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Construction of barley consensus map showing chromosomal regions associated with economically important traits

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In the past, it has been difficult to accurately determine the location of many types of barley molecular markers due to the lack of commonality between international barley linkage maps. In this study, a consensus map of barley was constructed from five different maps (OWB, VxHs, KxM, barley consensus 2 and barley consensus 2003) to produce the consensus AD-2005 map with 1536 markers. The QTL that have been identified in previous barley studies were then incorporated into the integrated consensus map to provide a quick method of aligning and comparing barley linkage maps and to identify markers closely linked to barley traits. The markers placed on this map are consistent with respect to order on the chromosomes with the individual maps and other barley maps with a few minor differences. The consensus AD-2005 was compared with rice Cornell RFLP map to examine the reliability of the constructed map in comparative genomic studies. Unlike previous consensus maps, the purpose of this consensus map (containing QTL) is to provide a tool for scientists to accurately locate molecular markers to chromosome regions responsible for economically important traits. It is estimated that markers placed on the consensus map are located very close to their true positions as determined by the five maps used in this study. It is envisaged that the consensus map will benefit small-grain researchers by providing an efficient means of choosing markers of interest and identifying QTL regions for future genetic or plant breeding studies on a worldwide basis.

Key words: Barley, QTL, genetic linkage mapping, consensus map, comparative genome mapping.

INTRODUCTION

Several different types of DNA markers are currently available for genetic analysis and new marker types are being developed continuously. Markers differ from each other in many respects such as the initial workload and costs for building up the marker system, running costs and ease of use, level of polymorphism, dominance, number of loci analyzed per assay, reproducibility and distribution on the linkage groups of the genetic linkage maps. A genetic linkage map is a fundamental organizational tool for genomic research. The most important applications of genetic maps are towards:

(1) A basic knowledge of genome organization and evolution;

- (2) The localization of monogenic and oligogenic traits; and
- (3) Studies of genetic diversity.

Therefore, for any given species, individual genetic maps are often constructed with a specific goal in mind, thereby generating multiple maps for a single species that feature novel markers and genetic information. The information contained within these individual maps can be further enhanced when these maps are incorporated into a single consensus map to represent a given species.

Consensus maps have been constructed for a number of plant species such as *Arabidopsis thaliana* (Hauge et al., 1993), *Brassica oleracea* (Kianian and Quiros, 1992), *Helianthus annus* (Gentzbittel et al., 1995), *Hordeum* vulgare (Qi et al., 1996) and Zea mays (Beavis and Grant, 1991). Mapping with multiple populations provides several advantages over mapping based on a single population. In particular, a larger number of loci can be placed onto a single map. This is especially important when attempting to map specific genes of interest (e.g., morphological markers or candidate genes for economically important traits) that are unlikely to segregate within a single mapping population. These multi population mapping studies provided evidence for chromosomal rearrangements and gene duplication and have assisted in the assignment of linkage groups to chromosomes. The consensus maps provide the basis for comparative genomic studies among related species and sub species.

Barley (*Hordeum vulgare L.*) is a model species for genetic and physiological studies and shows a wide range of adaptations to various habitats. It is an annual, diploid self-pollinating species with a relatively short life cycle. Primitive landraces and the wild progenitor of barley (*H. spontaneum*) exhibit large variations in physiology, morphology and genetics, which might be used to improve cultivated barley (Nevo, 1992; Forster et al., 2000).

QTL mapping has been employed in several areas of biological sciences. In plant breeding; one of the major lines of research is the detection of useful traits in relatives of cultivated species (Fulton et al., 1997; Xiao et al., 1998; Bernacchi et al., 1998). There has been much interest in studying quantitative traits of agronomic importance, disease resistance (Young, 1996), drought tolerance (Teutat et al., 2001; Diab et al., 2004), and many other traits for biotic and abiotic stress tolerance in barley. QTL mapping has led to a vast body of genetic information in public database and provided the scientific community with powerful tools for comparative genomics (Gai et al., 2000; Mekhdov et al., 2000).

In the present study, an integrated consensus map of barley was constructed based on a common set of markers mapped onto the respective linkage groups and the QTL, identified in previous barley studies, were transferred to the integrated consensus map. The main objective of this work is to facilitate comparative mapping studies of cereals and gathering many mapping information to allow scientist to compare genetic information from diploid species such as barley to species with more complex genomic structure that could lead to the identification of highly conserved sequences and regulatory mechanisms by which it is possible to predict function and location of genes in different maps that have been traditionally studied separately.

MATERIALS AND METHODS

Genetic maps

Three Linkage maps and two consensus maps of barley were used in this study to construct the consensus AD-2005 barley map. Rice Cornell RFLP map was used as a test drive comparative model. The major feature of the five barley maps and the rice map are described below.

Hordeum-OWB linkage map

This map was built with a range of markers. These include 11 morphological markers (NEPs), 79 restriction fragment length polymorphisms (RFLPs), 19 intron fragment length polymorphisms (IFLPs) and 50 simple sequence repeats (SSRs). Additional information on the markers in the linkage map is available at http://barleyworld.org.

Hordeum-Graner1VxHs

This map was constructed using 135 individuals of an interspecific F2/F3 progeny (VADA x *H. spontaneum*). The map consisted of 160 markers with colinear arrangement covers a distance of 1,453 cM and identifies regions of varying map distances.

Hordeum KxM

This map is an RFLP linkage map that was constructed using 120 F2 plants from a cross between Ko A (a Japanese two-rowed malting barley) and Mokusekko 3 (a Chinese six-rowed barley landrace). 188 loci were mapped with an average distance of 6.5 cm between markers for a total of 1389 cM, and included 117 genomic DNA RFLPs, 69 cDNA RFLPs, one isozyme (Est1) and one morphological (vrs1) marker. This map showed three gap regions exceeding 25 cM.

