

Advanced backcross-QTL analysis in spring barley (*H. vulgare ssp. spontaneum*) comparing a REML versus a Bayesian model in multi-environmental field trials

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Received: 19 May 2008 / Accepted: 20 March 2009 / Published online: 11 April 2009
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Abstract A common difficulty in mapping quantitative trait loci (QTLs) is that QTL effects may show environment specificity and thus differ across environments. Furthermore, quantitative traits are likely to be influenced by multiple QTLs or genes having different effect sizes. There is currently a need for efficient mapping strategies to account for both multiple QTLs and marker-by-environment interactions. Thus, the objective of our study was to develop a Bayesian multi-locus multi-environmental method of

QTL analysis. This strategy is compared to (1) Bayesian multi-locus mapping, where each environment is analysed separately, (2) Restricted Maximum Likelihood (REML) single-locus method using a mixed hierarchical model, and (3) REML forward selection applying a mixed hierarchical model. For this study, we used data on multi-environmental field trials of 301 BC₂DH lines derived from a cross between the spring barley elite cultivar Scarlett and the wild donor ISR42-8 from Israel. The lines were genotyped by 98 SSR markers and measured for the agronomic traits “ears per m²,” “days until heading,” “plant height,” “thousand grain weight,” and “grain yield”. Additionally, a simulation study was performed to verify the QTL results obtained in the spring barley population. In general, the results of Bayesian QTL mapping are in accordance with REML methods. In this study, Bayesian multi-locus multi-environmental analysis is a valuable method that is particularly suitable if lines are cultivated in multi-environmental field trials.

Communicated by J.-L. Jannink.

Electronic supplementary material The online version of this article (doi:10.1007/s00122-009-1021-6) contains supplementary material, which is available to authorized users.

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Introduction

Detecting favourable exotic quantitative trait loci (QTLs) and introducing them into elite lines could greatly enhance breeding success. Tanksley and Nelson (1996) proposed an advanced backcross QTL analysis combining QTL discovery and variety development in a single step. Using advanced backcross populations derived from a cross of an elite cultivar with an exotic donor, it is possible to identify superior exotic QTLs, whereas the number of negative alleles from the unadapted material is reduced.

In order to map QTLs, the plant material is genotyped by DNA markers and measured on agronomic traits in multi-environmental field trials. In the following statistical

analysis, significant associations between DNA markers and phenotypic traits are determined. As quantitative traits are influenced by multiple genes having effects of different magnitudes, it is of primary interest in QTL mapping to select the appropriate model and to estimate the effects and locations of the QTLs (Broman and Speed 2002; Sillanpää and Corander 2002). A common difficulty in QTL mapping is that QTLs may show environment specificity, i.e., QTL effects may significantly differ across environments (Kang and Gauch 1996).

Several authors have examined multi-environmental data in composite interval mapping (Jansen et al. 1995), where selection of background markers is performed in several steps. Usually, uncorrelated residuals, i.e., no genetic (background) correlation among environments, are assumed in these models. Tinker and Mather (1995) implemented composite interval mapping to multi-environmental data using the least-squares estimation (Haley and Knott 1992). They included a test for QTL-by-environment interaction and used partial regression coefficients from background markers to control genetic variance due to non-target QTLs. Recently, Yandell et al. (2007) presented a software package called “R/qtlbim” providing Bayesian interval mapping by accounting for gene-by-environment interaction. Verbyla et al. (2003) computed a multiplicative mixed model for QTL-by-environment interaction of the factorial analysis type. The mixed-model method and the least-squares estimation were used by Piepho (2000). In this study, the genetic correlation among environments was also taken into account. In order to consider genetic correlations, Jiang et al. (1999) used a multi-trait approach of Jiang and Zeng (1995) and regarded expressions of the same trait in different environments as different traits. Fixed effects were pre-corrected by SAS software prior to the QTL analysis. Also, Boer et al. (2007) proposed a modeling approach of genotype-by-environment interactions accounting for genetic correlations between environments and error structure within environments of F₅ maize testcross progenies. A multi-locus analysis was applied by Crossa et al. (1999). In this study, partial least-squares regression and factorial regression models were used utilizing genetic markers and environmental covariables for studying QTL-by-environment interaction. Korol et al. (1998) presented an approach where the dependence of a putative QTL effect on environmental conditions is expressed as a function of environmental mean value of the regarded trait. This strategy allows for considering QTL-by-environment interactions across a large number of environments.

Concerning the known literature, a multi-locus QTL mapping approach that simultaneously considers model selection in multi-environmental data has not been fully developed. Since the magnitude of QTL effects can depend

on the specific environmental conditions, it is important to account for these effects in the model.

The objective of our research was to compare different approaches of multi-environmental QTL detection considering Bayesian and Restricted Maximum Likelihood (REML) methods: (i) REML single-locus analysis using a mixed hierarchical model, (ii) REML multi-locus analysis by a forward selection approach applying a mixed hierarchical model, (iii) Bayesian multi-locus mapping analyzing one environment at a time, and (iv) Bayesian multi-locus mapping in all environments jointly.

For this purpose, we used field data for an advanced backcross BC₂DH population derived from a cross of the malting barley cultivar Scarlett with the wild barley accession ISR42-8 from Israel (von Korff et al. 2006). In order to verify the results obtained with the real dataset, additionally a simulation study was performed. First, in a REML single-locus analysis, a mixed hierarchical model was computed in the Mixed procedure of the software package SAS 9.1 (SAS Institute 2004). Then, the same statistical model was applied by using a forward selection approach where the most significant marker of the current one-dimensional search round was always taken as a fixed cofactor in the model of the next estimation round. Furthermore, we applied a Bayesian multi-locus approach that was extended to handle multi-environmental data. In this approach, only marker points were considered as putative QTLs. In all cases, it was possible to account for QTL effects in multiple environments. This was compared to a Bayesian model where separate single-environmental analyses were executed for one environment at a time. In all analyses, we assumed the absence of genetic (background) correlation among environments.

Materials and methods

Real dataset of a spring barley population

A population with 301 BC₂DH lines originating from the cross of the German spring barley variety Scarlett with the Israeli wild barley accession ISR42-8 was developed. The BC₂DH population was genotyped by 98 SSR markers. Phenotypic evaluation of the traits “ears per m²” (Ear), “days until heading” (Hea), “plant height” (Hei), “thousand grain weight” (Tgw), and “grain yield” (Yld) was carried out under field conditions in unreplicated experiments at four different locations during the seasons 2003 and 2004. Data on the parental lines were collected but, as we considered the BC₂DH lines for QTL mapping, not included in the analysis. A detailed description is given in von Korff et al. (2004, 2006).

Simulation study

In the computer simulation, the real marker data of 301 BC₂DH lines were used by imposing known simulated genetic effects influencing the quantitative phenotype. For the genetic effects, marker main, marker interaction (crossover and non-crossover), and markers having both, a main and an interaction effect, were simulated. The positions and effect sizes of the simulated markers are presented in Table 5. As in the field dataset, a population of 301 DH lines was assumed being cultivated in six different environments. Normally distributed phenotypic values of a trait with a heritability of 0.59 were simulated. In the simulation, residuals were assumed to be independent (no correlation structure) with a standard deviation of 1.2 [N(0, 1.2)] and variance was considered to be the same for all environments. Also, no additional environmental effects were generated.

QTL mapping strategies

In our study, we compared different approaches of multi-locus multi-environmental QTL detection in the real and in the simulated dataset:

(1) REML single-locus analysis

The single-locus analysis was performed with SAS 9.1 software (SAS Institute 2004) using REML method of the Mixed procedure. Then, the applied mixed hierarchical model was as follows:

$$Y_{ijkm} = \mu + M_i + L_j(M_i) + E_k + M_i * E_k + \varepsilon_{m(ijk)}$$

With phenotypic observations Y_{ijkm} , general mean μ , fixed effect M_i of the i th marker, random effect $L_j(M_i)$ of the j th BC₂DH line nested in the i th marker, random effect E_k of the k th environment, random interaction effect $M_i * E_k$ of the i th marker with the k th environment, and residue $\varepsilon_{m(ijk)}$ of Y_{ijkm} .

In this analysis, the random factor $L_j(M_i)$ can be interpreted as a genetic background effect. The residuals were assumed to be identically and independently normally distributed. For each marker, a value of F -statistic, used to test the marker effect, is computed considering the residual mean of squares as an error term. The marker-by-environment interactions are tested by the value of t -statistic.

