

Towards understanding the genetic basis of adaptation to low rainfall environments

Jason K. Eglinton¹, Michael Baum², Stefania Grando², Salvatore Ceccarelli², Andrew R. Barr¹.

¹: Department of Plant Science, Waite Campus, The University of Adelaide, Glen Osmond, South Australia, 5064.

²: International Center for Agricultural Research in the Dry Areas (ICARDA), PO Box 5446, Aleppo, Syria.

Abstract

Water deficit is one of the most important constraints to cereal production in the Mediterranean-type dryland cropping environments of the world. The present project aims to identify and develop barley with improved adaptation to low rainfall environments, and to develop molecular markers for key traits associated with drought stress tolerance. While markers for these traits will find application within current breeding germplasm, this work also targets the identification of novel alleles from wild and landrace barley.

A population was developed from a cross between a Syrian landrace barley and an improved ICARDA line. The two parental lines are well adapted to low rainfall conditions, exhibit similar maturity, and also represent significant genetic diversity. In 1999/2000, this population was evaluated at two low rainfall sites in Syria and four sites in Jordan. The sites experienced significant drought stress and a number of lines out-yielded the parental lines and well adapted local varieties, and the differences in yield were not associated with maturity effects. A range of traits associated with performance under drought stress were measured including growth habit, early vigor, tiller number, leaf chlorophyll content, plant height, days to heading, biomass, kernel weight, grain yield and harvest index. A molecular map has been constructed with 247 molecular markers (73 SSR, 174 AFLP) used to genotype 94 RIL's from this population.

Tolerance to drought stress has been a difficult trait to characterise and quantify, and our current understanding is largely based upon comparative physiology. The application of molecular genetics strategies in conjunction with physiology and field evaluation promises to deliver significant advances in both our understanding of stress tolerance, and our ability to positively select for stress tolerance in crop improvement.

Introduction

Low rainfall environments are a major component of the cereal production areas in Australia. Almost one third of the total area sown to barley in Australia (979,000 ha) has returned mean grain yields of only 1.41 t/ha in the period 1986-1997 (area includes NSW central, SA and Vic mallee, WA eastern, mallee and sandplain zones – ABARE 1999). In most Mediterranean-type, dryland cropping environments of the world, including the Middle East where it was first domesticated, barley is the crop best adapted to the marginal fringes of cropping. In contrast, wheat is more widely grown within the marginal areas of southern Australia. This may, in part, be attributable to the general adaptation of germplasm used as sources for improved malt quality, including North American and European materials. Germplasm from ecogeographic regions similar to southern Australia, including wild and primitive landrace barleys, therefore provide an important resource to improve the adaptation of barley to low rainfall environments.

There is a significant lack of publications reporting on mapping of yield and related traits in low rainfall environments. Examination of published results from yield analysis of mapping populations demonstrates the importance of using appropriately adapted germplasm. While significant QTL for

yield and yield components have been identified under various field conditions, the map locations typically correspond to key loci influencing development, such as photoperiod sensitivity, dwarfing, growth habit, and vernalisation requirements (<http://www.css.orst.edu/barley/nabgmp/qtlsum.htm> and NBMMP, unpublished). The influence of developmental traits on yield tends to be amplified in high stress environments, significantly reducing the power of QTL analysis for detecting alleles conferring a yield advantage. The current study aims to develop and evaluate mapping populations suitable for investigating the genetic basis of adaptation to low rainfall environments, and is focused on novel germplasm that will contribute to the development of varieties with improved adaptation to southern Australia.

Materials and Methods

A population of 120 RIL's was generated from the cross Arta x Harmal-02/Esp//1808-4L by advancing lines through single seed descent to F₅ at ICARDA. Arta is a 2-row Syrian landrace and Harmal-02/Esp//1808-4L is an improved ICARDA breeding line. Both parents are well adapted to low rainfall conditions (250-375 mm) and are characterized by high yield stability.

In the 1999/2000 season, trial designs were incomplete blocks with 2 replicates with the 88 entries and 8 controls randomized within each block. Trials were evaluated at Tel Hadya and Breda (Syria), and Ramtha, Gweer, Khanasri, and Rabba (Jordan).

Traits assessed in the field trials included maturity, tiller number, plant height, growth habit, early vigour, kernel weight, grain yield, biological yield and harvest index. Chlorophyll content (SPAD) was obtained from the mean of 5 readings from intact leaves in the field using a portable chlorophyll meter [SPAD-502, Soil-Plant Analysis Development (SPAD), Minolta Camera Co., Osaka, Japan]. Spatial and MET analyses were performed by Ms Colleen Hunt, Biometrics SA.