Barley Consensus 2

This consensus map was constructed using four segregation data sets, Proctor x Nudinka, Igri x Franka, Steptoe x Morex, and Harrington x TR306. 22% of the markers were common to at least two of the independent data sets. The integrated map contains 882 markers.

Barley Consensus 2003

This consensus map, combining SSR, RFLP, and AFLP markers has been developed by combining five Australian barley linkage maps, Galleon x Haruna Nijo, Chebec x Harrington, Clipper x Sahara, Alexis x Sloop and Amaji Nijo x W12585. This consensus map consists of 705 markers, with 138 being SSRs.

Rice map

This map is an updated version of the Cornell RFLP 1994 map reported by Causse et al. (1994) and revised by Wilson et al. (1999). The mapping population was derived from a backcross between cultivated rice (*Oryza sativa*) and its wild African relative (*Oryza longistaminata*).

Construction of the consensus AD-2005 map

Five mapping data sets were downloaded from the publicly available Grain Genes database (http://www.graingenes.org). The consensus map was constructed in three stages with each stage adding a new layer of information. In the first stage, the initial map

Trait	Мар	Reference
Relative water content under stress treatment	Tad X ER	Diab et al., 2003
Relative water content under irrigated condition	Tad X ER	Diab et al., 2003
Osmotic potential under irrigated condition	Tad X ER	Diab et al., 2003
Osmotic potential at full turgor	Tad X ER	Diab et al., 2003
Water soluble carbohydrates	Tad X ER	Diab et al., 2003
Fusarium head blight resistance	F x S	Mesfin et al., 2003
		Ma et al., 2000
		Zhu et al., 1999
Flowering time	I x T	Jeremy et al., 1996
Malting quality	НхМ	Marquez et al., 2000

 Table 1. Quantitative trait loci for traits gathered from different barley studies and placed on barley consensus-AD 2005 map.

was constructed based on common markers (anchor loci) present in the five barley maps. In the second stage, the markers on the five maps were matched according to sequence similarity using the sequence similarity program (http://www.ncbi.nlm.nih.gov/blast/bl2 seq/bl2.html) and this information was used to identify additional links between the maps. Finally, the consensus AD-2005 map was constructed as described by Diab (2003).

To construct the consensus AD-2005 map, the consensus map 2 (Qi X et al., 1996) and consensus 2003 (Karakousis et al., 2003) were first integrated to produce the first framework map (AD1). The AD1 framework was then merged with OWB map (Wolfe et al., 1996) to produce a second framework map (AD2), then KXM map (Miyazaki et al., 2000) was incorporated into the AD2 map to produce a third framework map (AD3). Finally, the AD3 framework map was integrated with the VxHs map (Graner et al., 1991) to produce the consensus AD-2005 map with 1536 markers distributed on the seven chromosomes.

Comparative study for rice and barley maps

To examine the reliability of the consensus AD-2005 in comparative studies, the Cornell rice RFLP 2001 map (http://www.gramene.org) was downloaded and compared with the constructed barley consensus AD-2005 map, OWB, KXM and VXHs maps based on common markers (anchor loci).

Incorporation of QTL

The QTL that were previously identified in different barley studies were incorporated into the integrated barley consensus AD-2005 map for QTL comparison purpose. Quantitative trait loci for relative water content under stress condition (RWCs), relative water content under irrigated condition (RWCi), osmotic potential under irrigated condition (OPi), osmotic potential at full turgor (OP100), water soluble carbohydrates (WSC), *Fusarium* head blight resistance (FHB), flowering time (FT) and malting quality (MQ) were gathered from previous studies and placed on the constructed consensus AD-2005 (Table 1, Figure 1).

RESULTS AND DISCUSSION

Well developed barley genetic maps exist as a result of the efforts of numerous groups worldwide. These maps

include RFLPs, amplified fragment length polymorphisms (AFLPs), single sequence repeat or microsatellites (SSRs), isozyme protein markers; and morphological markers (Becker and Heun, 1995; Graner et al., 1991; Heun et al., 1991; Kleinhofs and Graner, 2001). These genetics maps were based on various markers, the most useful being those that are transferable from one mapping population to another. These markers have been incorporated into bin maps (Karakousis et al., 2003; Qi et al., 1996). In the present study, five different barley maps were integrated to produce a consensus map with 1536 markers distributed on the seven linkage groups with 240 common markers between the five maps. The 882 markers of the consensus 2 map were merged with the 705 markers of the consensus 2003 to produce the first framework integrated barley consensus map (AD1) with 1255 markers. The 1255 marker of the AD1 map were then merged with OWB map to produce the second framework integrated barley consensus map (AD2) with 1371 markers. Then the AD2 was incorporated with KxM map to produce the third framework map integrated barley consensus map (AD3) with 1461 marker. Finally, the AD3 map was merged with VXHs map to generate the barley AD-2005 consensus map with 1536 markers.

Description of the barley consensus AD-2005 map

The primary goal for the construction of this consensus map was to place, relative to one another, as many genetic markers as possible onto a single map. Therefore, the concern is raised more towards obtaining a general order and distance among these markers rather than the fine resolution of order and distance. The markers placed on this map are consistent with respect to order on the chromosomes with the barley consensus 2 (Qi et al., 1996), barley consensus 2003 (Karakousis et al., 2003) and with other published or consensus barley maps (Kleinhofs and Graner, 2001; Qi et al., 1996;

Chromosome	Barley consensus 2	Barley consensus 2003	Hordeum- OWB	Hordeum- KxM	Hordeum- Graner VxHs	Barley Consensus - AD 2005
1H	92	87	24	27	19	189
2H	163	160	30	28	28	306
3H	133	54	20	28	28	150
4H	81	59	24	24	18	136
5H	139	137	19	28	28	270
6H	98	81	22	25	20	175
7H	176	127	20	28	19	310
Total	882	705	159	188	160	1536

Table 2. Comparison between the five individual maps and barley consensus AD-2005 map in respect of number of markers on each chromosome.

