that traits like GY and DH are close to the target values. However, we still believe that drought tolerance and winter hardiness should be used for genetic improvement and will benefit from additional genetic diversity. Further enhancement to capture genetic variation may include use of measurements on additional traits and molecular markers to identify quantitative trait loci by association mapping. The latter will provide a basis to predict the performance of winter barley lines and select parents to increase the frequency of favorable alleles. This study was constrained to only drought environments; therefore, we need to diversify the testing environments that include cold tolerance as well.

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