Two hundred and fifty four molecular markers (80 SSR, 174 AFLP) were used to genotype the 94 RIL population from the cross Arta x Harmal-02/Esp//1808-4L. JoinMap 2.0 software was employed for map construction. Segregation ratios were tested using chi-square test at p=0.05, and p=0.01 respectively. Out of 254 molecular markers, 16 distorted markers were excluded from the linkage mapping. Markers were grouped using LOD thresholds at 6, and then the linkage groups were assigned to 7 chromosomes. The linkage map includes 189 molecular markers covering 646.3 cM on seven chromosomes (28, 1H; 42,2H; 16, 3H; 15, 4H; 16, 5H; 35, 6H; 37, 7H). QTL analysis of the adjusted site means was performed using MapQTL 3.0 software.

Results and Discussion

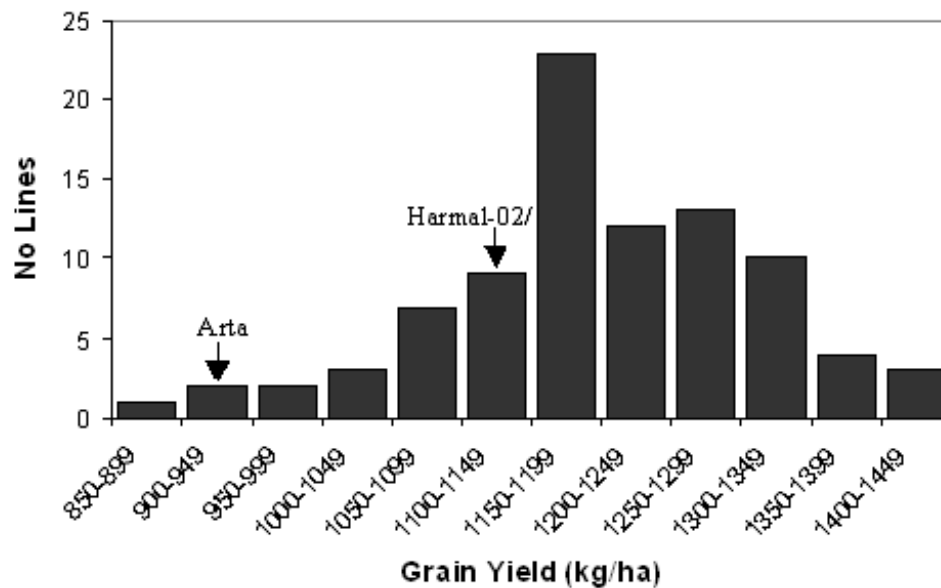


Figure 1: Distribution of grain yield in the mapping population compared to the parents tested at 6 locations in Syria and Jordan in the 1999/2000 season.

The trial sites in 1999/2000 experienced a range of drought stress, resulting in average adjusted mean yields of 3 t/ha at Tel Hadya, 1.3 at Breda, 0.99 at Ramtha, 0.86 at Rabba, 0.63 at Gweer, and 0.41 at Khanasri. No significant foliar diseases were observed in the trials. The correlation of grain yield at Tel Hadya to the other sites ranged from 0.72 to 0.77. The correlation between the remaining five sites ranged from 0.89 to 0.98. The heritability for grain yield was lowest at Tel Hadya at $h^2=0.56$, and highest at Breda at $h^2=0.83$. A significant number of lines from the population Arta x Harmal-02//Esp/1808-4L outyielded both parental lines, with the population means greater than the parental lines at both sites (Table 1). Furthermore, two lines yielded more than the best control varieties (data not shown). The best-performed lines did not exhibit significant maturity differences, suggesting the improved performance under drought stress is probably not due to escape mechanisms.

Figure 1 illustrates the grain yield distribution within the mapping population analysed across six sites in the 1999/2000 growing season. The population exhibits pronounced transgressive segregation, with a significant number of lines outperforming both parental lines, consistent with the results from 1998/1999. Very few lines produced grain yield lower than both parental lines.