Miyazaki et al., 2000; Graner et al., 1991; Wolfe et al., 1996; Ramsay et al., 2000) with a few minor differences. This conservative property of the barley genome makes the integrated maps reliable and successful. Based on this integrated map, geneticists and breeders can choose their favorite markers in any region of interest of the barley genome.

For comparable areas, the size of the consensus map constructed in this study (consensus AD-2005) is consistently larger than the consensus map constructed by Qi et al. (1996) and the consensus map constructed by Karakousis et al. (2003) despite the fact that each of those two maps has been constructed using five different maps (Table 2). Obvious explanation is that those two maps were integrated together with another three maps (OWB, VXHs and KXM) beside the step-wise procedure used to integrate the individual maps.

The utility of the constructed consensus map is enhanced with the availability of the SSR, RFLP, and AFLP markers integrated from the barley consensus map 2003 (Karakousis et al. 2003). The integrated map removes many large gaps present in the individual maps and in other consensus maps except a gap on chromosome 4H. The poor coverage in this region might be due to a lack of polymorphism for the markers screened in this region.

Incorporation of QTL

QTL analysis can be done in relation to mapped genetic markers and provide data on genome location and the relative effects both positive and negative of loci and alleles. The next step is the identification of the genes, alleles and physiological processes that are biologically important. Numerous studies identifying QTL for relative water content (RWC), osmotic potential (OP), water soluble carbohydrates (WSC), Fusarium head blight resistance (FHB), flowering time (FT) and malting quality (MQ) have been conducted in barley (Teulat et al., 2001; Diab et al., 2004; Mesfin et al., 2003; Ma et al., 2000; Zhu et al., 1999; Jeremy et al., 1996; Marquez et al., 2000; Hayes et al., 1993; Tinker et al., 1996). Presently, 143 QTL were gathered from previous barley studies and placed on the consensus AD-2005 map. Seventy seven QTL for Fusarium head blight resistance, 32 for malting quality, 24 for flowering time, 1 for relative water content under stress condition, 1 for relative water content under irrigated condition, 2 for osmotic potential at full turgor, 1 for osmotic potential under irrigated condition and 5 for water soluble carbohydrates (Figure 1).

For Fusarium head blight resistance trait, 7 QTL were located on chromosome 1H, 12 on chromosome 2H, 9 on 3H, 8 on 4H, 13 on 5H, 12 on 6H and 16 on chromosome 7H (Figure 1). Mesfin et al. (2003) reported the presence of QTL for FHB on all chromosomes except chromosome 6H, and Zhu et al. (1999) found QTL for FHB resistance on all barley chromosomes except chromosome 5H, while Ma et al. (2000) reported QTL for FHB resistance located on chromosomes 2H, 3H, 5H, 6H and 7H. Taken together, these studies indicate that resistance is conditioned by many loci and that the low resolution of the mapping populations has resulted in a limited assessment of the FHB. Integrating these QTL from different studies on a single consensus map gives the opportunity for scientist to compare between QTL and might solve the problem of low resolution maps hence detecting false negative QTL during trait analysis. Two markers (ABG317 and ABC153) on chromosome 2H were found to be associated with QTL for Fusarium head blight resistance. Those two markers were located on the same chromosomal region on the consensus barley AD-2005 (Figure 1). This indicates the reliability of placing QTL on consensus maps.

For flowering time trait, 6 QTL were placed on chromosome 1H, 4 on 2H, 1 on 4H, 7 on 5H, 3 on 6H and 7H each, while no QTL were found on chromosome 3H (Figure 1). This result agrees with the finding of Jeremy

1H(a)			1H(b)	
1H(a) 0.000 MW 0.000 MW 0.000 MW 0.000 Hc 0.013 Hc 0.025 P1 0.030 AB 0.035 P1 0.036 P1 0.037 MW 0.041 MW 0.036 P1 0.037 MW 0.040 MW 0.051 AB 0.054 MW 0.054 MW 0.054 MW 0.057 BC 0.054 MW 0.057 BC 0.054 MW 0.057 BC 0.054 MW 0.1057 BC 0.1057 BC 0.1057 BC 0.1057 BC 0.1056 P1 0.1176 BC 0.1176 BC 0.1222 P1 0.2233 BC 0.2249 P1	VG36A AB G59 VG337 ZenG11b ue18a rr5 MWG938 rr1 Chs3 rr2 4/M49-70 4/M49-70 4/M49-70 G310A G158 BCD1434 VG2083 dMIa6 3/M47-221 2/M52-181 P13/M55-308 4/M48-363 VG2148 VG2148 VG2148 VG2148 VG2148 VG2148 VG2148 VG2148 VG214 G316f MWG2021a VG2048 MWG645 siC10b A4 .1 iSC5 uD14 G180 2/M50-95 2/M50-95 2/M50-95 2/M50-95 2/M50-95 2/M50-95 2/M50-95 3/M50-114 P14/M47-111 nac32 ALAAT VBMA5 D099 BCD98 3/M50-114 P14/M47-111 nac32 ALAAT VBMA5 D099 BCD98 3/M50-242 CD0580a M20 1/M48-132 CD098 1/M48-33 BCD207 R544 EBmac501 2/M50-242 CD0580a M20 1/M48-132 CD098 1/M48-133 BCD207 R544 EBmac501 2/M50-111 AWRM1 R929a AWBMS80 11 r8542 CD04 VG755 VG20 C2 G74 CD22 UD14B MWG913 G500A VG758 VG20 Intromere-1H 2/M50-78 C164(SM) nag0211 G54 UF2A RisBPP161C G452 MWG789B SBPP7 ABC152B G494 BCD351C VG506 Pcr2		1H(b 0.475 0.478 0.494 0.529 0.535 0.545 0.591 0.644 0.623 0.644 0.623 0.644 0.643 0.645 0.644 0.643 0.645 0.644 0.643 0.644 0.643 0.644 0.643 0.644 0.643 0.644 0.643 0.644 0.643 0.644 0.643 0.644 0.643 0.644 0.643 0.644 0.779 0.778 0.778 0.778 0.778 0.885 0.885 0.885 0.885 0.885 0.885 0.885 0.885 0.885 0.885 0.885 0.904 0.904 0.904 0.935 0.954 0.955 0) Bmac213 AWB(45 AWB(45) AWG45 AWG45 MWG800 CD0105B CD01396 DD0136 CD01396 JBC773D X5.3 ABC151E MWG930 P12/M50-94b ABC151D MWG78 PSR162a CD0419A ABC160 MWG77 FEI ABC706B HVM2 JBG77C J	
	Fusarium h	ead blight re	er irrigated c	condition	