Missing marker data are handled by omitting each observation with a missing marker value from the dataset. Thus, the amount of phenotypic information is reduced due to missing marker data.

The relative performance of the homozygous exotic genotype ($RP[Hsp]$) was calculated by $RP[Hsp] = \frac{Hsp - Hv}{Hv} * 100$, where Hsp represents the least square mean of the

homozygous exotic genotype and Hv the least square mean of the elite genotype.

The computing time was about 1 min for one trait of both, the spring barley population and the simulated dataset on a Pentium IV 2.0 GHz processor.

(2) REML multi-locus analysis using a forward selection approach

The same mixed hierarchical model as described above was applied here for stepwise variable selection in SAS Proc Mixed. The stepwise variable selection strategy is described in Sillanpää and Corander (2002) and has been applied for example in Kilpikari and Sillanpää (2003). The first round of forward selection procedure corresponds to the single-locus analysis. Next, the marker with the most significant effect (based on the P value of hypothesis test Type III F -statistic) is chosen as a fixed cofactor in the model of the following estimation rounds. Using this extended model, the marker effects are estimated again. This procedure is repeated until no further significant markers can be found. The computing time for this method was about 20 min for one trait of the real and of the simulated dataset.

(3) Bayesian multi-locus analysis using multi-environmental data

Additionally, we performed Bayesian multi-locus QTL mapping using multi-environmental data.

The statistical model for phenotypic trait values Y_{jk} was as follows:

$$Y_{jk} = \mu + \sum_{i=1}^n M_{ij} + E_k + \sum_{i=1}^n M_{ijk} + \varepsilon_{jk}$$

where μ is the overall sample mean of the phenotypes, M_{ij} is the effect of the i th marker genotype of the j th line, E_k is the effect of the k th environment, M_{ijk} is the effect of the i th marker genotype of the j th line in the k th environment (i.e. genotype-by-environment interaction), and, n is the number of markers.

Residuals are assumed to be independently and identically normally distributed as $\varepsilon_{jk} \sim N(0, \sigma_0^2)$, where $\sigma_0^2 =$ residual variance common to all environments.

In the Bayesian setting, we parametrized the statistical model so that for each marker one genotype effect was assigned a value of zero; thus, for each marker we only needed to estimate one main effect M_{ij} . Similarly, in each environment for each marker, one environment-specific genotype effect was assigned a value of zero, resulting in one estimable coefficient M_{ijk} at each environment. By denoting the genotype (A or B) of line j at marker i with X_{ij} , the effects can be written as $M_{ij} = \beta_i 1(X_{ij} = B)$ and $M_{ijk} = \beta_{ik} 1(X_{ij} = B)$. The parameters β_i and β_{ik} are

interpreted as the difference of the main genotype effects and the differences of environment-specific genotype effects. Note, however, that unlike REML, this model is still oversaturated. The prior densities of the unknown marker effect differences in a K -environment model, $\theta = (\beta_1, \dots, \beta_n, \beta_{11}, \dots, \beta_{nk})$, were specified following Xu (2003); Hoti and Sillanpää (2006), where each effect θ_r , $r = 1, \dots, (K + 1)n$, in the statistical model is assigned a zero mean normal distribution with its own variance parameter σ_r^2 combined with Jeffreys' scale invariant prior $p(\sigma_r^2) \propto \frac{1}{\sigma_r}$. The prior of the overall mean was $p(\mu) \propto 1$, and the priors of the environmental effects were $p(E| \sigma_E^2) = \prod_k p(E_k | \sigma_E^2)$, where $p(E_k | \sigma_E^2)$ is a normal distribution with zero mean and a common variance σ_E^2 . The variance of the environmental effects and the variance of the residual term were assigned improper uniform priors, $p(\sigma_E^2) \propto 1$ and $p(\sigma_0^2) \propto 1$, respectively.

In order to obtain Markov Chain Monte Carlo (MCMC) samples of the joint posterior distribution of marker effects, Gibbs sampling (Geman and Geman 1984) and Metropolis-Hastings algorithms (Hastings 1970) were used. Here, we give the fully conditional posterior distributions of the environmental effects E_k and the effect variance σ_E^2 . The sampling distributions/updating steps of the remaining parameters and handling of missing data are described in Hoti and Sillanpää (2006). The fully conditional posterior distribution of the environmental effect E_k is a normal distribution with mean $\sum_{j=1}^N e_{j,k} \left(N + \frac{\sigma_0^2}{\sigma_E^2}\right)^{-1}$ and variance $\sigma_0^2 \left(N + \frac{\sigma_0^2}{\sigma_E^2}\right)^{-1}$, where N is the total number of lines. For the effect variance σ_E^2 , the fully conditional posterior distribution is the scaled inverted chi-squared distribution with the degree of freedom parameter K and the scale parameter $\sum_{k=1}^K \sum_{j=1}^N e_{j,k}^2$.

The Bayesian analysis was implemented using Matlab 7 (2007). The missing values were randomly assigned initial values from their empirical distributions. The MCMC algorithm was run for 400,000 rounds in the field dataset and 50,000 rounds in the simulated dataset. In order to reduce autocorrelation, only every 10th round was stored. In all cases, in the field data the first 380,000 MCMC-rounds (simulated data: 20,000 rounds) were considered to be "burn-in" rounds and were thus not considered in the final results. Computing time was about 33 h for one trait of the real dataset and about 20 min for the simulated dataset.

In the QTL analysis, we obtained estimates of marker main (M_{ij}) and interaction (M_{ijk}) effects. For each MCMC-sample, the sum of main and corresponding environment

interaction effect was calculated. Then, to interpret the results at each marker locus the median of the posterior distribution of marker effect over all MCMC-rounds was computed. If this median was non-zero in all environments, this marker had a main effect on the specific trait value. Otherwise, if the median was non-zero in some environments only, it was interpreted as a specific kind of a marker-by-environment interaction effect.

(4) Bayesian multi-locus analysis using single-environmental data

In order to determine whether multi-environmental QTL testing improves the results, we also conducted the same Bayesian multi-locus mapping as described above, but used data of each environment separately. Thus, the statistical model was reduced to:

$$Y_j = \mu + \sum_{i=1}^n M_{ij} + \varepsilon_j.$$

In this analysis, computing time of the main analysis was about 9 h for one trait of the real dataset and about 15 min for the simulated dataset.

Analogous to the multi-environmental Bayesian QTL analysis, the posterior median of the marker effects over all MCMC-rounds was computed. In both single- and multi-environmental Bayesian analysis, model selection and parameter estimation were based on adaptive shrinkage (Xu 2003; Hoti and Sillanpää 2006). Note that this approach is closely related to the so-called genome-wide selection (Meuwissen et al. 2001). In the genome-wide selection approach, breeding values are predicted based on molecular markers covering the whole genome. This strategy is in contrast to the use of genetic similarities, which are calculated based on the molecular marker data, in the prediction of breeding values (Bauer et al. 2006, 2008).

Convergence of the MCMC—chain

The convergence assessment of the Bayesian mapping strategies was performed by plotting the MCMC paths for the markers with estimated non-zero effects as suggested by Kass et al. (1998).

Significance threshold of estimated marker effects

In order to determine whether the detected QTL effects were due to spurious effects, we estimated an experimentwise critical value following Churchill and Doerge (1994). In this estimation, the data are shuffled by computing random permutations of the phenotypic observation vector. The i th observation is assigned to the i th line whose

index is given by the i th element of the permutation. Thus, the association between marker data and observations is destroyed. The shuffled data were analysed for Bayesian single-environmental and REML single-locus analysis. Overall, 50 permutations were calculated. In order to obtain the experimentwise critical value for a trait analysed by Bayesian single-environmental mapping, first the maximum median of the marker effects of every QTL analysis of permuted data is selected. In REML single-locus analysis, the maximum F value (for marker main effects) and the maximum t value (for marker interaction effects) of all permuted QTL analyses are chosen. In each mapping strategy, these values are ordered. The experimentwise critical value then corresponds to the $100(1 - \alpha)$ percentile, where α equals 0.05. In order to detect QTL effects in the original data and to determine statistical significance, the results of the QTL analysis can be compared to this critical value.

