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1 **Spanish barley landraces outperform modern cultivars at low productivity sites**

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1 **Summary**

2 Barley landraces from the western Mediterranean area have not been thoroughly exploited by modern  
3 breeding. This study aims at assessing the agronomic value of a core collection of lines derived from  
4 landraces of Spanish origin, and to compare them with sets of successful old and modern cultivars.  
5 The agronomic performance of a set of 175 barley genotypes, comprising 159 landrace-derived lines  
6 and 26 cultivars, was evaluated in a series of 10 field trials, carried out over 3 years and several  
7 locations. The most relevant trait of the landraces was higher grain yield at low production sites than  
8 cultivars, which may be related with better ability to fill the grain under stressful conditions. On the  
9 other hand, lateness, excessive plant height and lodging were negative traits frequently found in the  
10 landraces. Large genotype-by-environment interaction (GEI) for grain yield was detected, related  
11 partly with differences among germplasm groups, probably indicating local adaptation. GEI was also  
12 associated with the interaction of heading time and powdery mildew resistance with temperature.

13

14 **Keywords:** barley, phylogenetic resources, landraces, grain yield

15

## 1 **Introduction**

2 Over the 20<sup>th</sup> century, barley producers in Europe chose to substitute their landraces or primitive  
3 cultivars by newly bred cultivars. New materials were readily adopted because they were specifically  
4 improved for the challenges of modern agriculture and consumer demands. Old landraces were  
5 gradually abandoned, and are currently kept mostly in germplasm banks.

6 Nevertheless, landraces and old cultivars persisted in some areas in Europe, probably due to a  
7 combination of agronomic and socio-economic factors. A better stability of landraces compared to  
8 modern cultivars under largely unpredictable environmental conditions (as in Mediterranean climates)  
9 has been recurrently mentioned in plant breeding literature (van Oosterom et al., 1993, Voltas et al.,  
10 1999; Lasa et al., 2001).

11 This could be the case of some Spanish landraces, which persisted under cultivation longer than in  
12 other Western European regions. The best example is cultivar Albacete, a selection from a landrace  
13 made around 1955, which continues to be popular in some regions of Spain due to its reliability. In the  
14 semi-arid region of Aragón, it still occupied 69% of the area devoted to six-row barley in 2002 (DGA,  
15 2002).

16 In general, landraces constitute one of the most valuable sources of genetic diversity. This diversity  
17 has become now more accessible thanks to the advances in genomics and recombinant DNA  
18 technology (Newton et al., 2010). Spanish barleys have long been known as a distinct phylogenetic  
19 resource with potential to contribute favourable traits to barley breeding. The genetic singularity of the  
20 Spanish barleys was described by Tolbert et al. (1979), Moralejo et al. (1994), Lasa et al. (2001), and  
21 especially by Yahiaoui et al. (2008). This genetic distinctiveness may be related to the presence of  
22 adaptation traits specific to Mediterranean conditions, which is worth investigating. The Spanish  
23 Barley Core Collection (SBCC) was assembled as a tool to systematize the study of the genetic  
24 diversity of local landraces of barley (Igartua et al., 1998).

25 So far, the Western Mediterranean barley landraces have not been widely used in modern breeding,  
26 probably with the exception of the Coast types (of Spanish or North-African origin) that were

1 introduced in California by Spanish settlers in the 18<sup>th</sup> century (Florell, 1929). These landraces were  
2 later one of the founding germplasm groups of current North-American barleys (Knüpffer et al, 2003).  
3 The reasons for this overlook are, on one hand, the association of favourable and unfavourable traits of  
4 unknown genetic control and, also, an insufficient phenotyping effort. This study is part of an effort to  
5 overcome this lack of systematic phenotyping. A thorough evaluation of this collection for disease  
6 resistance has been already published (Silvar et al., 2010, 2011a). The objectives of this work are to  
7 describe Spanish barleys from the agronomic point of view, to assess their potential to contribute  
8 favourable traits, to compare their behaviour with old and modern cultivars widely grown in Spain,  
9 and to analyze the relationships of grain yield with various phenotypic and environmental traits. The  
10 final purpose of this study is to spur the interest of the barley community over this valuable  
11 phylogenetic resource.

## 12 **Material and Methods**

### 13 Plant material

14 A total of 182 genotypes were evaluated in field trials. The set comprised the following subsets: 145  
15 six-row and 11 two-row Spanish inbred lines, derived from landraces after at least three generations of  
16 head-to-row purification; sixteen old cultivars, widely used in Spain during the 20<sup>th</sup> century, 8 two-row  
17 (Alpha, Beka, Hassan, Kym, Pallas, Union, Wisa and Zaida) and 8 six-row (Ager, Albacete, Almunia,  
18 Barberousse, Dobra, Hatif de Grignon, Monlon and Pané); and, finally, ten cultivars, recently bred or  
19 currently grown in Spain, used as controls of good agronomic performance (Candela, Orria, Plaisant  
20 and Steptoe six-row; Gaelic, Graphic, Nevada, Seira, Tipper and Volga two-row). The first three  
21 groups, six-row and two-row landrace-derived inbred lines and old cultivars, constitute the Spanish  
22 Barley Core Collection (SBCC, Igartua et al., 1998).

### 23 Field trials

24 A total of 10 field trials were sown in standard dates (Table 1) in three provinces, representing relevant  
25 barley growing areas of Spain (Table 1). The climatic data for the locations were provided by the  
26 Spanish Meteorology State Agency (AEMET), and were gathered from stations either in the same

1 location of the trial (Zuera, Sádaba), or in locations within a 20 km radius (the rest). Potential  
2 evapotranspiration (ETP) was estimated based on the daily data of precipitation, maximum and  
3 minimum temperatures, using the method of Hargreaves (Hargreaves et al., 1985). Daily temperature,  
4 precipitation, ETP, and precipitation/ETP ratio were converted to monthly and seasonal (autumn,  
5 winter and spring) averages (Table 1).

6 Each trial occupied a large area (0.7 ha). Therefore, soil heterogeneity was a concern. To minimize its  
7 effect, the trials were subdivided in four sub-trials at each location. Each sub-trial included 44 SBCC  
8 accessions plus the 10 modern check cultivars, for a total of 54 accessions per sub-trial. One check  
9 was sown twice to fill up the last sub-trial. The allocation of genotypes to sub-trials was done in a  
10 stratified manner, keeping the original proportions of the groups (six-row lines, two-row lines, old  
11 cultivars), and also maintaining a balance of geographic origins between the four sub-sets.

12 The experimental design for each sub-trial was an alpha-lattice, with 3 replications. Therefore, the ten  
13 modern cultivars were replicated 12 times, 3 at each sub-trial, whereas the rest of the accessions were  
14 replicated three times. Incomplete blocks were arranged in two directions, row ( $k=9$ ) and column  
15 ( $k=6$ ). Each genotype was sown in 6 row plots, 6 m long, 0.2 m between rows, with a rate of 350 seeds  
16  $m^{-2}$ . Each sub-trial had a width of 27 plots, with an alley of 1 m between tiers. The disposition of the  
17 sub-trials in the field was in quadrants, conforming a square plot of 81 m side length. Replications  
18 were nested within sub-trials.

## 19 Traits

20 The traits recorded were plant height (PHT), measured at maturity, in one representative plant of each  
21 plot, as the height from the tillering node to the point of insertion of the flag leaf; heading date (HED),  
22 as the number of days from January 1<sup>st</sup> until the day when 50% of the stems of each plot displayed 2  
23 cm protruding awns; lodging (LDG), recorded only at the trials in which it was present, following the  
24 visual scale of IPGRI (1994), with values from 1 (very low) up to 9 (very high); grain yield (YLD), as  
25 grain weight per plot in  $q\ ha^{-1}$ ; test weight (TW), determined with a grain analyzer (Dickey-John);  
26 thousand kernel weight (TKW); yield components (only at Zuera, Zaragoza, 2003), namely, number of  
27 ears  $m^{-2}$  (SPM), number of grains by ear (KS), number of grains  $m^{-2}$  (KM), and weight of 1000 grains

1 (TKW), from hand-harvest of a segment 1 m long of two central rows of each plot, for two  
2 replications; incidence of foliar diseases (leaf rust, LR; net blotch, NB; powdery mildew, PM) at trials  
3 in which the attacks were severe enough to reveal apparent genotypic differences (visual scores from  
4 1-resistant to 9-susceptible on plot basis); malting quality traits, carried out at the DAMM company  
5 facilities in Bell-lloc, Lleida, with samples from the FOR03 trial, which produced good grain quality.  
6 The traits recorded were caliber of grains, as the percentage of grains that passed through a sieve of  
7 2.2 mm (screening, SCR), the percentage of grains retained by a sieve of 2.5 mm (kernel plumpness,  
8 KP); the percentage of the malt rendered soluble upon mashing in the laboratory, i.e., the solids  
9 content of wort (MEX), and the percentage of protein in the grain (PRT). A complete list of trials  
10 where these traits were recorded is provided in Table S1.