- Malting quality
- Flowering time
- Relative water content under stress treatment
- Osmotic potential at full turgor
- Relative water content under irrigated condition
- Water soluble carbohydrates

Figure (1). Integrated barley Consensus AD-2005 map with QTL for some biotic and abiotic traits.

0.000

0.063

0.067

0.129

2H(b) 2H(a) MWG64 ABG358 MWG64 ABG356 MWG516 Pox P13/M47-275 P12/M50-240 P12/M51-265 PBI21a 0.132 0.006 0.163 0.014 CDO57 MWG996 ABC162 0.020 0.021 0.207 MWG950 DGD18 BG140B 0.023 0.235 ABG8 BCD221A MWG222A P13/M48-123 P13/M54-107 P13/M55-306 P14/M48-279 P14/M59-287 P14/M62-238 0.240 0.252 0.267 0.024 0.025 0.342 0.344 cdo506a BCD175 HVM36 P14/M47-275 0.026 0.027 0.374 0.030 0.401 AWBMA14 CDO370 ABC167B 0.031 0.406 0.035 0.040 0.041 0.429 ABC16/B Hot1 MWG763 P14/M48-94 BCD355 MWG223 bBE54D ABG453 PSR131a MWG858 ABG2 MWG222B MWG789A 0.432 0.455 0.468 0.477 0.045 0.054 0.055 0.485 0.056 0.057 P13/M47-399 PSR666a MWG647 MWG646a MWG887a MWG2133 MWG874 0.491 0.494 0.501 0.510 0.511 0.512 MWG663 RbcS EBmac0684 ABG714a 0.519 0.071 ksuA1B WG405A BCD402B Bmac132 0.077 0.522 HVM23 BCD351B MWG636(HT) MWG2054 ABG602 _ 0.527 0.079 0.530 ABC256 0.083 0.084 0.088 0.535 0.543 0.545 ABG397 MWG65 BCD351F CDO667 AWBMA27b EBmac607 0.089 0.550 0.092 0.094 0.555 MBmag341a ABG318 PSR108a 0.557 0.558 ~ 0.096 iiiiii ABG19 ABG716 CDO537 MWG557 P14/M48-332 P12/M50-199 P14/M59-176 0.576 -0.100 0.578 0.103 P12/M50-199 F 14/m55 MWG889(IF) MWG578 MWG553b BCD339B BCD334 MWG2058 0.607 0.105 0.608 0.619 0.629 0.107 Bry2 CDO770 CDO64 PSR933b ABC156A 0.630 0.635 0.108 0.644 0.647 0.648 MWG949B BCD111 0.110 0.112 0.115 Centromere-2H ksuD22 Bmac93 Bmag518 EBmac684 PSR126 0.651 0.116 0.118 0.656 CDO675A ABC306 ABG316C ABC468 BCD221B 0.119 0.668 0.676 0.679 0.121 0.123 JBG299 ABG459 0.128 0.684

P12/M51-270 P13/M54-224	0.690
P13/M61-58 ABC309	0.702
Bmy2 CDO474a	0.720
ksul32 MWG996a	0.720
EBmac715 HVHOTRI	0.728
ABG14 ABC451	
X2 2	0.730
GMS3	0 740
MWG520a	0.740
Bmag692	0.744
MWG737 MWG9	0.743
CD0537	0.700
	0.702
ABG5	0.792
MWG71	0.794
JBC495 JBG282	0.790
MWG84a	0.757
JBC582	0.014
MWG657	0.010
P13/M49-59 AWBMA33	0.017
Bmag381	0.020
BCD334	0.037
JBG255	0.044
MWG2067	0.845
MWG656	0.846
MWG844F	0.050
X2.3	0.000
BCD453B	0.855
CDO474C	0.863
KFP203 ABG619 CD0474C	0.873
AdhIntC	0.879
ABG72	0.891
EBmatc39	0.040
MWG882A	0.910
DGF15 BCD266	0.913
ABC152D MWG865	0.914
AAW605 EBmac571a	0.928
	0.937
P13/M59-275 CD0665B	0.939
CD01335a	0.945
EXO2F PSR117a	0.948
CDO680	0.950
MWG726	0.955
P13/M59-256	0.957
Bmag0113E	0.962
P14/M59-226 EBmac793	
ksuF15A	0.964
cdo665a	0.965
JBG63B MWG2081	0.968
MWG801 MWG699	0.973
hex-v	0.974
ABG072	
P11/M51-170	0.975
P12/M51-157	
P13/M59-288 BCD386	
Bmag378 EBmac623	11
MWG581	