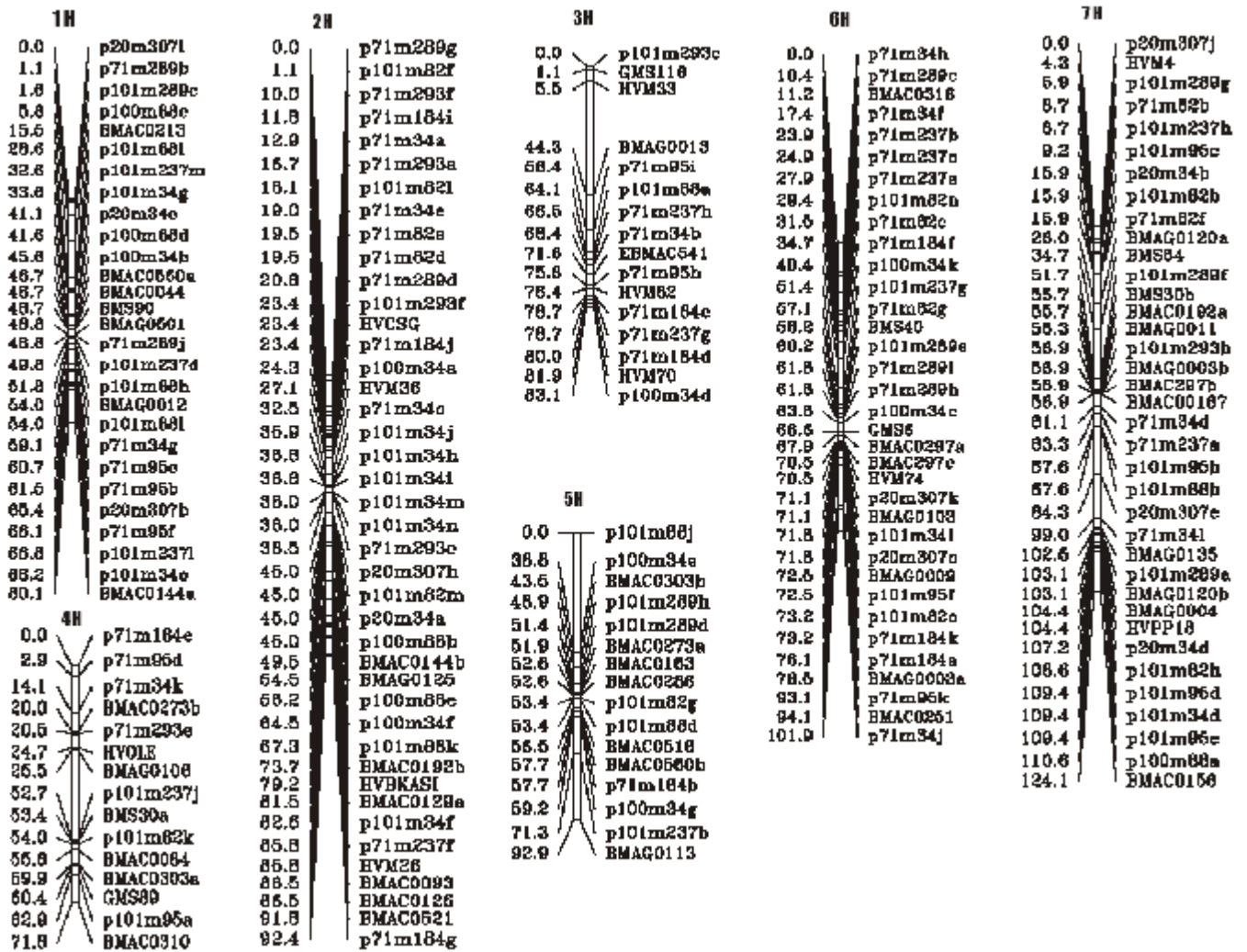
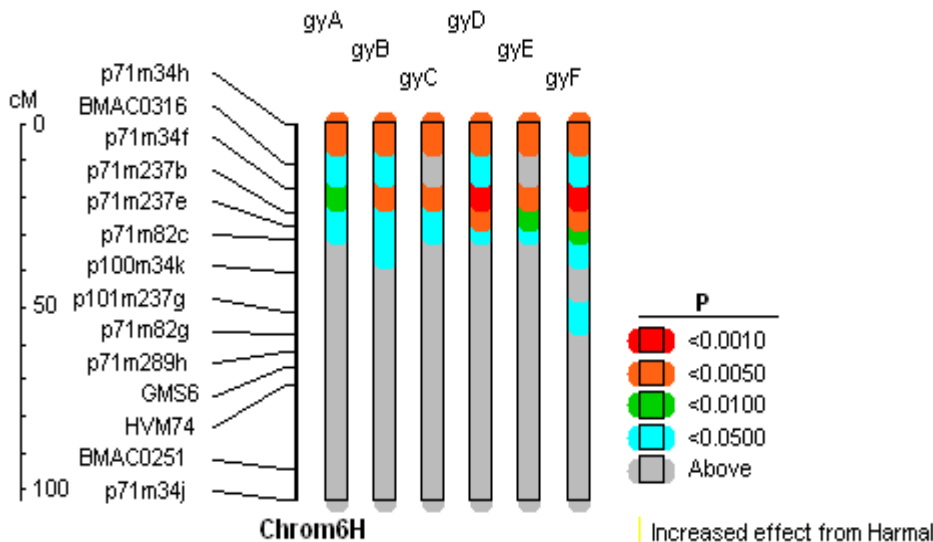