The forward selection approach utilizes the significance threshold obtained from REML single-locus analysis. As computing time was demanding for a Bayesian multi-environmental analysis, the calculation of a permutation analysis was not possible. Therefore, following Hoti and Sillanpää (2006) the MCMC-samples of all traits and markers were standardized to a common scale by multiplying each MCMC-sample with $\hat{\sigma}_g/\hat{\sigma}_p$, where $\hat{\sigma}_g$ is the empirical standard deviation of each marker and $\hat{\sigma}_p$ corresponds to the empirical standard deviation of phenotypic data. In the field dataset, a marker was defined to be significant if its standardized effect was greater than +0.17 or smaller than -0.17. In the simulated dataset, a significance threshold of ± 0.10 was chosen, thus, all markers having an effect greater than -0.10 or smaller than +0.10 are not considered to be significant.

Putative QTLs

Following Pillen et al. (2003), for each QTL mapping strategy linked significant markers that had a distance of ≤ 20 cM were interpreted as a single putative QTL.

Bin marker map

A Bin marker class was assigned to all used SSR markers following Kleinhofs and Graner (2001); Costa et al. (2001). Additionally, for the markers HVM62, GBM1015, HVM67, HVLTPPB, HVM36, and GBM1052, Bin classes were also available from the high-density consensus map recently published by Marcel et al. (2007). In the following, Bin classes obtained from Marcel et al. (2007) are given in italics.

Genetic variance explained by a marker

The genetic variance explained by a marker (R^2) was computed by:

$$R^2 = [\text{SQ}_M / (\text{SQ}_M + \text{SQ}_{L(M)})] * 100$$

with SQ_M = sum of squares of markers obtained from hypothesis test Type I; $\text{SQ}_{L(M)}$ = Type I sum of squares of lines nested in markers.

In order to obtain SQ_M and $\text{SQ}_{L(M)}$ we calculated the following mixed model in SAS Proc Mixed:

$$Y_{ijkm} = \mu + M_i + L_j(M_i) + E_k + \varepsilon_{m(ijk)}$$

where all parameters have been fixed factors.

Heritability

The heritability of the traits was obtained by REML variance component estimation using the Varcomp procedure in the SAS software package:

$$Y_{jkm} = \mu + L_j + E_k + \varepsilon_{jkm}$$

Then the heritability follows from $h^2 = \frac{V_g}{V_g + V_e}$, where V_g = genetic variance of the BC₂DH lines and V_e = residual variance.

Results

Field data of a spring barley population

In general, similar QTLs were detected using REML single-locus analysis, the REML forward selection approach, Bayesian multi-locus multi-environmental method considering all environments jointly in the analysis, and Bayesian multi-locus single-environmental mapping where each environment is analysed separately (Table 1). Depending on the heritability of the trait, some QTLs could be found to have a significant effect in all four mapping strategies. For example, considering “plant height,” a trait with a high heritability h^2 of 0.76, three of nine QTLs were detected with all analyses. In contrast, regarding “ears per m²,” a trait with a low heritability of 0.21, only one of 11 QTLs could be found to be significant with all approaches. In addition, only marker main effects were detected using a REML mapping method, whereas both marker main and interaction effects could be found by using a Bayesian approach.

In the following, detailed results of the QTL analyses will be described for every trait separately, where traits are grouped according to their heritability (Table 1):

Table 1 Detected QTLs of REML single-locus analysis (I), REML forward selection (II), Bayesian single-environmental (III), and Bayesian multi-environmental (IV) mapping for several traits in the spring barley population

QTL ^a	Coded marker number ^b	SSR-marker group	Chr. ^c	Pos. ^d	Bin ^e	R ² (%) ^f	RP(%) ^g	QTL mapping strategies			
								I ^h	II ⁱ	III ^j	IV ^k
<i>Days until heading</i> ($h^2 \approx 0.77$)											
QHea.S42-1H.1	5	GBM1042	1H	39	6	4.4	2.7	M ^{sl}	MxE ^m		
QHea.S42-1H.2	14	GBM1061	1H	115	13	0.7	0.9			M ^m	
QHea.S42-1H.3	16	HVABAIP	1H	144	13	4.0	1.8		MxE	MxE	
QHea.S42-2H.1	20	GBM1052	2H	42	4 (4)	21.6	-9.0	M*	M*	M	MxE
QHea.S42-2H.2	22–23	EBmac684, GMS3	2H	80–86	7–8	4.9, 5.0	-1.9, -2.0	M*	M*	MxE	MxE
QHea.S42-2H.3	29	EBmac415	2H	146	13	4.2	-3.3				MxE
QHea.S42-3H.1	31–32	HVLTTPB, EBmac705	3H	25–30	3 (3)	4.9, 4.5	-4.4, -4.3	M*	M*	MxE	
QHea.S42-3H.2	39	GBM1043	3H	130	10	4.3	-1.9	M*	M*	MxE	
QHea.S42-3H.3	40–41	HV13GEIII, HVVM62	3H	155–165	13–14 (15)	7.3, 4.6	-2.9, -2.2	M*	M*	MxE	M
QHea.S42-4H.1	54	EBmac701	4H	130	10	0.5	0.7				M
QHea.S42-4H.2	59–61	HVJASIP, HVVM67, HDAMYB	4H	180–190	12–13 (12)	4.3, 4.9, 6.1	1.8, 1.9, 2.2	M*	M*	MxE	
QHea.S42-5H.1	65	Bmag337	5H	43	5	0.3	-0.6				MxE
QHea.S42-5H.2	68	MGB338	5H	85	8	0.4	1.0			MxE	
QHea.S42-6H.1	77	EBmac624	6H	107	7	4.5	-2.1	M*			
QHea.S42-7H.1	92	BMS64	7H	146	8	4.1	-2.6	M*	M*		
<i>Plant height</i> ($h^2 \approx 0.76$)											
QHei.S42-2H.1	18–20	HVM36, GBM1035, GBM1052	2H	17–42	2–4 (3–4)	6.0, 5.3, 3.0	-8.9, -8.6, -11.5	M*	M*	MxE	
QHei.S42-2H.2	22–24	EBmac684, GMS3, HVTUB	2H	80–92	7–8	13.5, 16.3, 9.9	-10.8, -12.0, -8.9	M*	M*	M	
QHei.S42-3H.1	31–35	HVLTTPB, EBmac705, HVITR1, MGB410, Bmag603	3H	25–70	3–6 (3)	5.4, 5.4, 8.2, 6.1, 6.8	16.7, 16.7, 24.0, 12.9	M*	M*	MxE	MxE
QHei.S42-3H.2	39	GBM1043	3H	130	10	7.6	8.9	M*	M*	M	MxE
QHei.S42-3H.3	40–43	HV13GEIII, HVVM62, MGB358, Bmac29	3H	155–190	13–16 (15)	22.0, 16.9, 10.5, 3.9	17.9, 15.1, 11.7, 7.3	M*	M*	MxE	MxE
QHei.S42-4H.1	53–56	TACMD, EBmac701, EBmac635, EBmac679	4H	125–132	9–10	4.8, 6.3, 4.7, 5.1	-7.3, -8.4, -7.0, -7.3	M*			
QHei.S42-4H.2	58–61	GBM1015, HVJASIP, HVVM67, HDAMYB	4H	170–190	12–13 (11–12)	9.2, 14.6, 15.2, 5.8	-8.8, -11.0, -11.0, -7.1	M*	M*	MxE	
QHei.S42-5H.1	65	Bmag337	5H	43	5	6.4	9.6	M*			
QHei.S42-7H.1	83	Bmag7	7H	27	2	4.6	12.7	M*			
<i>Grain yield</i> ($h^2 \approx 0.70$)											
QYld.S42-1H.1	6	MGB325	1H	52	6	5.0	-13.0	M*			
QYld.S42-1H.2	8–11	HVM20, Bmag211, Bmag149, Bmag105	1H	65–75	7–8	4.9, 4.1, 4.8, 7.2	-12.9, -11.8, -12.8, -18.3	M*	M*	MxE	M
QYld.S42-1H.3	16	HVABAIP	1H	144	13	5.8	-9.3			MxE	MxE