#### 11 Statistical analyses

12 Each sub-trial was analyzed following the alpha-lattice design, using the procedure *proc mixed* of SAS  
13 (1988). BLUPs for the genotypes for each trait at each sub-trial were calculated accordingly. In a  
14 second analysis, the 10 check cultivars included in all sub-trials were analyzed, following a  
15 randomized complete block design (RCBD), with three replications nested within the four sub-trials  
16 (analyzed with *proc glm*, SAS, 1988). When the averages of the 10 checks for a particular trait were  
17 significantly different between sub-trials, this was interpreted as a true difference due to uncontrolled  
18 environmental conditions (possibly soil), and a correction was carried out. A factor, K, was calculated  
19 dividing the general average of the field trial by the average of the sub-trial. The corrected data were  
20 obtained multiplying the corresponding K value by the trait value of the genotypes included in each  
21 sub-trial. This correction was actually rather light, and was preferred over the option of correcting on  
22 the basis of the values of the 10 common checks, as this apparently overcorrected the data.

23 A previous diversity study based on molecular markers, revealed the occurrence of four different  
24 groups of accessions, or populations, in the landrace-derived Spanish lines, based on genetic  
25 differences (Yahiaoui et al., 2008). These populations were taken into account as possible sources of  
26 variation for the phenotypic traits measured in this study. The four groups (numbered G1 to G4)  
27 comprised 17, 9, 48 and 82 genotypes, respectively. For the purpose of this analysis, the SBCC sets of

1 old six-row cultivars, old two-row cultivars, and the 10 modern check cultivars were also considered  
2 as groups, G5 to G7, respectively.

3 Genotype was considered as a random factor, as the genotypes are a representative sample of all  
4 Spanish landrace barleys, and of cultivars widely grown in Spain. Environment, a combination of  
5 location and year for each field trial was considered fixed, because of the low number of degrees of  
6 freedom. This choice was justified because the number of field trials used was enough for an  
7 agronomic evaluation, but it is uncertain whether their frequencies are a representative sample of all  
8 possible environments in our conditions.

9 An AMMI analysis (Gauch, 1988, 1992) was carried out to describe the genotype-by-environment  
10 interaction (GEI) for grain yield, the main trait under study. This analysis was performed with routines  
11 *proc glm* and *proc princomp* in SAS (SAS, 1988). The number of significant terms in the AMMI  
12 model was evaluated with the method of Gollob (1968). The graphical representation of the AMMI  
13 model was enriched by plotting additional genotypic, phenotypic and environmental (climatic)  
14 variables, to study their relationship with the GEI of grain yield. A regression analysis of these  
15 variables with the genotypic principal component scores of the AMMI axes was performed. The  
16 regression coefficients were represented on the biplots, with length proportional to the coefficient of  
17 determination (percentage of variation of AMMI axes explained) of each external variable. Some of  
18 the environmental covariates were highly correlated among themselves. To reduce redundancy among  
19 them, a principal component analysis for these variables was carried out and only the most  
20 representative variables were shown in the AMMI graphical representations.

21 Finally, sets of external genotypic and environmental variables were introduced in the analysis of  
22 variance for grain yield by means of factorial regression (van Eeuwijk, 1995). These sets of variables  
23 were introduced as covariate for the GEI in a sequential manner as shown in Baril et al. (1995). Then,  
24 the two subsets of best covariates were combined in a single analysis, testing all their possible  
25 interactions until arriving at the most parsimonious model possible (the one that explained the largest  
26 proportion of the GEI sums of squares, using a minimum number of degrees of freedom).

27



## 1 **Results**

2 The values of trial ART02 were not included in the analysis of grain yield, because severe lodging  
3 impeded a good separation of plots during harvest. The results of three six-row Spanish accessions  
4 originally included in the analysis are not reported, as they turned out to be duplicates, after analysis  
5 with molecular markers (Yahiaoui et al., 2008).

6 Corrections due to differences among sub-tests were necessary at eight trials for grain yield, four for  
7 test weight, two for thousand kernel weight, and three for plant height. The correction factors were  
8 quite low, with the most extreme values being 0.9447 and 1.0618 for plant height at SAD02 and  
9 ART02, respectively, which means correction of approximately  $\pm 6\%$ .

### 10 Responses of groups of genotypes

11 There were noticeable differences between landraces and cultivars for all traits (Fig. 1). The analyses  
12 of variance for each trait are presented in Tables 2 and S2. The genotypic differences were broken  
13 down into *between* and *within* genetic groups (as defined in the M&M section). For most traits, mean  
14 squares for *between groups* were larger than *within groups*, especially for plant height, lodging and  
15 test weight, but also for powdery mildew resistance, grain yield, leaf rust resistance, thousand kernel  
16 weight and heading time. The GEI was also broken down in the same manner. The mean squares for  
17 this interaction were also larger *between* than *within* groups by trial for all traits.

18 Grain yield was higher overall for cultivars than for landrace-derived lines. The mode for cultivars and  
19 landraces was on the same yield class, but there were only cultivars at the highest yielding class. In a  
20 further step, trials were divided into two subsets according to overall productivity, with the threshold  
21 around 3000 kg ha<sup>-1</sup>: high productivity (YLD-H) for trials BEL02, VLD02, ART04 and SAD04, and  
22 low productivity (YLD-L) for trials SAD02, FOR03, SAD03, VED03, and VLD03. At high  
23 productivity trials, the cultivars yielded more than landrace lines, with most cultivars placed at the two  
24 highest yielding classes, in which there were no landrace lines. At the low productivity trials, however,  
25 landraces outyielded cultivars on average. Only 2 out the 25 highest yielding genotypes averaged over  
26 low productivity trials were cultivars, and the first 9 were landraces. There were differences among the

1 landrace groups as well (Table 2), with accessions from G4 showing a clear advantage over the other  
2 landrace groups at low yielding sites (Table S3). In these trials G4 and G3 actually performed on  
3 average as well as the best groups of cultivars.

4 Landraces were, overall, later flowering than cultivars, with an average delay ranging from 2.3 to 5.8  
5 days among trials (Table S4). Ranges of flowering dates were larger for landraces (between 17.5 and  
6 26.0 days) than for cultivars (between 9.7 and 19.0 days, Table S4). The most frequent flowering date  
7 for cultivars was around April 24-26, whereas for the landraces the mode was on April 28<sup>th</sup> (Fig. 1).  
8 Plant height was another trait in which landrace lines and cultivars presented striking differences.  
9 Most cultivars were very short, below 64 cm, whereas all landraces surpassed this height, with a mode  
10 around 83 cm, with the exception of G2 lines, which were shorter (Table S4). The pattern for lodging  
11 was similar to plant height, most cultivars being lodging resistant, whereas most landraces were prone  
12 to lodging.

13 Regarding yield components, the number of spikes and the number of kernels per square meter were  
14 larger for cultivars, though these traits were calculated only for one location. The two groups of two-  
15 row materials (G2 and G6) presented higher number of spikes per area than the rest. Number of  
16 kernels per spike was larger for landrace lines, but this was expected as 93% of them are six-row,  
17 whereas only 46% of cultivars are six-row. Test weight was larger for cultivars than for landraces, but  
18 thousand kernel weight was superior for landraces overall, particularly for groups G3 and G4, which  
19 had larger values than cultivars. This was true for 7 out of the 8 trials in which this trait was  
20 calculated.

21 Besides the main field trials reported here, the whole SBCC or the subset of landrace-derived  
22 accessions were tested in additional locations in smaller, unreplicated plots (6 rows, 25 cm apart, 3.5  
23 m long). In two of these trials there were disease attacks severe enough to reveal apparent genotypic  
24 differences. One trial at the province of Gerona (north-western tip of Spain), in 2000, suffered attacks  
25 of leaf rust (LR) and powdery mildew (PM), whereas one trial at Valladolid, also in 2000, had a  
26 powdery mildew attack. Also, noticeable damage due to net blotch (NB) was observed in trials ART02

1 and FOR03, and due to PM at BEL02 and SAD02. There seems to be ample diversity for powdery  
2 mildew and leaf rust resistance in landrace lines, and less for the reaction to net blotch (Table 2).