Figure 2: Linkage map constructed from 94 individuals from the cross Arta x Harmal-02/Esp//1808-4 genotyped with 189 AFLP and SSR markers.



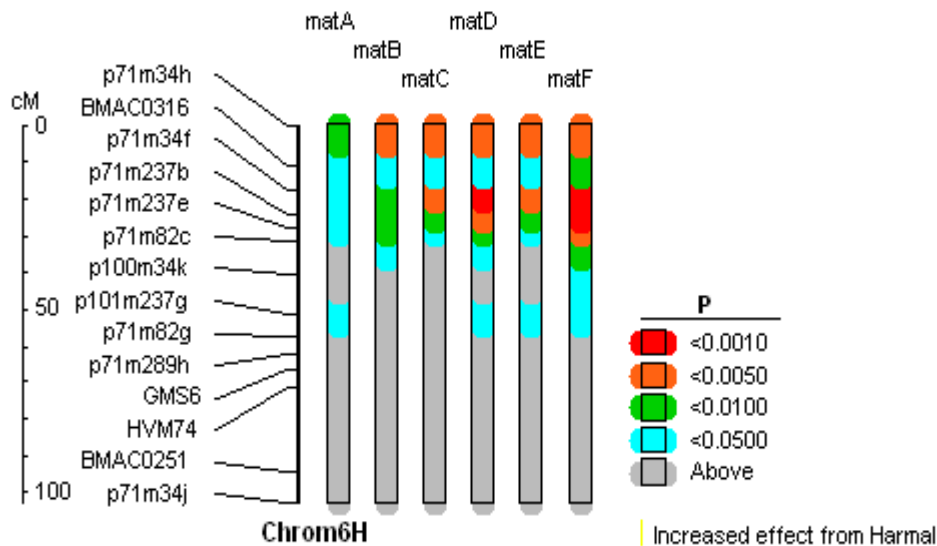
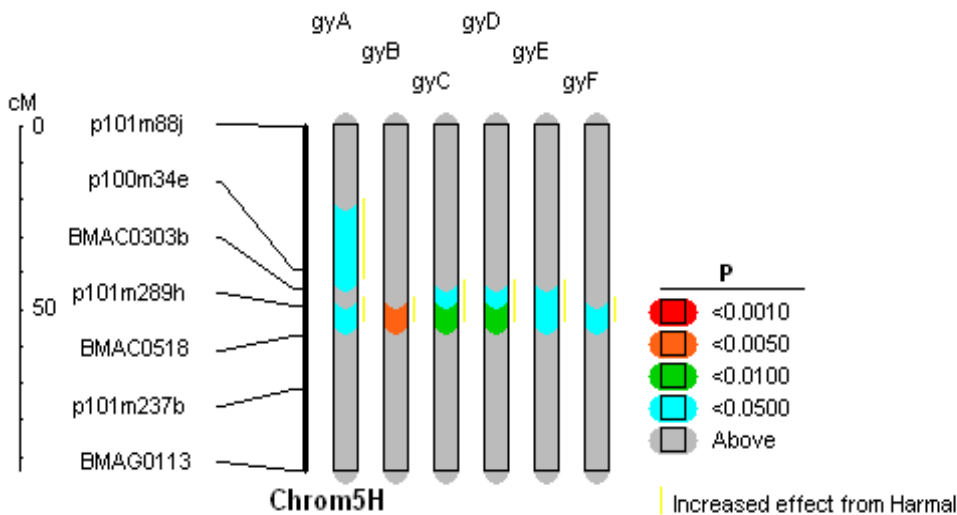


Figure 3: QTL analysis of chromosome 6H for grain yield (left panel) and maturity (right panel) for each of the six trial sites. Tel Hadya (A), Breda (B), Ramtha (C), Gweer (D), Khanasri (E), and Rabba (F).