Table 1 continued

QTL ^a	Coded marker number ^b	SSR-marker group	Chr. ^c	Pos. ^d	Bin ^e	R ² (%) ^f	RP(%) ^g	QTL mapping strategies					
								I ^h	II ⁱ	III ^j	IV ^k		
QYid.S42-2H.1	25–26	Bmag381, Bmag125	2H	107–122	9–10	3.0, 4.2	–6.5, –8.4	M*	MxE				
QYid.S42-3H.1	31–35	HVLT7PB, EBmac705, HVITR1, MGB410, Bmag603	3H	25–70	3–6 (3)	13.8, 13.9, 13.7, 10.7, 12.4	–32.6, –32.5, –39.8, –22.8, –24.7	M*	M*	MxE	MxE		
QYid.S42-3H.2	39	GBM1043	3H	130	10	2.0	–5.3	M*	M*	MxE	MxE		
QYid.S42-3H.3	40–41	HV13GEIII, HVM62	3H	155–165	13–14 (15)	8.2, 6.1	–12.8, –10.7	M*		MxE	MxE		
QYid.S42-3H.4	43	Bmac29	3H	190	16	0.1	–1.1				MxE		
QYid.S42-5H.1	65	Bmag337	5H	43	5	3.6	–9.6				MxE		
QYid.S42-5H.2	69	GMS61	5H	126	10	2.6	–12.9				MxE		
QYid.S42-7H.1	92	BMS64	7H	146	8	4.2	–11.1	M*					
<i>Thousand grain weight (h² ≈ 0.54)</i>													
QTgw.S42-1H.1	8	HVM20	1H	65	7	1.5	–2.1				MxE		
QTgw.S42-1H.2	16	HVABAIP	1H	144	13	0.5	1.0				MxE		
QTgw.S42-2H.1	23	GMS3	2H	86	8	1.9	1.9				M*	MxE	MxE
QTgw.S42-2H.2	25–26	Bmag381, Bmag125	2H	107–122	9–10	0.3, 0.5	0.9, 0.9				MxE		MxE
QTgw.S42-3H.1	38	HVM60	3H	110	9 (8)	4.5	3.1	M*					
QTgw.S42-3H.2	40–42	HV13GEIII, HVM62, MGB358	3H	155–175	13–15 (15)	3.3, 4.3, 6.5	–2.8, –3.1, –3.8	M*	M*	MxE			
QTgw.S42-4H.1	53–56	TACMD, EBmac701, EBmac635, EBmac679	4H	125–132	9–10	16.6, 16.3, 17.1, 16.8	–5.6, –5.7, –5.5, –5.5	M*	M*	M*	MxE	MxE	
QTgw.S42-4H.2	59–61	HVJASIP, HVM67, HDAMYB	4H	180–190	12–13 (12)	8.8, 8.4, 8.7	–3.7, –3.6, –3.7	M*	M*	M*	MxE		
QTgw.S42-6H.1	75	GMS6	6H	96	5	1.4	–1.8				MxE		
QTgw.S42-6H.2	79	GBM1008	6H	135	10	1.6	1.8				MxE		
QTgw.S42-7H.1	92–95	BMS64, Bmag120, MGB317, EBmac755	7H	146–166	8–11	4.6, 4.7, 4.4, 4.2	–4.2, –4.3, –4.6, –3.6	M*	M*	M*	M*	MxE	
<i>Ears per m² (h² ≈ 0.21)</i>													
QEar.S42-1H.1	16	HVABAIP	1H	144	13	6.0	8.4				M*		
QEar.S42-2H.1	18	HVM36	2H	17	2 (3)	5.8	9.5				M*		
QEar.S42-2H.2	21–24	MGB391, EBmac684, GMS3, HVTUB	2H	67–92	6–8	6.4, 21.5, 24.2, 21.2	11.1, 15.3, 16.5, 14.7	M*			M*	MxE	MxE
QEar.S42-3H.1	34–35	MGB410, Bmag603	3H	65–70	5–6	6.7, 6.5	–13.7, –13.8	M*			M*		
QEar.S42-3H.2	40–41	HV13GEIII, HVM62	3H	155–165	13–14 (15)	5.2, 4.6	–8.8, –7.9	M*			M*		
QEar.S42-4H.1	45–46	HVOLE, HVB23D	4H	21–25	3	5.2, 4.5	–9.7, –9.3	M*			M*		
QEar.S42-4H.2	53–56	TACMD, EBmac701, EBmac635, EBmac679	4H	125–132	9–10	10.0, 9.6, 9.5, 9.1	11.4, 11.3, 10.6, 10.6	M*			M*		
QEar.S42-4H.3	58–61	GBM1015, HVJASIP, HVM67, HDAMYB	4H	170–190	12–13 (11–12)	13.6, 23.9, 22.7, 9.0	12.0, 16.0, 15.4, 9.8	M*	M*	M*	M*	MxE	MxE
QEar.S42-5H.1	62	MGB384	5H	0	2	6.8	–10.8	M*			M*		

Table 1 continued

QTL ^a	Coded marker number ^b	SSR-marker group	Chr. ^c	Pos. ^d	Bin ^e	R ² (%) ^f	RP(%) ^g	QTL mapping strategies			
								I ^h	II ⁱ	III ^j	IV ^k
QEar.S42-5H.2	65	Bmag337	5H	43	5	4.6	-8.3				M*
QEar.S42-6H.1	79	GBM1008	6H	135	10	5.1	-7.6				M*

^a Names of the QTLs consisting of the qualifier "Q", the trait abbreviation, the determined population, the mapped chromosome and a QTL number to distinguish between QTLs on the same chromosome. Markers with a distance ≤ 20 cM were considered to be a single QTL

^b The markers were coded according to their chromosomal location

^c Chromosomal location of the SSR markers

^d Position of the SSR markers on the chromosome in centiMorgan (cM) (von Korff et al. 2004). If several markers were significant, the cM range is given

^e Bin marker class following Kleinhofs and Graner (2001); Costa et al. (2001). In the case of several significant markers, the Bin class range is displayed. An additional number in brackets gives the Bin class following Marcel et al. (2007). As the Bin class of Marcel et al. (2007) was available only for some markers, in the case of several significant markers belonging to the same QTL, these markers are given in italics

^f Genetic variance explained by a marker calculated using REML method in SAS Proc Mixed

^g Relative performance of the homozygous exotic genotype

^h REML single-locus QTL mapping

ⁱ REML forward selection approach

^j Bayesian multi-locus single-environmental analysis

^k Bayesian multi-locus multi-environmental analysis

^l Marker main effect obtained from REML analysis

^m *M* Marker main effect, *MxE* Marker interaction effect. Both effects are derived from Bayesian analysis and have to be interpreted differently as in REML method. In Bayesian mapping the model was oversaturated so that marker main and interaction effects are not independently identifiable

“Days until heading” ($h^2 \approx 0.77$)

Overall, 15 QTLs distributed over all chromosomes were found to be significant for the trait “days until heading.” Two QTLs were significant for four analyses, three QTLs for three analyses, four QTLs for two analyses, and six QTLs were found in one analysis.

“Plant height” ($h^2 \approx 0.76$)

For “plant height,” nine QTLs on the chromosomes 2H, 3H, 4H, 5H, and 7H were detected. Three QTLs were found in all four approaches, in three analyses, and with only one strategy, respectively.

“Grain yield” ($h^2 \approx 0.70$)

Eleven QTLs for the trait “grain yield” were located on the chromosomes 1H, 2H, 3H, 5H, and 7H. Two QTLs were found with all QTL mapping strategies, two QTLs were detected with three analyses, two QTLs with two analyses, and five QTLs were found in only one mapping strategy.

“Thousand grain weight” ($h^2 \approx 0.54$)

For the trait “thousand grain weight” the analyses revealed 11 QTLs on all chromosomes with the exception of 5H. One QTL was detected with all mapping approaches, four QTLs with three analyses, one QTL with two analyses, and five QTLs were found to be significant in only one analysis.

“Ears per m^2 ” ($h^2 \approx 0.21$)

For the trait “ears per m^2 ,” overall, 11 QTLs could be detected on all chromosomes except 7H. One QTL was found to be significant in all four mapping strategies, one QTL in three analyses, two QTLs in two analyses, and seven QTLs were detected in only one approach.

In order to illustrate the QTL mapping strategies, the results of all statistical analyses will be presented in more detail for the trait “grain yield.” Considering REML single-locus analysis, overall, 14 markers on chromosomes 1H, 2H, 3H, and 7H (Table 2) showed a F value greater than the significance threshold (obtained from permutation test). The P value of F test ranged between 0.001 and 0.017, and the estimated marker effects of the exotic allele ranged between -11.46 and -2.46 . If a REML forward selection approach was performed, only four markers had a value of F -statistic greater than the significance threshold. These markers showed a P value of F test ranging from 0.001 to 0.009 and estimated effects from -7.35 to -3.35 .