MWG738 MWG655B ABC157 ABC252 MWG520B F3hA CDO373 PSR540 EBmac415 MWG2123 MWG882 GIn2 P13/M47-256 CDO373 GS1 HVM54 EBmac0415 MWG180 MWG1 cnx1 vrs1 JBG303 ABC620 P13/M50-203 ABG72 P13/M50-127 HyCSG P14/M60-299 CDO474B ksuF41 Bmag114 Bmag125 Rrn5S1 ABC165 ABG317 P12/M54-94 P14/M47-378 ABG317B ABC153 DGF41 Zeo P14/M61-348 BCD512 Bmag749 ABG316E ABG317A AWBMS56 P14/M61-111 DGG43 Bmac0144F ABC171A PSR934 ABG609A Bmag0125 ABG316D Pcr1 MWG503 BCD292 MWG636(IF) PSR609 PSR370a MWG90 MWG866 Prx2 MWG892 MWG876 ABG613 BCD339C MWG989 X2.4 MWG338A MWG829 MWG949 MWG80 MWG2076 RWTHBE54c BG123a P14/M55-156 CDO36 Rich4Bama Rich4NcoC P13/M47-192 CDO366

Osmotic potential under irrigated condition

0.685

0.687

Fusarium head blight resistance

DGE12 MWG658

ABR338 ABG356

- Malting quality
- Flowering time
- Ē Relative water content under stress treatment
- **W** Osmotic potential at full turgor
- Relative water content under irrigated condition
- Water soluble carbohydrates

Figure 1. contd.



3H(b)

Figure 1. contd.

Flowering time

Relative water content under stress treatment

Relative water content under irrigated condition

Osmotic potential at full turgor

Water soluble carbohydrates

4H(a)

0 000 1	MWG58 MWG622a
0.000	BCD351B Dhn6
0.002	CDO541 MWG181
0.002	bBE54A
0.006	AB G3
0.009	MWG1026B
0.010	P13/M50-110 AWBMS62
0.010	Pm
0.011	HVM3
0.012	MWG180B
W W	CDO650 CDO795
0.013	Mne1a MWG232
	AWBMS90
0.021 \	MWG2135 MWG57
0.025	ABC303
	MWG2036 AB A3
0.028	Adh4 ABG484
	Pgk2A MWG2110
	MWG939 bAI57
0.035	MWG793 Ris2A2
	dMig
0.036 ///日\\\	Mne1b
0.038 //	AB G461C MW G635a
	MWG2097 MWG948
0.044 ′	MWG2134 PBI25
0.064	MWG880
	CD0586
0.070	AB G472
0.073	FBmac635 FBmac701
0.096	Bmag 375
0 100	Tub A1 BCD265B
0.102	P13/M50-371
	AB G715 Bmac181
0.106	EBmac906
0.112	MWG35C
0.125	MWG677
0 127	P13/M51-252 P13/M51-90
0.127	PSR141
0.129	BCD453B(69.8)
0.135	MWG464
0.138	P14/M47-328
0.141	Centromere-4H
0.144	BCD453c
0.166	WG719
0.173	X4.1
0.188	Bmag0353
0.203	X4.2
0.204	AB G394
0.221	P12/M50-292 P13/M61-318
0.253	Bmac0186
0.254	AB G319 A
0.259	JBC970
0.265	BCD15a
0.274	CDO1406
0.352	AB G618
0.356	
0.376	MWG655C
0.388	MWG114 EBmac788
0.397	AB G4B
0.404	P13/M47-454
0.411	AB G498 PSR164
0.450	
0.458	BG125 iAco2
0.463	IDO1312 HVMLOHIA
0.472	JDG1300
0.485	AD 00000 019



0.407	IBC 47B
0.487	/ JBG47B
0.503	
0.504	DOD4420
0.513	
0.514	AL 88/2 DAP91
0.521 -/	CD0677
0.525	X4.3
0.538	MWG2159 cMWG652B
0.570	AB G397
0.572 //	P11/M48-119
0.580 ///	AB G366
0.593 //	\ [\] MWG464B
0.602 /	[\] MWG464 A
0.661	— КГР221
0.736	Bmag419
0.738	EBmac0701
0.740	EBmac679
0.753 //	AB G319C
0.757 //	ABC151C
0.774	ABG3a GMS89
0.795	AB G54
0.816	│
0.834 /	X4.4
0.880	AB G601
0.909 🔪	BCD402 MWG199
0.945 \	/ AB A306C MW G2047b
0.949 \\	// P14/M51-122
0.962	// CDO465 MWG2112
0.972	// ABC305B
0.983	// ASE1C
0.985	// Hsh
0 993	EXO2a
Æ	K MWG542 HVM67
1.000	Bmv1
	, , . , , , , , , , , , , , , , , , , ,
Usmotic po	otential under irrigated condition
Fusarium h	nead blight resistance
Malting qu	ality

- Flowering time
- Relative water content under stress treatment
- Osmotic potential at full turgor
- Relative water content under irrigated condition
- Water soluble carbohydrates

Figure 1. contd.