A single QTL was detected for maturity positioned on the short arm of chromosome 6H (Figure 3), with the positive allele conferred by Arta. The QTL ranged from a LOD score of 3.0, explaining 20.5 % of the observed phenotypic variation at Rabba, to a weak association at Tel Hadya. The 6H locus was associated with grain yield at all six sites (Figure 3), with the strongest association explaining 18.4% of the observed phenotypic variation in grain yield. This locus is distinct from the locations typically associated with days to heading, however maturity effects have previously been identified in this chromosomal region in the Blenheim x E224 population (Thomas *et al.* 1995).



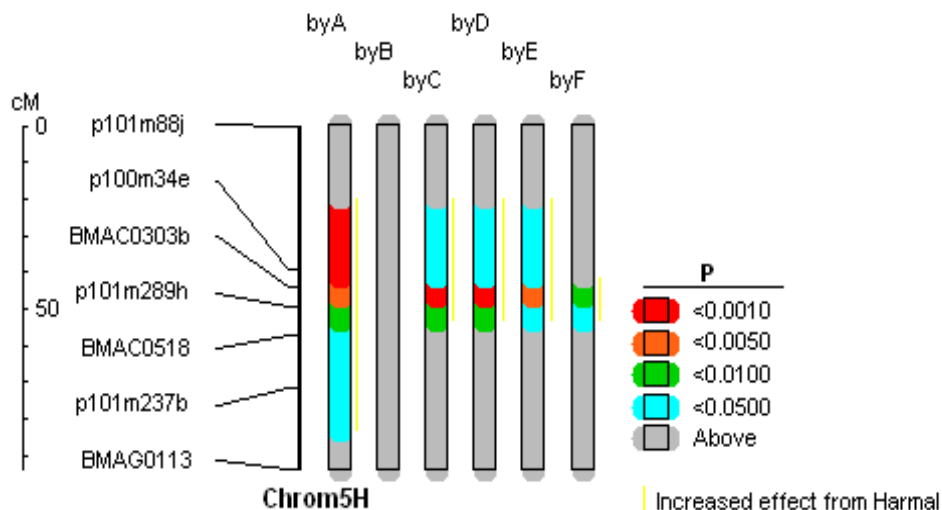


Figure 4: QTL analysis of chromosome 5H for grain yield (left) and biological (right) for each of the six trial sites. Tel Hadya (A), Breda (B), Ramtha (C), Gweer (D), Khanasri (E), and Rabba (F).

A QTL for biological yield (LOD = 2.9, explaining 14.9% of the phenotypic variance) was detected at Tel Hadya (Figure 4). The positive allele was from the parent Harmal-02/Esp//1808-4. The same QTL was detected with lower significance at the four sites in Jordan, but was absent in the trial at Breda. This locus had a detectable, but not statistically significant, association with grain yield at the six locations (Figure 4).

A QTL below the LOD threshold of 3.0 was detected at the same location on chromosome 1H at each of the five lowest rainfall sites (Figure 5), but was not observed at Tel Hadya (adjusted mean yield 3 t/ha). The positive allele was conferred by the Syrian landrace Arta. Grain yield QTL have previously been reported at the *hor1* locus on the telomeric region of the short arm of chromosome 1H (Hayes et al 1996), and at the telomeric region of the long arm of chromosome 1H (Hayes et al. 1996, Marquez et al. 2000). Confirmation of the effect of the 1H locus in further analysis of this population would verify a novel grain yield locus that does not appear to be confounded by developmental effects. The population has been evaluated again in the 2000/2001 season at the same six sites in Syria and Jordan, and is currently being grown in multiplication and observation trials in South Australia, prior to yield trials in low rainfall regions.