3 Regarding quality traits, grain size parameters (SCR, KP) for the landrace lines were comparable to  
4 the results of cultivars. Differences in malt extract and grain protein were almost non-existent,  
5 probably due to low replication of these measurements, and are just a rough indication of the malting  
6 quality potential of the genotypes tested.

### 7 Joint analysis for grain yield

8 The analysis of variance for grain yield revealed large differences between genotypes, and also a  
9 significant GEI. For both the principal effect (genotype) and the GEI, the mean squares *between*  
10 *groups* were much larger than *within groups*. Furthermore, when the GEI *between groups* was broken  
11 down, it was evident that the larger share of this interaction was contributed by the comparison of high  
12 vs. low productivity trials (Table 3).

13 The AMMI analysis for grain yield suggested some trends in the GEI (Figs.2 and S1). The first three  
14 axes were significant, explaining 48.0%, 28.0% and 15.5% of the sum of squares of the GEI,  
15 respectively (Table 3). Actually, the third axis may represent mostly noise, as we could expect a  
16 maximum of 81% of the GEI sums of squares due to pattern, as estimated by the method proposed by  
17 Gauch (1992). Therefore, the AMMI2 model is more parsimonious, and will be kept for further  
18 analyses. The trials could be classified roughly in three groups: two highly interactive groups, one  
19 with trials from the province of Valladolid (VLD03, VLD02) and the other with trials from the  
20 province of Lleida (BEL02, ART04), and the last group with the trials showing the least interaction,  
21 four from the province of Zaragoza (SAD02, SAD03, SAD04, VED03) and one from Lleida (FOR03).  
22 The first axis indicated a contrast between trials BEL02 and ART04 on one side, and VLD02 and  
23 VLD03 on the other. The second axis was driven mostly by the contrast between SAD03 and FOR03  
24 vs VLD02 and ART04. The separation between most cultivars (particularly those belonging to G5 and  
25 G7) and the landraces indicated different GE responses. Most cultivars had negative scores on both  
26 axes, whereas the landraces were distributed over the other three quadrants of the plot, although some  
27 were placed close to the origin, meaning that their GEI was minimal. There were differences between

1 groups of landraces as well. Almost all accessions from G3 had positive scores on the first axis. The  
2 accessions from the other 3 landrace groups were more scattered, but it is remarkable that, almost  
3 exclusively, accessions from G4 were found in the second quadrant. Therefore, there were apparent  
4 differential adaptations between cultivars and landraces, but also among landrace groups.

5 The genotypic covariate with largest positive correlations with the first axis was the reaction to  
6 powdery mildew, followed by plant height, lodging, leaf rust and heading time. Test weight, on the  
7 other hand, showed a strong negative correlation with the first axis. This axis also was significantly  
8 (and positively) correlated with maximum temperatures and evapotranspiration in the fall. We can  
9 speculate that good growing conditions during vegetative growth promoted plant development (higher  
10 plant height and lodging) at VLD02 and VLD03, but also favoured the development of diseases,  
11 particularly for the accessions with positive scores on the first axis, mostly landraces from all groups.  
12 The landraces and cultivars with negative scores on the first axis probably combined smaller size with  
13 some tolerance to diseases. The fact that no landrace had sizeable negative scores on both axes means  
14 that there was no line combining reduced plant height and lodging and good tolerance to disease.  
15 Actually, this may be one of the reasons of the overall superiority of modern cultivars in Spain. The  
16 second component showed less strong correlations with genotypic and environmental covariates. The  
17 strongest one was with plant height which, overall, appears as the main genotypic factor causing GEI  
18 in this study. Test weight was the other genotypic covariate with a remarkable correlation, negative,  
19 with the second axis.

20 In general, the cultivars showed relatively better performance at the higher yielding sites, except  
21 VED03, whereas G3 accessions showed an opposite pattern. The cultivars, in general, did not present  
22 a relatively good performance at the lowest yielding trials (SAD02, FOR93, SAD03, VLD03),  
23 whereas some landraces from groups G1, G2 and G3 had better relative adaptation at these trials.

24 The results of the factorial regression pointed at several genotypic and environmental covariates as  
25 related to the GEI of grain yield. Actually, the mean squares of the interaction terms including some of  
26 these covariates were remarkably larger (Table 3) than those derived from other partitionings of GEI  
27 (AMMI and genotypic groups). The reaction to powdery mildew was the main genotypic factor related

1 to grain yield GEI, particularly when considered together with the maximum fall temperature. Heading  
2 time, again in interaction with maximum fall temperature, was the second most important genotypic  
3 factor, followed by lodging which in turn, did not show any significant interaction with environmental  
4 covariates. Only 1.7 % of the degrees of freedom of GEI, corresponding to the interaction of the three  
5 genotypic covariates with Trial, explained 38.8% of its sums of squares. Moreover, just two degrees of  
6 freedom of the GEI (0.14%), corresponding to the interaction of powdery mildew resistance and  
7 heading time with maximum fall temperature, explained 21.1 % of the GE sums of squares.

## 8 **Discussion**

9 This study aimed at the characterisation of a potentially useful genetic resource, the Spanish landraces  
10 of barley, which has been scarcely used in modern plant breeding. Previous studies determined that  
11 they show clear genetic differences with the germplasm used in mainstream barley breeding in Europe  
12 (Yahiaoui et al., 2008) and also that they may carry adaptations to environmental conditions that may  
13 be useful for other regions in a climate change scenario (Casas et al., 2011). The present study gives a  
14 complete overview of the agronomic potential of Spanish landraces. The main finding of this study is  
15 the identification of drastic changes of genotype order between productivity levels, revealing that  
16 landraces are superior under mid-to-low production conditions. This is a relevant message for  
17 European breeders, because it means that some of these landraces possess traits that may have not  
18 been well captured in current cultivars. This finding is particularly interesting at this moment, in which  
19 breeders are looking for sources of favourable traits to increase resilience of crops to respond to  
20 climate change challenges.

21 The large differences found between landraces and cultivars were not unexpected. Variety  
22 replacement over the 20th century occurred for a reason, and this study hints at several traits as the  
23 possible basis underlying this replacement. From the agronomic point of view, a detrimental trait of  
24 the landraces is the excessive plant height that induces lodging under mid-high yielding conditions.  
25 Lower plant height and lodging in cultivars compared to landraces may have resulted from adaptation  
26 to modern fertilization levels. In fact, reduced plant height has been one of the main outcomes of  
27 modern breeding in winter cereals (Austin et al., 1980; Friedt, 2011). The longer growth cycle of the

1 landraces may be affected by the age in which they were developed. The original landraces were  
2 collected mostly in the first half of the 20th century, whereas the cultivars were bred in the second half  
3 of the century, mostly in the last quarter. Several studies have found an increase of temperatures in  
4 many regions of the world and, specifically, in Northern Spain over the second half of the past century  
5 (an average of 1.4°C, reported by Peñuelas et al., 2002) and in Southern Spain from 1986 until 2008  
6 (García-Mozo et al., 2010). These increases have caused, for instance, an advancement of leaves  
7 unfolding in trees of 16 days over 49 years (Peñuelas et al., 2002), and an advancement of flowering  
8 time of arboreal and herbaceous species, correlated with temperature increase (García-Mozo et al.,  
9 2010). This shift of phenological events must have affected crops as well. For instance, by advancing  
10 the occurrence of stressful situations during grain filling for winter cereals, due to earlier episodes of  
11 high temperatures. This increase of risk of high temperature stress for Southern Europe over the last  
12 century was indeed detected by the IPCC (IPCC, 2007). Therefore, an advancement of heading time in  
13 modern varieties, to avoid increasingly early terminal stress, is not surprising. A similar shortening of  
14 growth cycle due to breeding was observed for durum wheat (De Vita et al., 2007, Royo et al., 2008).  
15 On the other hand, the earliest heading time observed in landraces and cultivars was the same,  
16 suggesting that there is a minimum safety threshold to achieve heading, after the period of high risk of  
17 late frosts is over.