In Bayesian single-environmental mapping, overall, 14 markers showed a significant effect resulting in nine QTLs (Fig. 1; Table 1). None of the markers showed a significant effect in all six environments (Fig. 1). In contrast,

Table 2 Significant SSR markers with their chromosomal positions, estimated effects of the exotic allele, F and P values from REML single-locus analysis and the REML forward selection approach for the trait “grain yield” of the spring barley population

SSR marker	Chromosome	Position (cM)	Effect	F value	P value
<i>REML single-locus analysis</i>					
MGB325	1H	52	-3.80	15.8	0.011
HVM20	1H	65	-3.78	15.5	0.011
Bmag211	1H	68	-3.45	12.2	0.017
Bmag149	1H	70	-3.74	14.5	0.013
Bmag105	1H	75	-5.36	19.7	0.007
Bmag125	2H	122	-2.46	12.8	0.016
HVLTPPB	3H	25	-9.54	39.3	0.002
EBmac705	3H	30	-9.48	40.4	0.001
HVITR1	3H	49	-11.46	28.7	0.003
MGB410	3H	65	-6.69	42.5	0.001
Bmag603	3H	70	-7.26	48.7	0.001
HV13GEIII	3H	155	-3.76	18.3	0.008
HVM62	3H	165	-3.15	14.4	0.013
BMS64	7H	146	-3.25	12.2	0.017
<i>REML forward selection</i>					
Bmag603	3H	70	-7.26	48.75	0.001
HVLTPPB	3H	25	-7.35	23.46	0.005
Bmag105	1H	75	-5.34	24.84	0.004
GBM1043	3H	130	-3.35	17.39	0.009

Significance threshold obtained from permutation test: 12.14 (F value)

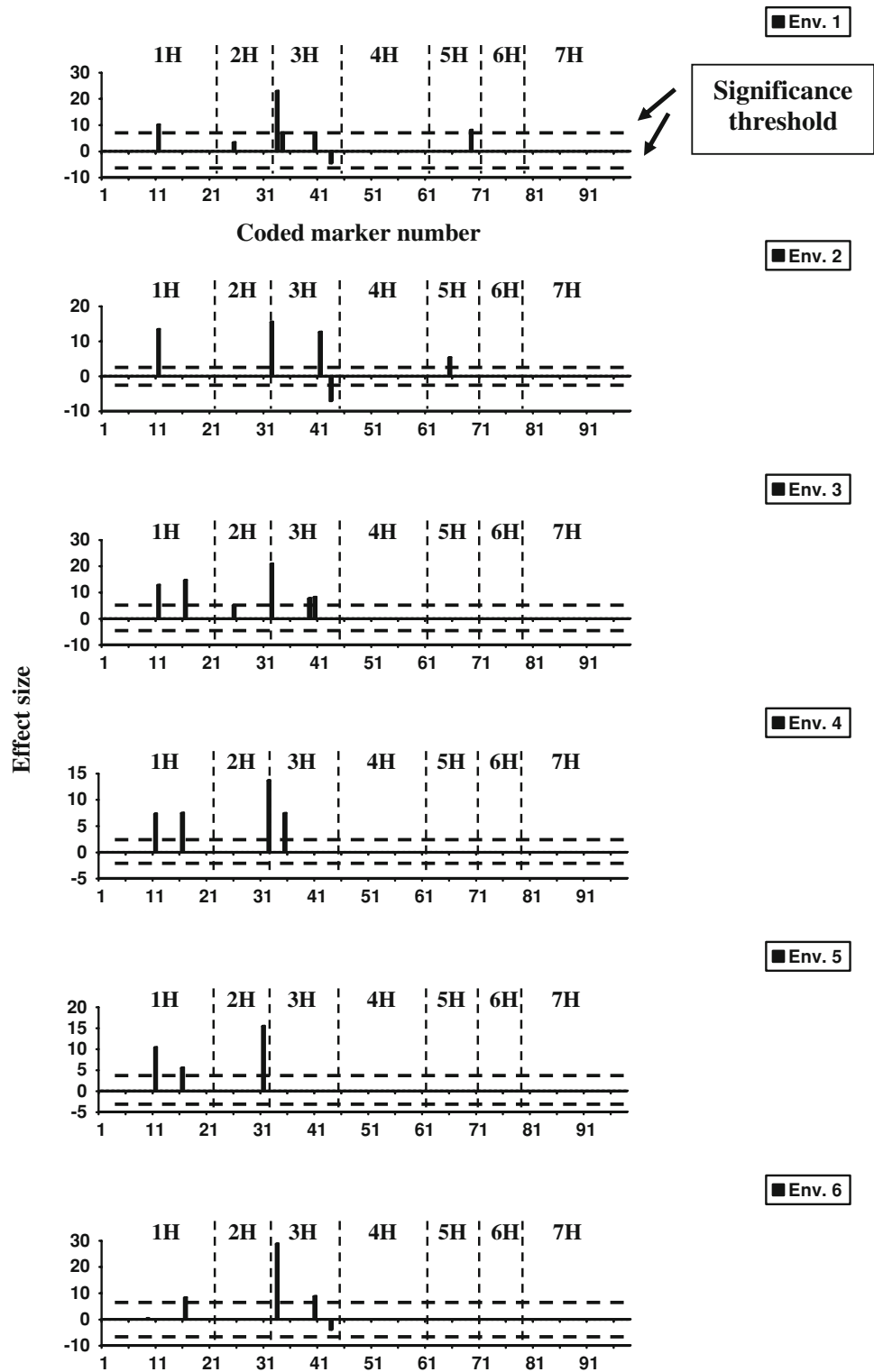
considering Bayesian multi-environmental analysis, only five markers having a significant effect were mapped, yielding five QTLs (Fig. 2; Table 1). In Bayesian multi-environmental mapping markers flanking a significant QTL on the same chromosome often showed negligible effects (Fig. 2). For example, the marker 11 has estimated (standardized) effects between 0.22 and 0.33, and is hence defined to be significant. The flanking markers with the numbers 12–15 have small (standardized) effects ranging from -0.05 to $+0.04$.

Simulation study

In the computer simulation, based on the real molecular marker data known genetic effects were assumed. Marker main and interaction (non-crossover and crossover) effects and combinations of both of them were simulated having different effect sizes (Table 5).

In Bayesian single- and multi-environmental QTL mapping, except for one marker with a main effect, all other markers with true (simulated) effects were detected regardless of the marker having an effect in all or in only some environments (Table 5). The marker that was not

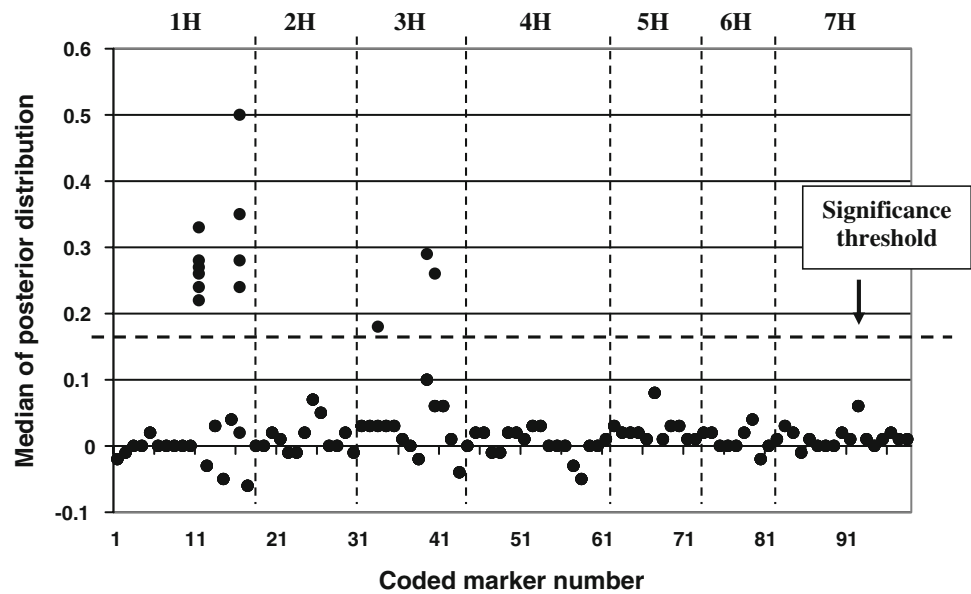
Fig. 1 Locus-specific point-estimates (posterior medians) of effect sizes of Bayesian multi-locus single-environmental QTL mapping for the trait “grain yield” in the spring barley population. The posterior medians are displayed for all environments separately. The significance threshold was obtained from permutation tests. The markers were coded according to their chromosomal location



found in Bayesian analyses (marker 79), has a true effect of 0.2 but estimated effect of 0 which could be due to the small effect size. The false-positive marker 32 was supported by both Bayesian methods (in one or two environments) although the marker has a true effect of zero.