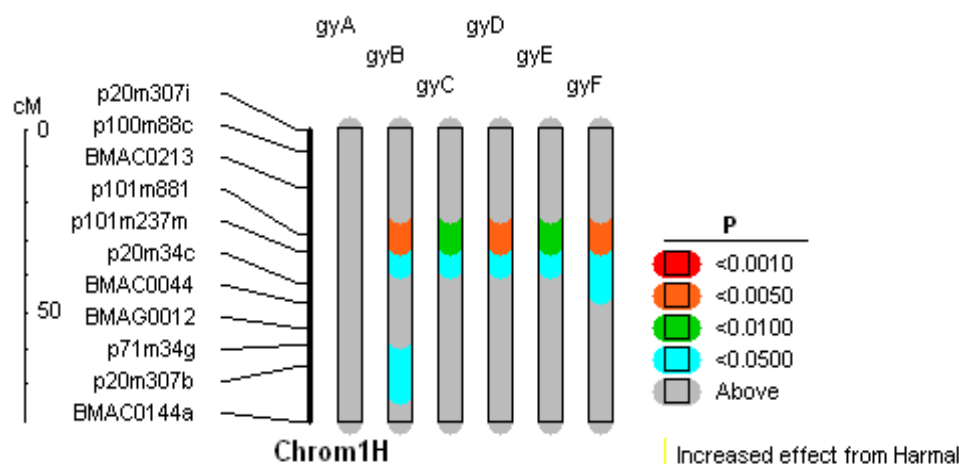


Figure 5: QTL analysis of chromosome 1H for grain yield for each of the six trial sites. Tel Hadya (A), Breda (B), Ramtha (C), Gweer (D), Khanasri (E), and Rabba (F).

In addition to the Arta x Harmal-02/Esp//1808-4L population, a number of other mapping populations

are currently under development, specifically targeting adaptation to low rainfall environments. Two advanced backcross populations have been produced, one from *H. spontaneum* 41-1 x Arta (at ICARDA), and the other CPI71284-48 x Barque (at the Waite). A population developed from Tadmor x ER/Apm has a complete map constructed (Teulat *et al.* 1998), and is currently in post entry quarantine prior to evaluation in Australia. This population is of particular interest given the encouraging performance of ER/Apm derivatives in SA field trials in 1999 and 2000.

Elite ICARDA breeding lines have been evaluated in SA during 1999 and 2000. The best of these lines have produced grain yield at least as high as the best Australian feed varieties analysed across two contrasting seasons. This is very significant given that imported barley lines are not normally comparable to Australian varieties, particularly under lower rainfall conditions. The four mapping populations provide the genetic resources to evaluate the potential of Syrian and Egyptian landraces, wild barley, and other adapted germplasm to improve the performance of barley in low rainfall areas. When combined with traits such as boron tolerance and disease resistance, we can reasonably expect this germplasm to contribute to increased in yield and yield stability across a significant proportion of Australia's barley production area.

Acknowledgements

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References

1. Australian Grains Industry: Performance by GRDC agroecological zones. ABARE, 1999.
2. Hayes PM, Liu BH, Knapp SJ, Chen F, Jones B, Blake T, Franckowiak J, Rasmusson D, Sorrells M, Ullrich SE, Wesenberg D, Kleinhofs A. (1993). Quantitative trait locus effects and environmental interaction in a sample of North American germplasm. *Theor. Appl. Genet.* 87(3):392-401.
3. Hayes PM, Prehn D, Vivar H, Blake T, Comeau A, Henry I, Johnston M, Jones B, and Steffenson B. (1996). Multiple disease resistance loci and their relationship to agronomic and quality loci in a spring barley population. *J. QTL*. <http://probe.nalusda.gov:8000/otherdocs/jqtl/index.html>
4. Marquez-Cedillo LA, Hayes PM, Jones BL, Kleinhofs A, Legge WG, Rosnagel BG, Sato K, Ullrich E, Wesenberg DM. (2000). QTL analysis of malting quality in barley based on the doubled-haploid progeny of two elite North American varieties representing different germplasm groups. *Theor. Appl. Genet.* 101(1-2):173-184.
5. Teulat B, This D, Khairallah M, Borries C, Ragot C, Sourdille P, Leroy P, Monneveux P, Charrier A. (1998). Several QTLs involved in osmotic adjustment trait variation in barley (*Hordeum vulgare* L.). *Theor. Appl. Genet.* 96(5):688-698.
6. Thomas WTB, Powell W, Swanston JS, Ellis RP, Chalmers KJ, Barua, UM, Jack P, Lea V, Forster BP, Waugh, R and Smith DB. (1996) Quantitative trait loci for germination and malting quality characters in a spring barley cross. *Crop.Sci.* 36: 265-273.

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