18 The landraces, in general, presented worse agronomic ability than cultivars. However, they also  
19 displayed large variability for most traits, suggesting a possible use for breeding. In this respect, one of  
20 the most important results of this study is that landraces presented better adaptation to low yielding  
21 environments. Finding as many as nine landrace-derived lines which outyielded 26 cultivars under our  
22 mid-to-low production conditions was an unexpected result of this study. These results suggest that  
23 modern breeding has not impacted Spain as it has impacted barley production in Central and Northern  
24 Europe. This phenomenon was already detected at a number of studies carried out in the  
25 Mediterranean region with different sets of local germplasm (Pswarayi et al., 2008a,b; Ceccarelli,  
26 1994; Ceccarelli and Grando, 1989, 1996). These studies, however, focused mostly on field trials with  
27 very low production levels, around or below 1 t ha<sup>-1</sup>, whereas average grain yields of our low yielding

1 are representative of a higher productivity level, between 1.7 and 2.4 t ha<sup>-1</sup> (Table S4). It was expected  
2 that, at this level, yield potential would still be the main feature determining grain yield, as found by  
3 Rizza et al. (2004) for Southern Italy, but this was not the case. This level of production is very  
4 common on large areas of barley cultivation in Spain and in other countries with Mediterranean  
5 climates, like Spain, Algeria or Australia, which are among the main barley producers (FAOSTAT,  
6 2013). Usually, the main limitation to realize higher yields in Mediterranean environments is limited  
7 water availability (Rizza et al., 2004) and, therefore, any superior germplasm under these conditions  
8 may carry some positive drought tolerance traits. Abundant research on drought tolerance of crops  
9 indicates that different mechanisms may be relevant at different productivity levels, (Cattivelli et al.,  
10 2008). Therefore, the best Spanish landraces represent useful resources for breeders to mine for traits  
11 useful for drought tolerance, particularly at moderate yielding levels.

12 The landrace lines were not homogeneous agronomically. Actually, the groups of landraces made  
13 according to their genetic diversity (Yahiaoui et al., 2008) also presented notable differences for  
14 several agronomic traits. It is remarkable that accessions from groups G3 and G4 had higher TGW  
15 than groups of cultivars, even though these two groups were significantly later heading than the  
16 cultivars and, therefore, experienced slightly worse grain filling conditions than the cultivars. This  
17 may be partially explained by a balancing effect between yield components but it also suggests the  
18 presence of stress tolerance mechanisms during grain filling in the Spanish accessions of groups G3  
19 and G4. Kernel weight is the yield component which is most affected in winter cereals suffering  
20 terminal stress (Stone and Nicolas, 1994; Brancourt-Hulmel, 1999), particularly under Mediterranean  
21 conditions (Voltas et al., 1999), and different mechanisms to maintain adequate grain filling under  
22 stress have been proposed (Blum, 2005). Actually, improvement of grain filling under stress has been  
23 identified as one of the main outcomes of breeding in durum wheat (Alvaro et al., 2008). The potential  
24 of some Spanish landraces to enhance grain filling under stress merits further exploration.

25 There were significant differences between accessions for grain yield, and also a large GEI term. In  
26 both cases, a large part of both terms was due to the differences between genotypic groups,  
27 particularly landraces and cultivars, although the differences within groups were still significant.

1 Cultivars, in general, presented plant height, heading time and lodging susceptibility better suited to  
2 modern cultivation. The results of the factorial regression also indicated a large relevance of powdery  
3 mildew resistance in the determination of grain yield GEI. This was also visible in Fig. 2, in which the  
4 reaction to powdery mildew and leaf rust seem to be driving the spread of the genotypes over the first  
5 axis. Brancourt-Hulmel (1999) found that heading time, lodging and powdery mildew resistance were  
6 the main genotypic features that drove GEI in winter wheat trials in France, the same traits we have  
7 found for barley in Spain in this study. Most likely, all these traits had some relevance in the process  
8 of the substitution of modern cultivars for landraces in Spain.

9 The genotypic groups showed some specific features that can be used for their focused use in  
10 breeding. Group G1 was constituted by a clearly differentiated set of accessions. They had the longest  
11 growth cycle and were the tallest genotypes. Though no direct measures of biomass were made, it was  
12 evident that they produced larger biomass than the rest. It is possible that the original landraces were  
13 grown to be used as fodder, and thus may be interesting material for bioenergy uses. The accessions  
14 from G3 and G4 come from different parts of Spain (Yahiaoui et al., 2008). G3 comes from colder  
15 regions of the inland plateau, whereas G4 comes from warmer lowlands of the Southern part of the  
16 country, the coastal Mediterranean regions and the Ebro valley. The first axis of the AMMI analysis is  
17 a contrast between locations that are representative of these two areas: Valladolid (VLD02, VLD03) is  
18 in the centre of the Northern plateau, and Lleida (BEL02, ART04) is in the centre of the Ebro valley.  
19 Therefore, there was good agreement between the origin of the accessions and their position in the  
20 AMMI biplot (Fig. 2). All but one of the accessions from G3 had positive loadings in axis 1, same as  
21 VLD02 and VLD03. G4 accessions were actually more spread over the first axis, but many were on  
22 the same (negative) side as ART04 and BEL02.

23 Among all groups of genotypes studied, the best accessions from group G4 offer the highest potential  
24 to contribute favourable traits for grain yield and disease resistance. These lines, though later heading  
25 than cultivars, were the earliest landrace group and also showed the best scores for leaf rust and  
26 powdery mildew resistance among the landraces. Nevertheless, they should be introduced with care  
27 into breeding programs, to reduce their plant height and susceptibility to lodging. For this purpose,



1 introgression through backcross is advised. Also, care should be taken to ascertain the agronomic  
2 effects of possible adaptation syndromes that have been selected for in the landraces over time,  
3 affecting at the genes of the vernalization and photoperiod pathways (Casao et al., 2011a, b). Ongoing  
4 work using genome wide association mapping, and linkage mapping approaches with biparental  
5 populations derived from the best Spanish lines (Hofmann et al., 2013; Silvar et al, 2011b; Ponce-  
6 Molina et al., 2012) is already producing useful information on markers linked to economically  
7 important traits that can be used to facilitate targeted trait introgression with marker –assisted  
8 selection.

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### 16 **References**

- 17 Álvaro, F., J. Isidro, D. Villegas, L. F. García del Moral, and C. Royo, 2008: Breeding effects on grain  
18 filling, biomass partitioning and remobilization in Mediterranean durum wheat. *Agron. J.* **100**, 361–  
19 370.
- 20 Austin, R. B., J. Bingham, R. D. Blackwell, L.T. Evans, M.A. Ford, C. L. Morgan, and M. Taylor,  
21 1980: Genetic improvement in winter wheat yields since 1900 and associated physiological changes. *J.*  
22 *Agr. Sci.* **94**, 675–689.
- 23 Baril, C. P., J.B. Denis, R. Wustman, and F. A. van Eeuwijk, 1995: Analysing genotype by  
24 environment interaction in Dutch potato variety trials using factorial regression. *Euphytica* **84**: 23-29.
- 25 Blum, A., 2005: Drought resistance, water-use efficiency, and yield potential: are they compatible,  
26 dissonant, or mutually exclusive? *Crop Pasture Sci.* **56**, 1159-1168.
- 27 Brancourt-Hulmel, M., 1999: Crop diagnosis and probe genotypes for interpreting genotype  
28 environment interaction in winter wheat trials. *Theor. Appl. Genet.* **99**, 1018-1030.

1 Casao, M.C., E. Igartua, I. Karsai, P.R. Bhat, N. Cuadrado, M.P. Gracia, J.M. Lasa, and A.M. Casas,  
2 2011a: Introgression of an intermediate *VRNHI* allele in barley (*Hordeum vulgare* L.) leads to reduced  
3 vernalization requirement without affecting freezing tolerance. *Mol. Breeding* **4**, 475-484.

4 Casao, M.C., I. Karsai, E. Igartua, M.P. Gracia, O. Veisz, and A.M. Casas, 2011b: Adaptation of  
5 barley to mild winters: A role for *PPDH2*. *BMC Plant Biol.* **11**, 164.

6 Casas, A. M., A. Djemel, S. Yahiaoui, L. J. Ponce-Molina, B. Contreras-Moreira, M. P. Gracia, J. M.  
7 Lasa, and E. Igartua, 2011: *HvFT1* (*VrnH3*) drives latitudinal adaptation in Spanish barleys. *Theor.*  
8 *Appl. Genet.* **122**, 1293-1304.

9 Cattivelli, L., F. Rizza, F. W. Badeck, E. Mazzucotelli, A. M. Mastrangelo, E. Francia, C. Maré, A.  
10 Tondelli, and A.M. Stanca, 2008: Drought tolerance improvement in crop plants: an integrated view  
11 from breeding to genomics. *Field Crops Res.* **105**, 1-14.

12 Ceccarelli, S. 1994: Specific adaptation and breeding for marginal conditions. *Euphytica* **77**, 205–219.

13 Ceccarelli, S., and S. Grando, 1989: Efficiency of empirical selection under stress conditions in barley.  
14 *J. Genet. Breeding* **43**, 25-31.

15 Ceccarelli, S., and S. Grando, 1996: Drought as a challenge for the plant breeder. *Plant Growth Regul.*  
16 **20**, 149–155.