Considering REML single-locus analysis and the REML forward selection approach, all markers with an interaction effect (non-crossover or crossover) were not detected (Table 6). Also, only two of the four markers having a marker main effect were found. However, using REML

Fig. 2 Locus-specific point-estimates (posterior medians) of standardized effects of Bayesian multi-locus multi-environmental QTL mapping for the trait “grain yield” in the spring barley population. The posterior medians of all environments are displayed jointly in the graph. The markers were coded according to their chromosomal location



single-locus mapping in several cases on the same chromosome, a marker near to a marker with a true effect was found to be significant although this marker has an effect of zero in the simulation. In the forward selection approach, a less number of false-positive markers were detected than in REML single-locus analysis.

Discussion

In this study, a QTL mapping approach was developed that accounts for both multiple marker loci and marker-by-environment interactions simultaneously in the statistical model. For comparison, a Bayesian multi-locus single-environmental analysis, a REML single-locus approach, and REML forward selection analysis were computed. In order to determine which markers showed significant effects, a permutation test was calculated for the REML single-locus and Bayesian single-environmental analysis. In general, this permutation test is used in frequentist approaches and only rarely in Bayesian data analysis. In a permutation test, multiple hypothetical datasets obtained from shuffling the phenotypic observations that could have given rise to the observations are considered. The objective here is to determine how extreme our observed dataset is (in the sense of producing the mapping signal). This means we examine the strength of the mapping signal in the observed dataset compared to the random mapping signals in the shuffled datasets.

Using REML single-locus QTL mapping, each marker locus was considered separately in the analysis. That means that, as the lines were genotyped by 98 SSR markers, 98 analyses had to be performed. All markers with an F value

greater than the significance threshold were considered to be significant. In the single-locus analysis, many significant QTLs were detected in the real and in the simulated dataset (Tables 2, 6). This could be due to the consideration of only a single marker point at a time, which complicates the detection of a marker with a significant effect at the exact position on the chromosome. Hence, it can be observed that in several cases not the marker with a non-zero simulated effect itself (i.e., marker 22 in Table 6), but a marker with an effect of zero located near to the true marker on the same chromosome was found instead (i.e., marker 21). As both markers are within an interval of 20 cM, in the field dataset both markers were interpreted to belong to the same QTL. Compared to the REML single-locus mapping, using a REML forward selection approach, fewer markers were found to be significant (Tables 2, 6). Thus, as expected, the forward selection analysis seems to be more powerful for QTL mapping. Since the markers with the most significant effect in previous estimation rounds are included as fixed cofactors in the statistical model of the next estimation cycle, similar to composite interval mapping, the forward selection approach accounts for multiple marker loci in the analysis.

In Bayesian multi-locus analysis using multi-environmental data of the spring barley population, several significant QTLs were found (Table 1). However, some of these QTLs showed only negligible effects (Fig. 2). Remarkably, the observed small peaks were found around larger ones in the same region on the chromosome. One reason for detecting several candidates can be the increased power, in particular for identifying markers with low effects. Also, having multiple coefficients at single marker in the model is likely to improve mixing

Table 3 Occupancy probabilities P of marker effects being higher than the significance threshold in Bayesian multi-environmental mapping for all traits in the spring barley population

Ears per m ²		Days until heading		Plant height		Thousand grain weight		Grain yield	
QTL	P	QTL	P	QTL	P	QTL	P	QTL	P
QEar.S42-2H.2	1	QHea.S42-1H.2	0.55	QHei.S42-3H.1	0.63–0.8	QTgw.S42-2H.1	0.91	QYld.S42-1H.2	0.83–1
QEar.S42-4H.3	0.53–1	QHea.S42-1H.3	1	QHei.S42-3H.2	0.89	QTgw.S42-2H.2	0.63	QYld.S42-1H.3	0.94–1
		QHea.S42-2H.1	0.98–1	QHei.S42-3H.3	0.49–1	QTgw.S42-4H.1	0.99	QYld.S42-3H.1	0.66
		QHea.S42-2H.2	0.91					QYld.S42-3H.2	1
		QHea.S42-2H.3	0.52					QYld.S42-3H.3	0.98
		QHea.S42-3H.3	1						
		QHea.S42-4H.1	0.63						
		QHea.S42-5H.1	1						

For each QTL, the range of probabilities over all environments and significant markers is given

properties of the MCMC sampler, especially in the case of closely linked loci. Aside from this, we assumed an independent residual structure. According to Piepho (2000), omitting genetic (background) correlations among observations of the same genotype measured in different environments can cause spurious QTL signals. Accounting for this genetic correlation, however, was not possible in our study, as phenotypic observations of the traits were not replicated within each combination of line and environment in the dataset leading to confounded polygenic and residual variation and covariation. Nevertheless, compared to Bayesian single-environmental mapping, a Bayesian approach using multi-environmental data seems to be more stringent (based on our subjective significance criterion) (Table 1). This is in contrast to the simulation study where both, Bayesian single- and multi-environmental mapping yielded comparable results (Table 5). Based on the experimenting with different significance thresholds (around the true threshold value), it seems that the results of Bayesian multi-environmental analysis are not very sensitive to our choice of the threshold value (results not shown). Considering the estimated marker effects, the true marker effect was estimated more accurately using a Bayesian mapping strategy than a REML approach.

In a multi-locus analysis a potential complication is that in the case of a strong correlation between markers it could be difficult to determine which marker is significant. It can be assumed that the higher the number of markers, the stronger this correlation among markers could be. In the present study, 98 SSR markers were used in total. Still, on chromosome 6H there was a gap where no polymorphic markers could be found. Thus, in this research a strong correlation between markers is not probable, but this situation could arise in future studies where the lines are

genotyped by hundreds of markers. This problem could be alleviated by collecting a large number of individuals.

Marker interaction effects were detected to a greater extent in Bayesian QTL mapping; whereas, using the REML method, all found marker effects were interpreted as a main effect in the analysis (Tables 5, 6). In the REML forward selection approach of the simulated dataset, all markers having a combined main and interaction effect were found to be a significant marker main effect (Table 6). Markers with an effect in some environments only were not found by REML methods. However, marker main and interaction effects have to be interpreted in different ways using the REML and Bayesian methods. In REML analysis, it is possible to interpret marker main and interaction effects separately. In contrast, in Bayesian implementation an oversaturated model was used, which means that more parameters were actually estimated than would be necessary. This oversaturated model was used because all environments were treated equally in the prior distribution during the model selection process. For each MCMC iteration, the sum of main effect and corresponding environmental effect was calculated. Thus, marker main and interaction effects were not independently identifiable. If the estimated effects in all environments were greater than the significance threshold, this effect was interpreted as a marker main effect; otherwise, there would be an interaction effect. This fact should be considered when comparing the QTL results from REML and Bayesian methods (Table 1).

As Bayesian multi-environmental mapping was computationally demanding, the calculation of a permutation test was not possible, and therefore a significance threshold was derived subjectively for this QTL analysis. This raises the question of whether the threshold is comparable/realistic, or if it is still too low or too high. Additionally, for

Table 4 Detected QTLs by REML and Bayesian analyses in the spring barley population compared to QTL mapping studies using other barley populations and different molecular markers