5H(a)	5H(b)		5H(c)	
0.000 0.004 0.006 0.017 0.019 0.032 0.043 0.043 0.043 0.043 0.043 0.043 0.050 0.065 0.076 0.085 0.076 0.087 0.094 0.097 0.099 0.097 0.099 0.105 0.126 0.131 0.137 0.138 0.146 0.155 0.155 0.156 0.155 0.155 0.156 0.155 0.126 0.152 0.155 0.155 0.155 0.155 0.155 0.155 0.155 0.155 0.126 0.152 0.155 0.155 0.155 0.155 0.155 0.155 0.155 0.155 0.126 0.152 0.155 0.155 0.126 0.152 0.155 0.155 0.126 0.152 0.155 0.126 0.152 0.155 0.155 0.126 0.152 0.155 0.156 0.2153 0.215 0.2213 0.2215 0.225 0.255	MWG696 AB G705 A ABC483 ABC483 P13/M50-437 AB G610 AWPCB7b pTAG354a AWWWM1a HVTL Brac2273B AB G610 MWG609 MWG609 CD0669B MWG717 MWG561b MWG889 JBC96 JBC134 JBC96 JBC485 MWG561 D075 JBC467 MWG8920 AWBS53 MWG920 ABC156A ksu M49-211 P13/M48-180 P13/M49-211 P13/M48-360 <p14 m48-223<="" td=""> P13/M48-360 PSR1204 psr11 PSR1204 psr11 PSR1204 psr11 PSR1204 psr11 PSR1204 psr161 MWG405 AB G497 MWG405 AB G497</p14>	0.261 JB G87 0.286 XrDNA 0.285 MWG5 0.285 ABC32 0.302 JB C28 0.325 ABC32 0.334 MWG65 0.334 DC33 0.344 DC33 0.344 DC33 0.344 DC33 0.430 MWG5 0.433 MWG5 0.446 BCD33 0.446 BCD33 0.446 BCD33 0.540 BCC37 0.551 Bmag2 0.563 DF11/MWG67 0.563 <td>6 0.787 10 BCD410B 0.787 11 0.821 92 12 18 0.823 8 0.835 0.835 90 BG123b 0.835 91 0.836 0.835 94 0.836 0.836 17-220 AWBMA3 0.853 11-386 0.870 0.872 11-386 0.870 0.872 11-386 0.870 0.872 11-386 0.870 0.872 11-386 0.870 0.883 11-386 0.872 0.883 11-386 0.872 0.883 11-386 0.872 0.883 11-386 0.883 0.891 11-38 0.905 0.883 114 MWG549b 0.891 12-294 0.923 0.942 12-294 0.942 0.942 12-294 0.942 0.942 12-294 0.942 0.942 12-294 0.942 0.942 <t< td=""><td>7 MWG2121 1 MWG181 EBmaa 3 AB G495A MWG3 5 MWG583 MWG65 6 MWG79a 6 MWG70a 7 MWG1026 C DO675B MWG3 8 MWG740 PSR637a C DO400b CDO6 0 PSR394 2 PB139 5 MWG654 MWG2 0 ABC168 MWG76 PB139 MWG654 MWG2 0 ABC310A MWG76 1 MWG827 MWG34 MWG34 MWG650 BCD298 ABG707b BCD3 psr115 ABC310b ABG33 1 PH4/M55-135 1 CD0457 ABC483 4 ABG69 MWG2 ABG463 2 ABG57B 1 MWG2037a ABC 4 ABG57E 1 MWG364 4 ABG57B 12 ABG57B 14/M55-146 G5 ABG314A MWG891 15 ABG314A MYG6</td><td>24 522 78b 8 1020 701a 50 139e 139 139 139e 139 139e</td></t<></td>	6 0.787 10 BCD410B 0.787 11 0.821 92 12 18 0.823 8 0.835 0.835 90 BG123b 0.835 91 0.836 0.835 94 0.836 0.836 17-220 AWBMA3 0.853 11-386 0.870 0.872 11-386 0.870 0.872 11-386 0.870 0.872 11-386 0.870 0.872 11-386 0.870 0.883 11-386 0.872 0.883 11-386 0.872 0.883 11-386 0.872 0.883 11-386 0.883 0.891 11-38 0.905 0.883 114 MWG549b 0.891 12-294 0.923 0.942 12-294 0.942 0.942 12-294 0.942 0.942 12-294 0.942 0.942 12-294 0.942 0.942 <t< td=""><td>7 MWG2121 1 MWG181 EBmaa 3 AB G495A MWG3 5 MWG583 MWG65 6 MWG79a 6 MWG70a 7 MWG1026 C DO675B MWG3 8 MWG740 PSR637a C DO400b CDO6 0 PSR394 2 PB139 5 MWG654 MWG2 0 ABC168 MWG76 PB139 MWG654 MWG2 0 ABC310A MWG76 1 MWG827 MWG34 MWG34 MWG650 BCD298 ABG707b BCD3 psr115 ABC310b ABG33 1 PH4/M55-135 1 CD0457 ABC483 4 ABG69 MWG2 ABG463 2 ABG57B 1 MWG2037a ABC 4 ABG57E 1 MWG364 4 ABG57B 12 ABG57B 14/M55-146 G5 ABG314A MWG891 15 ABG314A MYG6</td><td>24 522 78b 8 1020 701a 50 139e 139 139 139e 139 139e</td></t<>	7 MWG2121 1 MWG181 EBmaa 3 AB G495A MWG3 5 MWG583 MWG65 6 MWG79a 6 MWG70a 7 MWG1026 C DO675B MWG3 8 MWG740 PSR637a C DO400b CDO6 0 PSR394 2 PB139 5 MWG654 MWG2 0 ABC168 MWG76 PB139 MWG654 MWG2 0 ABC310A MWG76 1 MWG827 MWG34 MWG34 MWG650 BCD298 ABG707b BCD3 psr115 ABC310b ABG33 1 PH4/M55-135 1 CD0457 ABC483 4 ABG69 MWG2 ABG463 2 ABG57B 1 MWG2037a ABC 4 ABG57E 1 MWG364 4 ABG57B 12 ABG57B 14/M55-146 G5 ABG314A MWG891 15 ABG314A MYG6	24 522 78b 8 1020 701a 50 139e 139 139 139e 139 139e
	 Osmotic potential Fusarium head blig Malting quality Flowering time Relative water con Osmotic potential Relative water con Water soluble carb 	under irrigated cor ght resistance tent under stress tr at full turgor tent under irrigated ohydrates	dition eatment l condition		

Figure 1. contd.