17 De Vita P., O. L. D. Nicosia, F. Nigro, C. Platani, C. Riefolo, N. D. Fonzo, and L. Cattivelli, 2007:  
18 Breeding progress in morpho-physiological, agronomical and qualitative traits of durum wheat  
19 cultivars released in Italy during the 20th century. *Eur. J. Agron.* **26**, 39–53.

20 DGA. 2002. Encuestas productivas de cultivos herbáceos de invierno. Campaña 1999-2000.  
21 Departamento de Agricultura del Gobierno de Aragón.

22 FAOSTAT, 2013: <http://faostat.fao.org/site/567/default.aspx#ancor>. Last accessed 09-13-2013.

23 Florell, V. H., 1929: Effect of date of seeding on yield, lodging, maturity, and Nitrogen content in  
24 cereal varietal experiments. *Agron J.* **21**, 725-731.

25 Friedt, W., 2011: Barley breeding history, progress, objectives, and technology: Europe. In: *Barley:*  
26 *Production, Improvement and Uses*, SE Ullrich (ed), 160-171. Wiley-Blackwell.

27 García-Mozo, H., A. Mestre, and C. Galán, 2010: Phenological trends in southern Spain: A response  
28 to climate change. *Agr. Forest Meteorol.* **150**, 575-580.

29 Gauch, H. G., 1988: Model selection and validation for yield trials with interaction. *Biometrics* **44**,  
30 705-715.

31 Gauch, H. G., 1992: *Statistical analysis of regional yields trials*. Elsevier, Amsterdam. 278 p.

1 Gollob, H. F., 1968: A statistical model that combines features of factor analysis and analysis of  
2 variance techniques. *Psychometrika* **33**, 73-115.

3 Hargreaves, G. L., G. H. Hargreaves, and J. P. Riley, 1985: Irrigation water requirements for Senegal  
4 River Basin. *J. Irrig. Drain. E.-ASCE* **III**, 265-275.

5 Hofmann, K., C. Silvar, A.M. Casas, M. Herz, B. Büttner, M. P. Gracia, B. Contreras-Moreira, H.  
6 Wallwork, E. Igartua, and G. Schweizer, 2013: Fine mapping of the *Rrs1* resistance locus against scald  
7 in two large populations derived from Spanish barley landraces. *Theor. Appl. Genet.* DOI  
8 10.1007/s00122-013-2196-4.

9 Igartua, E., M. P. Gracia, J. M. Lasa, B. Medina, J. L. Molina-Cano, J. L. Montoya, and I. Romagosa.  
10 1998. The Spanish barley core collection. *Genet. Resour. Crop Ev.* **45**, 475-481.

11 IPCC, 2007: The Physical Science Basis. Contribution of Working Group I to the Fourth Assessment  
12 Report of the Intergovernmental Panel on Climate Change. S. Solomon et al., Eds. Cambridge Univ.  
13 Press, Cambridge, 2007; [www.ipcc.ch/publications\\_and\\_data/ar4/wg1/en/spm.html](http://www.ipcc.ch/publications_and_data/ar4/wg1/en/spm.html).

14 IPGRI, 1994: Descriptors for barley (*Hordeum vulgare* L.). International Plant Genetic Resources  
15 Institute, Rome, Italy, 45 p.

16 Knüpffer, H., I. Terentyeva, K. Hammer, O. Kovaleva, and K. Sato, 2003: Ecogeographical  
17 diversity—a Vavilovian approach. In: *Diversity in Barley (Hordeum vulgare)*; R. von Bothmer, T. van  
18 Hintum, and H. Knüpffer (Eds.), pp 53-76. Series: *Developments in Plant Genetics and Breeding*, 7,  
19 Elsevier, Amsterdam.

20 Lasa, J. M., E. Igartua, F. J. Ciudad, P. Codesal, E. V. García, M. P. Gracia, B. Medina B, I.  
21 Romagosa, J. L. Molina-Cano, and J. L. Montoya, 2001: Morphological and agronomical diversity  
22 patterns in the Spanish barley core collection. *Hereditas* **135**, 217-225.

23 Moralejo, M., I. Romagosa, G. Salcedo, R. Sánchez-Monge, and J. L. Molina-Cano. 1994: On the  
24 origin of Spanish two-rowed barleys. *Theor. Appl. Genet.* **87**, 829-836.

25 Newton, A. C., T. Aker, J. P. Baresel, P. Bebeli, E. Bettencourt, K. V. Bladenopoulos, J. H. Czembor,  
26 D. A. Fasoula, A. Katsiotis, K. Koutis, M. Koutsika-Sotiriou, G. Kovacs, H. Larsson, M. A. A.  
27 Pinheiro de Carvalho, D. Rubiales, J. Russell, T. M. M. dos Santos, and M. C. Vaz Patto, 2010: Cereal  
28 landraces for sustainable agriculture: a review. *Agron. Sustain. Dev.* **30**, 237–269.

29 Peñuelas, J., I. Filella, and P. Comas, 2002: Changed plant and animal life cycles from 1952 to 2000 in  
30 the Mediterranean region. *Global Change Biol.* **8**, 531-544.

31 Ponce-Molina, L. J., A. M. Casas, M. P. Gracia, C. Silvar, E. Mansour, W. T. B. Thomas, G.  
32 Schweizer, M. Herz, and E. Igartua, 2012: Quantitative trait loci and candidate loci for heading date in  
33 a large population of a wide barley cross. *Crop Sci.* **52**, 2469-2480.

1 Pswarayi, A., F. A. van Eeuwijk, S. Ceccarelli, S. Grando, J. Comadran, J.R. Russell, E. Francia, N.  
2 Pecchioni, O. Li Destri, T. Akar, A. Al-Yassin, A. Benbelkacem, W. Choumane, M. Karrou, H.  
3 Ouabbou, J. Bort, J.L. Araus, J.L. Molina-Cano, W.T.B. Thomas, and I. Romagosa, 2008a: Barley  
4 adaptation and improvement in the Mediterranean basin. *Plant Breeding* **127**, 554–560.

5 Pswarayi, A., F. A. van Eeuwijk, S. Ceccarelli, S. Grando, J. Comadran, J. R. Russell, N. Pecchioni,  
6 A. Tondelli, T. Akar, A. Al-Yassin, A. Benbelkacem, H. Ouabbou, W. T. B. Thomas, and I.  
7 Romagosa, 2008b: Changes in allele frequencies in landraces, old and modern barley cultivars of  
8 marker loci close to QTL for grain yield under high and low input conditions. *Euphytica* **163**, 435–  
9 447.

10 Rizza, F., F. W. Badeck, L. Cattivelli, O. Lidestri, N. Di Fonzo, and A. M. Stanca, 2004: Use of a  
11 water stress index to identify barley genotypes adapted to rainfed and irrigated conditions. *Crop Sci.*  
12 **44**, 2127–2137.

13 Royo, C., V. Martos, A. Ramdani, D. Villegas, Y. Rharrabti, and L. F. García del Moral, 2008:  
14 Changes in yield and carbon isotope discrimination of Italian and Spanish durum wheat during the  
15 20th century *Agron. J.* **100**, 352–360.

16 SAS Institute, 1988: *SAS/STAT™ User's Guide*, Release 6.03. Edition. Cary, NC: SAS Institute  
17 Inc., 1028 p.

18 Silvar, C., A. M. Casas, D. Kopahnke, A. Habekuß, G. Schweizer, M. P. Gracia, J. M. Lasa, F. J.  
19 Ciudad, J. L. Molina-Cano, E. Igartua, and F. Ordon, 2010: Screening the spanish barley core  
20 collection for disease resistance. *Plant Breeding* **129**, 45-52.

21 Silvar, C., K. Flath, D. Kopahnke, M. P. Gracia, J. M. Lasa, A. M. Casas, E. Igartua, and F. Ordon,  
22 2011a: Analysis of powdery mildew resistance in the Spanish barley core collection. *Plant Breeding*  
23 **130**, 195-202.

24 Silvar, C., A. M. Casas, E. Igartua, L. J. Ponce-Molina, M. P. Gracia, G. Schweizer, M. Herz, K. Flath,  
25 R. Waugh, D. Kopahnke, and F. Ordon, 2011b: Resistance to powdery mildew in Spanish barley  
26 landraces is controlled by different sets of quantitative trait loci. *Theor. Appl. Genet.* **123**, 1019-1028.

27 Stone, P. J., and M. E. Nicolas. 1994. Wheat cultivars vary widely in their responses of grain yield and  
28 quality to short periods of post-anthesis heat stress. *Funct. Plant Biol.* 21:887-900.