QTL ^a	Chr. ^b	Pos. ^c	Bin ^d	Candidate gene	Literature
<i>Days until heading</i> ($h^2 = 0.77$)					
QHea.S42-1H.1	1H	39	6		Thomas et al. (1995) (DH-lines)
QHea.S42-1H.2	1H	115	13		
QHea.S42-1H.3	1H	144	13	<i>Vrn-H3</i>	Laurie et al. (1995) (DH-lines), Sameri and Komatsuda (2004) (RILs), Sameri et al. (2006) (RILs; mapped in Bin class 14)
QHea.S42-2H.1	2H	42	4 (4)	<i>Ppd-H1</i>	Laurie et al. (1995) (DH-lines), Sameri and Komatsuda (2004) (RILs), Li et al. (2005) (BC ₃ DH), Emebiri and Moody (2006) (DH-lines), Sameri et al. (2006) (RILs)
QHea.S42-2H.2	2H	80–86	7–8		Pillen et al. (2003) (BC ₂ F ₂)
QHea.S42-2H.3	2H	146	13		Pillen et al. (2003) (BC ₂ F ₂)
QHea.S42-3H.1	3H	25–30	3 (3)		
QHea.S42-3H.2	3H	130	10		
QHea.S42-3H.3	3H	155–165	13–14 (15)	<i>Denso</i>	Barua et al. (1993) (NILs and DH-lines), Laurie et al. (1995) (DH-lines), Thomas et al. (1995) (DH-lines), Tinker et al. (1996) (DH-lines)
QHea.S42-4H.1	4H	130	10		
QHea.S42-4H.2	4H	180–190	12–13 (12)	<i>Vrn-H2</i>	Laurie et al. (1995) (DH-lines), Pillen et al. (2003) (BC ₂ F ₂)
QHea.S42-5H.1	5H	43	5		Thomas et al. (1995) (DH-lines), Pillen et al. (2003) (BC ₂ F ₂)
QHea.S42-5H.2	5H	85	8		Pillen et al. (2003) (BC ₂ F ₂)
QHea.S42-6H.1	6H	107	7		
QHea.S42-7H.1	7H	146	8	<i>eps7HS</i>	Pillen et al. (2003) (BC ₂ F ₂), Emebiri and Moody (2006) (DH-lines)
<i>Plant height</i> ($h^2 = 0.76$)					
QHei.S42-2H.1	2H	17–42	2–4 (3–4)	<i>Ppd-H1</i>	Laurie et al. (1994) (DH-lines)
QHei.S42-2H.2	2H	80–92	7–8	<i>sdw3</i>	Gottwald et al. (2004) (F ₄ -progenies), Kraakman et al. (2006) (cultivars)
QHei.S42-3H.1	3H	25–70	3–6 (3)		Sameri et al. (2006) (RILs)
QHei.S42-3H.2	3H	130	10		Yin et al. (1999) (RILs; mapped in Bin class 11)
QHei.S42-3H.3	3H	155–190	13–16 (15)	<i>Denso</i>	Thomas et al. (1995) (DH-lines), Bezant et al. (1996) (DH-lines)
QHei.S42-4H.1	4H	125–132	9–10		
QHei.S42-4H.2	4H	170–190	12–13 (11–12)		
QHei.S42-5H.1	5H	43	5		
QHei.S42-7H.1	7H	27	2		
<i>Grain yield</i> ($h^2 = 0.70$)					
QYld.S42-1H.1	1H	52	6		Li et al. (2005) (BC ₃ DH; mapped in Bin class 8)
QYld.S42-1H.2	1H	65–75	7–8		Thomas et al. (1995) (DH-lines), Tinker et al. (1996) (DH-lines)
QYld.S42-1H.3	1H	144	13		
QYld.S42-2H.1	2H	107–122	9–10		Yin et al. (1999) (RILs)
QYld.S42-3H.1	3H	25–70	3–6 (3)		Thomas et al. (1995) (DH-lines), Pillen et al. (2003) (BC ₂ F ₂), Kraakman et al. (2004) (cultivars)
QYld.S42-3H.2	3H	130	10		Yin et al. (1999) (RILs)
QYld.S42-3H.3	3H	155–165	13–14 (15)	<i>Denso</i>	Thomas et al. (1995) (DH-lines), Tinker et al. (1996) (DH-lines), Li et al. (2005) (BC ₃ DH)
QYld.S42-3H.4	3H	190	16		
QYld.S42-5H.1	5H	43	5		Pillen et al. (2003) (BC ₂ F ₂)
QYld.S42-5H.2	5H	126	10		Kraakman et al. (2004) (cultivars; mapped in Bin class 12–13)
QYld.S42-7H.1	7H	146	8		Pillen et al. (2003) (BC ₂ F ₂)
<i>Thousand grain weight</i> ($h^2 = 0.54$)					
QTgw.S42-1H.1	1H	65	7		
QTgw.S42-1H.2	1H	144	13		
QTgw.S42-2H.1	2H	86	8		Pillen et al. (2003) (BC ₂ F ₂), Sameri and Komatsuda (2007) (RILs; mapped in Bin class 10)
QTgw.S42-2H.2	2H	107–122	9–10		Li et al. (2005) (BC ₃ DH; mapped in Bin class 15)

Table 4 continued

QTL ^a	Chr. ^b	Pos. ^c	Bin ^d	Candidate gene	Literature
QTgw.S42-3H.1	3H	110	9 (8)		
QTgw.S42-3H.2	3H	155–175	13–15 (15)		
QTgw.S42-4H.1	4H	125–132	9–10		
QTgw.S42-4H.2	4H	180–190	12–13 (12)		
QTgw.S42-6H.1	6H	96	5		
QTgw.S42-6H.2	6H	135	10		
QTgw.S42-7H.1	7H	146–166	8–11		Pillen et al. (2003) (BC ₂ F ₂)
<i>Ears per m² (h² = 0.21)</i>					
QEar.S42-1H.1	1H	144	13		
QEar.S42-2H.1	2H	17	2 (3)		
QEar.S42-2H.2	2H	67–92	6–8		
QEar.S42-3H.1	3H	65–70	5–6		
QEar.S42-3H.2	3H	155–165	13–14 (15)		
QEar.S42-4H.1	4H	21–25	3		
QEar.S42-4H.2	4H	125–132	9–10		
QEar.S42-4H.3	4H	170–190	12–13 (11–12)		
QEar.S42-5H.1	5H	0	2		
QEar.S42-5H.2	5H	43	5		
QEar.S42-6H.1	6H	135	10		

In brackets, the population used for QTL mapping is displayed (*BC* backcross, *DH* doubled haploid, *NILs* near-isogenic lines, *RILs* recombinant inbred lines). A detailed description of the QTLs is given in the Supplementary Material

^a Names of the QTLs consisting of the qualifier “Q”, the trait abbreviation, the determined population, the mapped chromosome and a QTL number to distinguish between QTLs on the same chromosome. Markers with a distance ≤ 20 cM were considered to be a single QTL

^b Chromosomal location of the SSR markers

^c Position of the SSR markers on the chromosome in centiMorgan (cM) (von Korff et al. 2004). If several markers were significant, the cM range is given

^d Bin marker class following Kleinhofs and Graner (2001) and Costa et al. (2001). In the case of several significant markers, the Bin class range is displayed. An additional number in brackets gives the Bin class following Marcel et al. (2007). As the Bin class of Marcel et al. (2007) was available only for some markers, in the case of several significant markers belonging to the same QTL, these markers are given in italics

each QTL locus, the probability of marker effects being higher than the chosen significance threshold was computed over all MCMC-rounds. If our significance threshold was too low, leading to “significant” QTLs that in reality are false-positives, then there would be a high number of markers that showed an effect greater than the threshold in each MCMC round. In this case, the probability of marker effects being higher than the threshold would be equal to 1 for most of the QTLs. In contrast, if the significance threshold was too high, then the markers would have effects greater than the threshold only in some MCMC rounds, so the probability would be much lower than 1. In our study, some QTLs show probabilities of 1, but a number of QTLs also show reduced probabilities in both, real and simulated datasets (Tables 3, 5). Thus, it seems that by applying the chosen significance threshold, the occurrence of false-positive QTLs is minimized. Tests with slightly different significance thresholds showed the chosen threshold to be most appropriate in reducing the number of false-positive QTLs. In the simulation study, with the chosen significance threshold only one false-positive

marker with a true effect of zero was detected to be significant, whereas another marker with a true effect of 0.2 was not found due to the small effect size.

Accounting for missing marker data in the analysis is handled differently in REML and Bayesian mapping. In REML analysis, each observation with a missing marker value is omitted from the dataset. Thus, the amount of phenotypic information is reduced due to missing marker data. Considering the REML forward selection approach where several markers are accounted for simultaneously as cofactors in the statistical model, the number of phenotypic observations omitted from the dataset is increased due to the larger probability that missing marker data occur in one or more of the markers. In contrast, in a Bayesian analysis, missing markers are imputed according to their posterior distribution (Hoti and Sillanpää 2006; Yu and Schaid 2007). There, the distance between the missing locus and the flanking markers is calculated based on the recombination frequency and the missing marker is more frequently assigned the genotypic value of the flanking marker with the smallest distance.