6H(<i>a</i>	l)	6H(b)
	MW G620 AB G466	0.700.0	DOFME
ן 0.000	Bmac316 Lth	0.762	BC164(IF) ksuD17
	PSR167 PSR312b	0.765 M	IWG2043 MWG2061
0.015	TAM10	0.769 C	entromere-6H
0.016	MWG663-2A Nar1	0.774	BG130A
0.020	BCD102 ABG378	0.776 0.783 1 / M	WG872
0.030	BCD21B	A	B G379 AB G388
0.035	HVM74	0.792 M	IWG2029 PBI9
0.038	MWG966	I R	
0.039	r PSR611	0.822 0.832 I B	Smac251
0.049	MWG573(IF)	0.841 P	14/M51-166
0.056	MWG59		BC170B ABG1A
0.061	/ MWG1UA	0.842	WG2100 MWG684B
0.083	AB G654 P14/M61-376		IW G951 MW G967D BC123
0.098	JBG130B	0.848 \	IAR7b
0.110	Bmag9 MWG405C	0.854 \	OGF2 ksu A3D
0.115	/ Cxp3	0.866 WH	Bmac571b HvACLIb
0.172	ABC152A	0.878	BG1C
0.179	/ His3D	0.881	13/M49-101 3CD269 EBmac602
0.184	/ ksu A1g P13/M61-331 MW/G690	0.896	13/M50-367
0.205	MWG652A	0.897	WG19 BCD221A
0.249	MWG602B	0.902 P	12/M51-191 PSR666b
0.314		0.904 / B	CD1 P13/M61-205
0.392	/ JBG259A	0.911 B	G140 A
0.419	X6.1	0.916	14/M49-91
0.427	P14/M61-171	0.920 M	IW G282
0.429	EBmac874	0.924 M	WG2137 MWG2141
0.455	/ JBG274	0.935 P	22/M58-151 BC154E Nir
0.469	MWG653 MWG664a	0.942 0.952	SR627
0.472		0.05C	BC264 BCD339B
0.474	/ MWG26	0.956	hn3 dhn5
0.504	MWG2065(HT)	0.962 B	
0.516	MWG79b	0.963 0.966	17/0684C MW/0/160 13/M61-272
0.534	MWG664b	0.967	lar7
0.548	JBG77B	0.968 P	13/M48-254
0.550	X6.2	0.969 B	CD221B PSR154
0.573	- MWG666 EBmac806 P14/M49-139b	0.975 ×	6.4 B G711
0.600	PSR167B	0.980 A	BC170A P14/M47-197
0.605	MWG996b	0.981 P	13/M51-205
0.612	ABR331 Ubi4	0.982 C	DO419A MWG549a
0.620	HVM31	0.984 A	B G 614 14/M51-308 BCD 15b
0.629	ABC163	^{0.986} C	DO836
0.633	ABC169B Ubi5	0.987 M	WG222B MWG684A
0.639	ABC175	0.989 A	B G461B
0.647	Rrn1	0.994 j P	13/M61-357 BC154 MWC897
0.650	Bmag0009		WG934 P11/M62-390
0.654	MWG286	^{1.000}	13/M61-216 P13/M61-328
0.001	ABR335 CDO497	B	CD339g MWG669
0.003	ksu A3B	·	
0.668	ABC156D MWG2235	Osmotic po	tential under irrigated condition
0.679	MWG679	Fusarium b	ead blight resistance
0.717	AB G474	Malting and	ality
0.726	AB G20 BCD340E		
0.746	AD G705B MWG984a	Flowering t	time
0.749	X6.3	Relative wa	ter content under stress treatment
		🛛 📶 Osmotic po	tential at full turgor
		🖾 Relative wa	ter content under irrigated condition
		Watar achi	hle opthohydrates
		water solut	one carbonyurates



7H(a		7
		'
	MWG905 ABG399B	0.569)
0.000	AB G312d Plc	0.573
0.0061	ABG704 RISBPP161a	0.500
0.008	AB G1B	0.616
0.018	BCD130 CDO545	0.678
0.010	MWG36B MWG851a	0.721
0.019	AB G77	0.726
0.033	Bmag0007	0.749
0.038	MWG555a	0.753
0.040	ABG75 RislC10a	0.754
0.051	ABC255	0.768
0.060	ABR303	0.771
0.070	iEst5 MWG2080	0.781
0.075	P12/M51-73 P14/M47-278 P14/M47-357 PSR160	0.782
0.079	GIx(Wx)	0.821
0.081	⁻ JBC401 P11/M51-341 P13/M50-237	0.826 1
0.083	BCD15c CDO1400	0.828)
	Bmag206	0.831
0.096	P11/M62-141 PSR637b	0.836
0.099	JBG235	0.840
0.101	P13/M50-272 P11/M62-353 P13/M4 <u>8-208</u>	0.845
0.102	P13/M48-85 ABC465	0.846.1
0.107	P14/M47-315	0.040
0.108	Prx1A MWG733B	0.849 \
0.109	BCD129	```
0.117	P13/M61-73 psr119b	0.850 ~
0.132	ABG320	/
0.141	MWG4a	0.851
0.162	BCD339h BCD135	0.853
0.203	HvWaxy4a HvWaxyG	0.856
0.211		0.858
0.235	MWG834	0.861
0.241	ABC152	0.865
0.249	MWG18	0.866
0.282	MWG89	0.870
0.300	MWG773	0.871
0.311	ABC167a	0.875
0.321	AB G380 dSbl	0.876
	AB G497b MWG721	0.878
0.349	MWG622 MWG980	0.885
	MWG527	0.886
0.378	P14/M47-164	0.888
0.443	AB G497 a	0.890
0.448 0.460	MWG606	0.891 ′
0.469	MWG39	0 804
0.492	HVCMA NANA ksuA1A	0.094
0.548	MWG66	0.898
0.562	WWWG2040D	0.033
		0.900
		0.902