29 Tolbert, D. M., C. O. Qualset, S. K. Jain, and J. C. Craddock, 1979: A diversity analysis of a world  
30 collection of barley. *Crop Sci.* **19**, 789-794.

31 van Eeuwijk, F. A., 1995: Linear and bilinear models for the analysis of multi-environment Trials: I.  
32 An inventory of models. *Euphytica* **84**, 1-7.

- 1 van Oosterom, E. J., S. Ceccarelli, and J. M. Peacock, 1993: Yield response of barley to rainfall and  
2 temperature in Mediterranean environments. *J. Agr. Sci. - Cambridge* **121**, 307-307.
- 3 Voltas, J., F. A. van Eeuwijk, A. Sombrero, A. Lafarga, E. Igartua, and I. Romagosa, 1999: Integrating  
4 statistical and ecophysiological analyses of genotype by environment interaction for grain filling of  
5 barley. I. Individual grain weight. *Field Crops Res.* **62**, 63–74.
- 6 Yahiaoui, S., E. Igartua, M. Moralejo, L. Ramsay, J. L. Molina-Cano, F. J. Ciudad, J. M. Lasa, M. P.  
7 Gracia, and A. M. Casas, 2008: Patterns of genetic and eco-geographical diversity in Spanish barleys.  
8 *Theor. Appl. Genet.* **116**, 271-282.
- 9

1 Table1. Geographic coordinates, climatic characteristics, sowing date of the field trials.

Location	Coordinate s	Altitude (m)	Harvest year	Trial code	Sowing date	Mean T (°C)			Min T (°C)			Max T (°C)			Rainfall (mm)				ETP <sup>4</sup>			Ratio <sup>5</sup>		
						A <sup>1</sup>	W <sup>2</sup>	S <sup>3</sup>	A	W	S	A	W	S	A	W	S	Total	A	W	S	A	W	S
Artesa de Segre (Lleida)	41°53'N 01°02'E	320	2002	ART02	31/10/2001	7.10	7.13	16.13	1.40	0.70	8.63	12.77	13.57	23.57	100	67	202	369	130	154	435	0.77	0.44	0.46
			2004	ART04	18/12/2003	9.30	5.67	16.00	4.97	0.20	9.30	13.67	11.77	22.67	130	126	167	423	113	133	410	1.15	0.94	0.41
Bell-lloc d'Urgell (Lleida)	41°38'N 00°47'E	210	2002	BEL02	07/11/2001	8.33	7.97	16.83	3.43	2.60	9.43	13.13	13.37	24.23	82	54	152	289	127	147	442	0.65	0.37	0.34
Foradada (Lleida)	41°52'N 1°00'E	455	2003	FOR03	07/11/2002	9.80	5.83	18.07	4.43	-0.63	10.30	15.13	12.33	25.80	165	178	35	378	133	147	467	1.24	1.21	0.07
Macotera (Salamanca)	40°49'N 05°17'E	892	2002	VLD02	08/11/2001	8.97	9.07	15.97	3.07	3.67	8.73	15.10	14.47	23.17	111	107	137	354	140	154	431	0.79	0.69	0.32
			2003	VLD03	11/11/2002	11.73	6.33	14.70	6.83	-3.40	5.17	16.57	16.50	23.60	199	169	72	440	137	142	419	1.46	1.19	0.17
Sádaba (Zaragoza)	42°16'N 01°16'E	440	2002	SAD02	28/11/2001	8.93	8.57	16.20	2.97	2.97	9.13	14.87	14.07	23.20	66	59	162	287	136	149	421	0.49	0.39	0.38
			2003	SAD03	27/11/2002	11.17	6.73	17.37	6.43	1.63	10.37	15.87	11.83	24.33	147	189	77	413	128	133	437	1.15	1.43	0.18
			2004	SAD04	23/12/2003	9.33	6.00	15.50	4.93	0.93	8.70	13.77	11.03	22.23	159	116	129	404	114	126	409	1.40	0.91	0.32
Zuera (Zaragoza)	41°52'N 00°39'E	298	2003	VED03	08/11/2003	11.07	7.13	18.10	6.53	2.17	11.33	15.60	12.07	24.80	138	127	106	371	125	134	439	1.10	0.95	0.24

1 Autumn; 2 Winter; 3 Spring; 4 ETP: total evapotranspiration calculated according to the method of Hargreaves; 5Ratio: rainfall divided by the ETP

Source: National Institute of Meteorology

1 Table 2. Separation of means among the genotypic groups for all traits (see description in text).  
 2 Numbers followed by the same letter in each column are not significantly different according to  
 3 an LSD ( $P < 0.05$ ).  
 4

Groups	HDN (days)		PHT (cm)		LDG (score)		YLD (q/ha <sup>-1</sup> )		YLD_L (q/ha <sup>-1</sup> )		YLD_H (q/ha <sup>-1</sup> )	
	1	122.9	A	85.4	A	4.0	B	23.27	D	18.86	B	28.8
2	118.5	B	73.7	C	3.6	BC	24.01	D	18.90	B	30.4	DE
3	118.8	B	81.4	B	5.5	A	25.96	C	21.63	A	31.4	D
4	116.9	C	80.8	B	5.5	A	27.08	BC	22.08	A	33.3	C
5	112.5	E	63.0	D	1.4	D	26.75	C	18.97	B	36.5	B
6	114.2	D	74.1	C	3.0	C	28.27	B	21.59	A	36.6	B
7	114.7	D	59.8	E	1.1	D	29.90	A	21.84	A	40.0	A
1	TW (kg. hl <sup>-1</sup> )		TKW (g)		SPM (number)		KNM (number)		KS (number)		LR (score)	
	65.5	D	35.8	D	213	C	6844	A	32.4	A	7.4	AB
2	69.3	B	38.5	C	340	A	6297	A	18.7	D	8.1	A
3	62.7	F	42.6	A	246	C	6506	A	26.3	B	8.2	A
4	63.6	E	42.6	A	259	BC	7043	A	27.8	AB	6.2	B
5	72.1	A	38.7	C	374	A	7236	A	19.1	CD		
6	67.0	C	41.0	B	259	BC	7558	A	28.5	AB		
7	69.3	B	39.1	C	323	AB	7759	A	24.6	BC		
1	NB (score)		PM (score)		SCR (%)		KP (%)		MEX (%)		PRT (%)	
	5.7	BCD	4.6	B	8.0	A	53.4	C	76.5	A	11.3	AB
2	4.9	E	4.5	B	3.9	B	66.4	BC	78.2	A	12.0	A
3	5.9	AB	5.9	A	3.4	B	73.2	AB	73.2	A	10.9	AB
4	5.8	BC	4.2	B	3.7	B	70.6	AB	72.3	A	11.9	A
5	5.2	DE	2.9	C	2.0	B	81.5	A	79.9	A	11.8	A
6	6.3	A	3.9	B	2.6	B	77.1	AB	77.5	A	10.5	B
7	5.3	CDE	2.5	C	8.0	A	53.4	C	76.5		11.3	AB