Table 5 Results from Bayesian single- and multi-environmental QTL mapping of the simulated dataset

Marker	Chr. ^a	Pos. ^b	Effect type ^c	Env. ^d	True effect	Bayes single ^e	Bayes multi ^f	
						Estimated effect	Estimated effect (unstandardized)	Occ. prob. ^g
16	1H	144	M	1	3.5	3.27	3.39	1
				2	3.5	3.30	3.39	1
				3	3.5	3.38	3.39	1
				4	3.5	3.63	3.39	1
				5	3.5	3.53	3.39	1
				6	3.5	3.64	3.39	1
22	2H	80	$M + I_c$	1	-2.1	-2.41	-1.98	1
				2	-3.5	-3.45	-3.33	1
				3	-2.1	-1.90	-1.98	1
				4	-2.1	-2.11	-1.98	1
				5	0.4	0	0.21	0.98
				6	-2.1	-2.14	-1.98	1
31	3H	25	I_c	1	0	0	0.24	0
				2	-3.3	-3.25	-2.85	1
				3	2.8	2.94	0.24	0
				4	1.7	2.16	2.12	0.90
				5	-2.3	0	0.24	0
				6	0	0	0.24	0
32	3H	30	-	1	0	0	-0.14	0
				2	0	0	-0.14	0
				3	0	0	2.04	0.99
				4	0	0	-0.14	0
				5	0	-1.71	-1.94	0.99
				6	0	0	-0.14	0
40	3H	155	I_{nc}	1	1.2	1.01	1.22	0.99
				2	0	0	-0.06	0
				3	0	0	-0.06	0
				4	2.1	2.29	2.56	1
				5	0	0	-0.06	0
				6	0.8	0	0.77	0.59
45	4H	21	M	1	-1.3	-1.37	-1.08	0.50
				2	-1.3	-0.96	-1.08	0.50
				3	-1.3	-1.53	-1.09	0.50
				4	-1.3	-1.77	-1.09	0.51
				5	-1.3	-1.09	-1.08	0.49
				6	-1.3	-1.38	-1.08	0.50
53	4H	125	I_{nc}	1	0	0	0.16	0
				2	-3.1	-3.21	-3.13	1
				3	0	0	0.16	0
				4	-2.2	-2.18	-2.13	1
				5	0	0	0.16	0
				6	-2.8	-2.77	-2.68	1

Table 5 continued

Marker	Chr. ^a	Pos. ^b	Effect type ^c	Env. ^d	True effect	Bayes single ^e	Bayes multi ^f	
						Estimated effect	Estimated effect (unstandardized)	Occ. prob. ^g
65	5H	43	I_c	1	0.3	0	-0.21	0.06
				2	0.9	0.92	0.98	0.86
				3	-0.8	-0.06	-0.43	0.01
				4	0	0	-0.42	0
				5	-0.2	0	-0.43	0
				6	-0.6	0	-0.42	0
75	6H	96	M	1	1.8	1.99	1.58	1
				2	1.8	1.62	1.58	1
				3	1.8	1.83	1.58	1
				4	1.8	1.86	1.58	1
				5	1.8	1.86	1.58	1
				6	1.8	1.28	1.58	1
79	6H	135	M	1	0.2	0	0.08	0
				2	0.2	0	0.08	0
				3	0.2	0	0.08	0
				4	0.2	0	0.08	0
				5	0.2	0	0.08	0
				6	0.2	0	0.07	0
92	7H	146	$M + I_{nc}$	1	2.5	2.45	2.06	1
				2	2.5	2.50	2.06	1
				3	0.6	0	0.84	0.02
				4	1.2	1.24	2.06	1
				5	2.5	2.32	2.06	1
				6	2.5	2.71	2.06	1

Significant markers with chromosomal positions, effect type, environment, true and estimated effects and occupancy probabilities of marker effects being higher than the significance threshold are shown

^a Chromosomal location of the markers

^b Position of the markers on the chromosome in centiMorgan (cM)

^c Effect type of the marker: M = marker main effect; I_c = marker interaction effect (crossover); I_{nc} = marker interaction effect (non-crossover); $M + I_c$ = marker main and interaction (crossover) effect; $M + I_{nc}$ = marker main and interaction (non-crossover) effect

^d In the computer simulation, the environment where the lines were cultivated

^e Bayesian single-environmental QTL mapping

^f Bayesian multi-environmental QTL mapping

^g Occupancy probability of marker effects being higher than the significance threshold in Bayesian multi-environmental mapping

Compared to QTL mapping studies using other barley populations and different molecular markers, several QTLs could be verified in our spring barley population (Table 4). Except for the trait “ears per m²,” for all other traits several QTLs detected in the spring barley population could be mapped in the same region on the chromosome by other authors. A detailed comparison of QTL positions detected here and in other barley QTL mapping studies is given in the Supplementary Material.

QTLs that were detected in three or four of our QTL mapping strategies and are not yet described in the literature might be “new” QTLs. These are the QTLs QEar.S42-

4H.3 (“ears per m²”), QHea.S42-3H.2 (“days until heading”), QHei.S42-4H.2 (“plant height”), and the QTLs QTgw.S42-3H.2, QTgw.S42-4H.1, and QTgw.S42-4H.2 for the trait “thousand grain weight.” In general, the power to detect a significant QTL with several statistical analyses is higher with increasing heritability of the regarded trait.

In conclusion, Bayesian multi-locus multi-environmental QTL mapping seems to be a valuable strategy accounting for both multiple loci and marker-by-environment interactions. This QTL analysis is suitable, especially if the lines are cultivated in multi-environmental field trials.

Table 6 Significant markers with their chromosomal positions, effect type, true (simulated) and estimated effects, F and P values from REML single-locus analysis and the REML forward selection approach of the simulated dataset

Marker	Chromosome	Position (cM)	Effect type ^a	True effect	Estimated effect	F value	P value
<i>REML single-locus analysis</i>							
15	1H	130	–	0	–0.89	47.41	0.001
16	1H	144	M	3.5	–1.44	130.22	0
21	2H	67	–	0	1.00	13.36	0.015
22	2H	80	$M + I_c$	–3.5 to 0.4	–	–	–
27	2H	139	–	0	–0.90	10.64	0.022
31	3H	25	I_c	–3.3 to 2.8	–	–	–
40	3H	155	I_{nc}	0 to 2.1	–	–	–
45	4H	21	M	–1.3	–	–	–
53	4H	125	I_{nc}	–3.1 to 0	–	–	–
57	4H	150	–	0	0.83	11.13	0.020
65	5H	43	I_c	–0.8 to 0.9	–	–	–
75	6H	96	M	1.8	–0.84	29.80	0.003
76	6H	103	–	0	–0.90	34.66	0.002
77	6H	107	–	0	–0.84	26.44	0.004
79	6H	135	M	0.2	–	–	–
91	7H	133	–	0	–0.57	12.00	0.018
92	7H	146	$M + I_{nc}$	0.6 to 2.5	–0.87	16.87	0.009
<i>REML forward selection</i>							
16	1H	144	M	3.5	–1.44	130.22	0
22	2H	80	$M + I_c$	–3.5 to 0.4	1.09	13.25	0.015
31	3H	25	I_c	–3.3 to 2.8	–	–	–
40	3H	155	I_{nc}	0 to 2.1	–	–	–
45	4H	21	M	–1.3	–	–	–
47	4H	31	–	0	0.43	35.09	0.002
53	4H	125	I_{nc}	–3.1 to 0	–	–	–
65	5H	43	I_c	–0.8 to 0.9	–	–	–
75	6H	96	M	1.8	–1.07	74.70	0
79	6H	135	M	0.2	–	–	–
92	7H	146	$M + I_{nc}$	0.6 to 2.5	–0.96	34.38	0.002

For the true marker effect, the range over all environments is given if the marker has an interaction effect

Significance threshold obtained from permutation test: 9.69 (F value)

^a Effect type of the marker: M = marker main effect; I_c = marker interaction effect (crossover); I_{nc} = marker interaction effect (non-crossover); $M + I_c$ = marker main and interaction (crossover) effect; $M + I_{nc}$ = marker main and interaction (non-crossover) effect

In comparing REML and Bayesian QTL mapping strategies, a Bayesian analysis can be computationally demanding. In this study, REML analysis took about 20 min, whereas Bayesian analysis needed about 33 h for the same trait in the spring barley population on a Pentium IV 2.0 GHz processor. So, when performing Bayesian QTL mapping, it is important to use efficiently programmed MCMC estimation methods. On the other hand, in a Bayesian framework all marker loci were considered jointly in a single analysis which resulted in a valuable method. Thus, the user has to decide if the gain of Bayesian

QTL mapping over other methods justifies the computational burden.

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