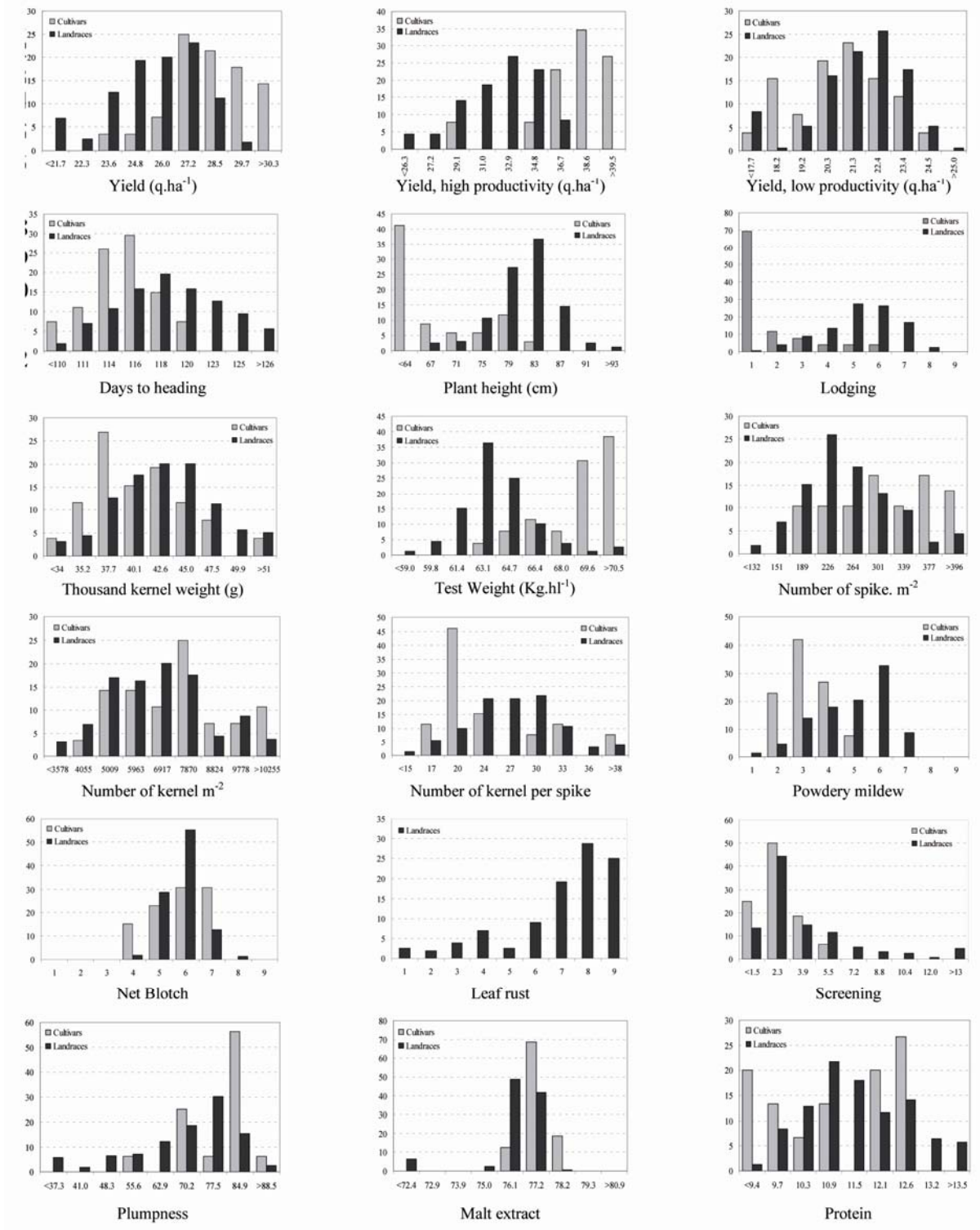
5  
6

1 Table 3. Joint analysis for grain yield, showing three different partitions of the genotype-by-  
 2 environment factor: genotypic groups (see text), AMMI and factorial regression with  
 3 genotypic and environmental covariates.  
 4

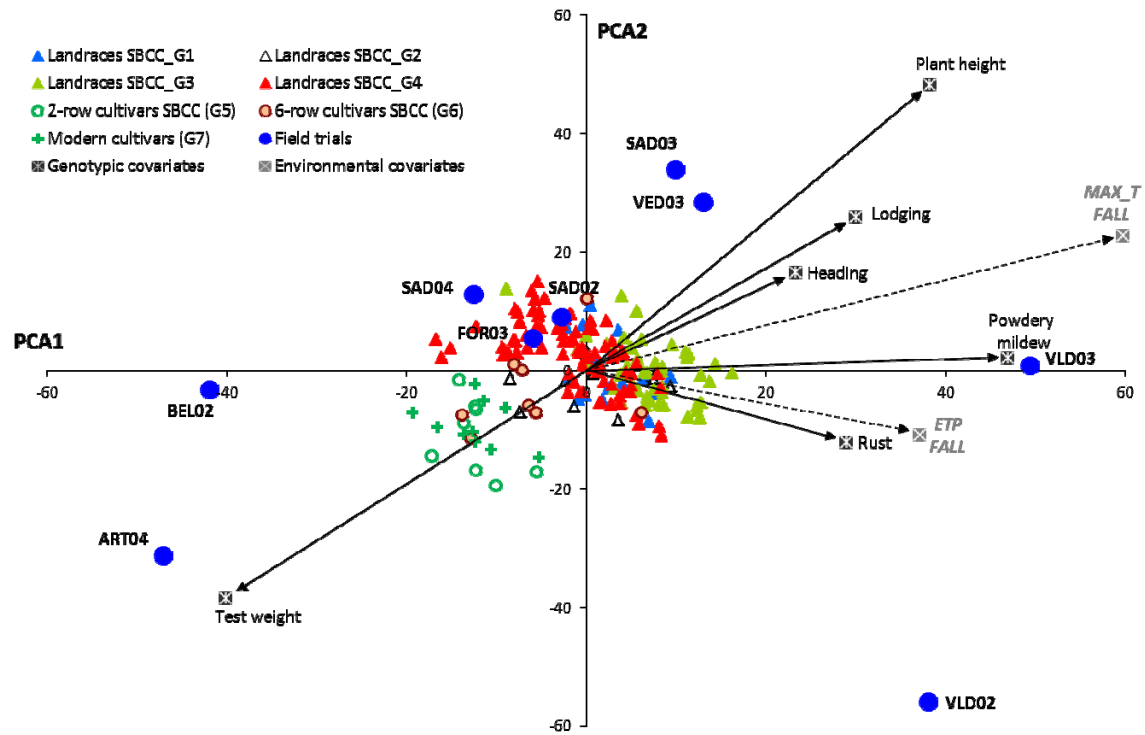
<b>Source</b>	<b>df</b>	<b>SS</b>	<b>MS</b>	<b>F</b>	
Trial	8	264928	33116	4088.4	**
Genotype	181	29322	162	20.0	**
Between groups	6	11248	1868	230.6	**
Within groups	175	18074	104	12.8	**
Genotype x Environment	1448	62942	44	5.4	**
<b>Genotypic groups</b>					
GE between groups	48	21667	451	55.7	**
GE bet. groups, high productivity	18	10102	561	76.1	**
GE bet. groups, low productivity	24	4747	198	24.4	**
GE bet. groups, high vs. low	6	6818	1136	140.2	**
GE within groups	1400	41275	29	3.6	**
GE with. groups, high productivity	525	21150	40	4.9	**
GE with. groups, low productivity	700	13150	19	2.3	**
GE with. groups, high vs. low	175	6975	40	4.9	**
<b>AMMI</b>					
AMMI1	188	30205	161	19.8	**
AMMI2	186	17594	95	11.6	**
AMMI3	184	9751	53	6.5	**
AMMI3 residual	890	5392	6	0.7	
<b>Factorial regression</b>					
PM*Trial	8	10978	1372	168.9	**
PM*Max T autumn	1	8049	8049	990.8	**
Deviation	7	2928	418	51.5	**
HDN*Trial	8	6903	863	106.2	**
HDN* Max T autumn	1	5204	5204	640.6	**
Deviation	7	1700	243	29.9	**
LDG*Trial	8	6539	817	100.6	**
Residual	1424	38522	27	3.3	**
Error	3276		8		

5 \*\*: Significant at level P <0.01

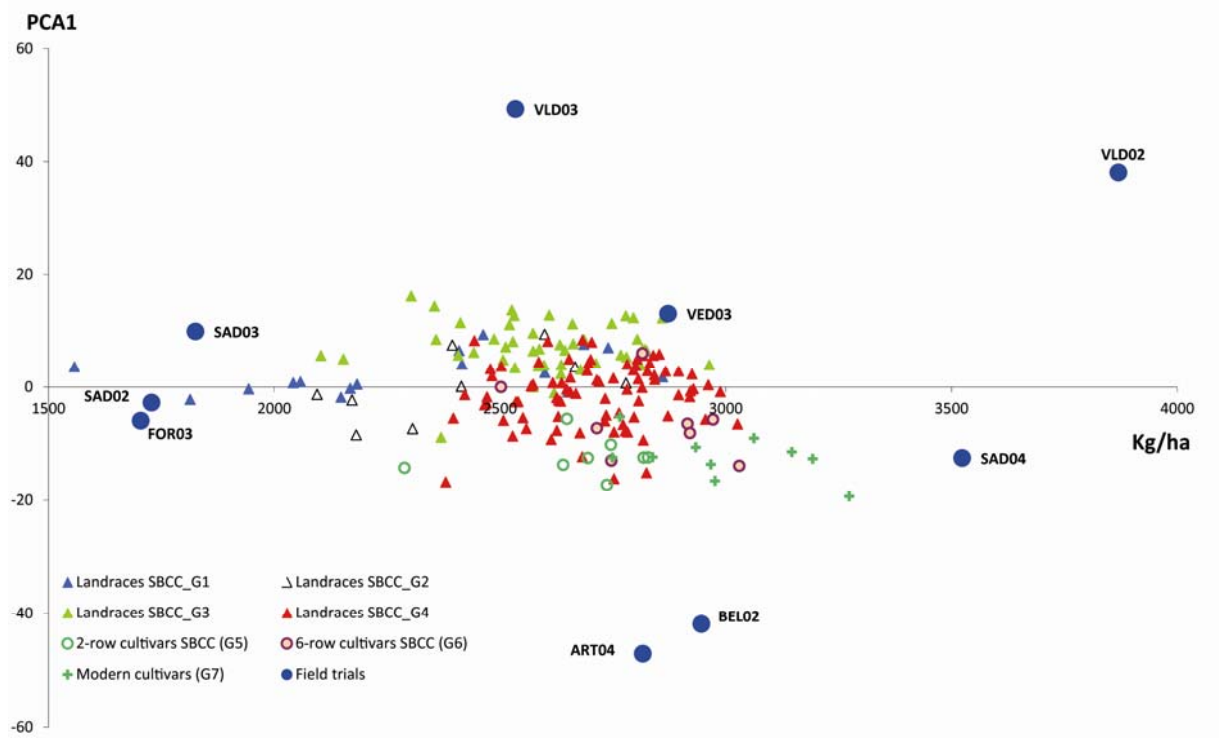




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1 Supplemental Table 1. Traits recorded at each field trial.

Trial	Plant height	Heading date	Lodging score	Grain yield	Test weight	Thousand kernel weight	Yield components	Malting quality traits	Leaf rust	Net blotch	Powdery mildew
ART02	x	x		x	x	x				x	
BEL02		x	x	x	x	x					x
SAD02	x			x							x
VLD02	x	x		x	x	x					
FOR03		x	x	x	x	x		x		x	
VLD03	x	x	x	x	x	x					
SAD03	x			x	x						
VED03	x	x	x	x	x	x	x				
ART04		x		x	x	x					
SAD04				x	x	x					
GER00									*		
VAL00											*

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1 Supplemental Table 2. Means and standard deviations of traits measured at each trial, split for landraces and cultivars.

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Trial	Groups	Variables															
		HED		PHT		LDG		YLD		TW		TKW		NBL		PML	
		Mean	Sd	Mean	Sd	Mean	Sd	Mean	Sd	Mean	Sd	Mean	Sd	Mean	Sd	Mean	Sd
ART02	Landraces	121.4	5.2	84.7	6.5	-	-	20.9	3.2	62.4	2.9	39.8	5.1	3.5	0.9	-	-
	Cultivars	119.1	4.0	74.0	10.1	-	-	27.8	2.7	69.4	3.5	40.0	4.9	3.3	1.2	-	-
BEL02	Landraces	112.1	4.7	-	-	6.5	1.3	28.5	5.0	63.5	3.0	39.8	5.0	-	-	3.9	1.6
	Cultivars	106.3	4.6	-	-	1.7	1.8	35.2	4.4	68.7	3.5	37.9	4.9	-	-	3.1	1.4
SAD02	Landraces	-	-	61.8	5.0	-	-	17.0	2.8	-	-	-	-	-	-	3.1	0.9
	Cultivars	-	-	50.1	7.3	-	-	18.9	2.4	-	-	-	-	-	-	3.0	0.8
VLD02	Landraces	124.0	5.1	89.5	6.7	-	-	38.4	5.9	65.6	3.0	46.2	3.7	-	-	-	-
	Cultivars	119.2	3.2	70.8	12.4	-	-	40.8	4.8	71.1	3.5	44.4	3.3	-	-	-	-
FOR03	Landraces	116.8	3.5	-	-	5.2	2.7	16.7	2.3	63.6	2.6	37.9	3.6	8.1	0.8	-	-
	Cultivars	114.1	2.6	-	-	2.0	1.8	19.2	2.5	69.3	3.3	36.9	3.7	7.9	1.1	-	-
VLD03	Landraces	123.4	6.2	92.3	11.4	5.2	2.5	25.8	4.0	65.6	2.3	44.0	5.0	-	-	-	-
	Cultivars	117.6	4.4	67.0	14.1	1.3	1.2	22.5	3.1	69.3	2.4	40.3	5.3	-	-	-	-
SAD03	Landraces	-	-	76.2	6.1	-	-	18.6	3.3	62.9	2.5	-	-	-	-	-	-
	Cultivars	-	-	61.9	8.3	-	-	16.1	3.3	68.0	2.8	-	-	-	-	-	-
VED03	Landraces	113.2	4.4	81.8	6.7	4.0	2.0	28.9	3.6	64.8	3.0	45.1	5.1	-	-	-	-
	Cultivars	109.5	3.5	67.6	11.5	2.0	2.0	27.7	3.3	69.4	3.5	40.3	5.2	-	-	-	-
ART04	Landraces	120.0	4.0	-	-	-	-	26.5	3.1	63.5	3.2	39.6	4.3	-	-	-	-
	Cultivars	116.6	2.5	-	-	-	-	38.4	5.6	70.6	4.4	38.4	4.2	-	-	-	-
SAD04	Landraces	-	-	-	-	-	-	34.9	4.5	63.0	3.4	40.6	4.9	-	-	-	-
	Cultivars	-	-	-	-	-	-	37.1	4.8	69.3	3.5	38.3	5.2	-	-	-	-

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Supplemental Table 3. Mean squares for the analyses of variance of a series of agronomic traits recorded at the field trials. Significant values (P<0.01) are highlighted in blue. Error terms for each trait are highlighted in red.

	df	HDN	PHT	LDG	TW	TKW	SPM	KNM	KS	PM	NB	LR	SCR	KP	MEX	PRT
Environment (E)	6	10528	53551	414	451	2870				619	57 43					
Genotype (G)	181	360	1047	41	176	229				10	3					
between groups	6	2868	19626	677	3733	2294	81506	8054221	584	127	13	44	68	1350	181	7.9
within groups	175	274	410	19	54	158	8865	7249772	64	6	3	3	9	180	82	1.2
GxE		13	99	10	8	14				3	1					
between groups		52	639	28	39	62				10	3					
within groups		11	80	9	7	13				3	1					
Error		3	21	3	4	4				2	1					

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Supplemental Table 4. Lists of the 25 best genotypes, according to grain yield over 9 trials (column “grain yield overall”), and over high productivity trials (column “grain yield – high”) and low productivity trials (column “grain yield – low”).

Ranking	Grain yield overall	Grain yield -high	Grain yield - low
1	Orria (G7)	Orria (G7)	73 (G4)
2	Graphic (G7)	Graphic (G7)	81 (G4)
3	Steptoe (G7)	Steptoe (G7)	16 (G4)
4	Candela (G7)	Gaelic (G7)	27 (G3)
5	Barberousse (G6)	Barberousse (G6)	91 (G4)
6	91 (G4)	Candela (G7)	38 (G4)
7	42 (G4)	Nevada (G7)	18 (G4)
8	Gaelic(G7)	Volga (G7)	75 (G4)
9	Monlón (G6)	Zaida (G5)	42 (G4)
10	Nevada (G7)	Kym (G5)	Orria (G7)
11	27 (G3)	Dobla (G6)	106 (G1)
12	81 (G4)	Ager (G6)	76 (G4)
13	18 (G4)	Alpha (G5)	39 (G4)
14	Volga (G7)	Monlón (G6)	31 (G3)
15	125 (G4)	Hassan (G5)	79 (G3)
16	73 (G4)	Tipper (G7)	51 (G3)
17	98 (G4)	91 (G4)	49 (G4)
18	Pané (G6)	Pané (G6)	14 (G4)
19	16 (G4)	145 (G4)	92 (G4)
20	Ager (G6)	Seira (G7)	109 (G4)
21	38 (G4)	42 (G4)	Steptoe (G7)
22	10 (G4)	98 (G4)	146 (G3)
23	14 (G4)	116 (G4)	11 (G3)
24	52 (G4)	4 (G1)	25 (G4)
25	4 (G1)	125 (G4)	125 (G4)

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1 Figure legends

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3 Fig. 1: Distribution of variables measured or recorded at a series of field trials for a collection of  
4 Spanish barley landraces, compared with a set of barley cultivars (see test for detailed description). The  
5 classes represent either 0.5 standard deviations for the continuous quantitative traits or a unit for the  
6 discreet traits

7 Fig. 2: Plot of the first two principal components of the AMMI analysis of grain yield for a series of  
8 Spanish barley landrace-derived lines and cultivars, grown in Spain in nine field trials. Genotypic and  
9 environmental covariates have been added to the plot, with vector lengths proportional to their  
10 correlation with the AMMI axes

11 Supplemental Fig. 1: Plot of the first principal component of the AMMI analysis of grain yield for a  
12 series of Spanish barley landrace-derived lines and cultivars, grown in Spain in nine field trials, versus  
13 the average yield of genotypes and trials.