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	40.04544	
[ADC134A Bmcc0497	
I	MW/G710a	
ŀ	MWG2040C	
ŀ	MWG836	
ŀ	MWG622a	
ŀ	LD	
	P11/M48-367 P14/M48-15	50
ł	AB G603	
l III.	lks2	
R	PSR933a YAtp57A	
	Brz	
	P12/M54-56	
	AWBMA15	
	MWG967a MWG2030	10000
	CD036	
	Amv2	
	AWBMA16	
	DO348	
	Bmac047B	
	MWG53	
	MWG940 MWG728	
	MWG599	
	Bmagu120 AWBMA11	
	PSR929b	
W.	CD0420B	
— N ,	MWG686	
	MWG996c Bmag120	***
	P14/M47-354 Bmac167	
	Bmag359a Bmag359b	
	EBmac827	
	JBG149 JBG26	
	AB G11 AB G701	
e/J	AWBMA26 CDO665d	
	PSR108b MWG2072	
	MWG729 ICIG11a	
 \	ADCAECA DASIMED 402	
	EBmac755	
	DAK642 P14/M55-102	
	EBmac764	
A.	B12D	
AL A	MWG380B	
	ABC305	i i i
A.	Bmag217	
	MWG5/3(HI) BCD351A	
	DBE54E PGK2B	
	MWG36C	
	Bmag183 HvSS1	
	PSR129	
	P14/M59-215 Bmac31b	
	MWG911 (SM) MWG3	
r	MWG696 MWG825	
	MWG808	
	P12/M51-200 ABC308a	
ľ	Bmag369 P13/M47-300	
- R	MWG704 MWG815	
6	ABG652a cdo57b	
n	AWBMS 37	
	ABC306 CDO583	
	EBmac757 P11/M48-364	
	Hv A22S	
- I	ksuF37 psr547	
[KSUE19D	
	ABG714b ABG476	
ļ,	ABC253	I I I
l	CD0595	

7H(c	:)	
0.9061	P11/M48-317 BCD263	
0.9101	MWG571D	***
0.913	CDO358 ksu A1h	
0.9181	HVM11b	
0.923	MWG889(HT)	
0.925	MWG539 BCD1476	HAVAY.
0.926	MWG669 BCD421	
0 927 1	CDO689 Bmag321	
0.929	Centromere-7H	
0.930	JBG13 P13/M59-277 P13/M59-1	209
0.934	Ubi1	
	MWG2041 ABC308	
0.936	BCD340D MWG511	
	MWG741 MWG10B	
0.940	AaWBI Bmac156	
0.942	CDO676 MWG878B	
0.947	P14/M51-228	
0.948	Adh7	
0.949	Cat3 BCD298B	
0.950	Tha Chi1	
0.954	P11/M48-292	
0.956	ABC321 P14/M61-275	
0.957	Ris44	
	mn BG143	
0.959	MWG719 ABC322A ABC254	
0.961	ksue18b	
0.962	AWBMS22	
0.965	ABC719	
0.968	ABG461	
0.970	JBG256	
	ABG461A PSR637c	
0.975	P12/M51-360 ksuE18c	
0.980	PSR680 MWG903 ABC455	
0.983	PSR117c ABC310b	I I I
0.984	ABC308b M501	
0.987	BCD512	
0.9887	P13/M59-118 ksuD14C MWG420	
	PSR150a MWG739	
	ABC151B MWG987	1000
	MWG681 PBI19	
0.992	ABC 621 Rip	
	Acl3 MWG626	
	CDO673 MWG725 MWG649a P13/M50-76	
	Bmag507	
0.994 0.996	AB G652	
0.998	AB G497b	
1.000	ABC154B MWG528	
	CDO347b	

- Osmotic potential under irrigated condition
- **Fusarium head blight resistance**
- Malting quality
- Flowering time
- Relative water content under stress treatment
- Osmotic potential at full turgor
- Relative water content under irrigated condition
- Water soluble carbohydrates



et al. (1996) as they identified QTL for flowering time on all chromosomes except the chromosome 3H. This indicates that the constructed consensus map is consistent with other barley maps used in QTL studies. In some genomic regions of the consensus map, markers associated with flowering time and *Fusarium* head blight resistance were co-located on the same place. Jeremy et al. (1996) reported a correlation between heading date and plant height but there is no reports for a correlation between heading date and *Fusarium* head blight resistance. This might reflect a possible correlation between the two traits. However, more studies and investigations are needed to be done in this area to verify this possibility.

Malting quality traits such as percentage of plump weight, protein kernels, test grain percentage, soluble/total protein ratio, L-amylase activity, diastatic power and malt-extract percentage are highly correlated and controlled by almost the same loci (Marguez et al., 2000). In the present study 32 QTL for malting guality were placed on the integrated map. Six of them were on chromosome 1H, 8 on 2H, 2 on 4H, 5 on 5H, 4 on 6H and 7 on 7H (Figure 1). In the progeny of Steptoe (feed) x More (malt), malting quality QTL were mapped to all seven chromosomes (Hayes et al., 1993). In the progeny of Harrington (malt) x TR306 (feed), malting quality QTL mapped to all chromosomes except 2H (Mather et al., 1997).

Ten QTL related to drought tolerance were incorporated into the consensus AD-2005 map. One for potential irrigated osmotic under condition on chromosome 2H, 1 for relative water content under stress condition on chromosome 7H, and one QTL for relative water content under irrigated condition on chromosome 5H. Two QTL for osmotic potential at full turgor were placed, one on chromosome 4H and one on 3H. While 5 QTL for water soluble carbohydrates were placed, two of them on chromo-some 7H and 5H each and one on chromosome 2H. This result agrees with Diab et al. (2004) and Teulat et al. (2001). QTL for water soluble carbohydrates and relative water content were found to be associated with the marker MWG626 and the marker Acl3 respectively on chromosome 7H. These traits are components of drought tolerance; therefore, the colocalization of these QTL is most likely due to pleiotropic effects of the same gene(s). The correlation between the 2 traits has been reported by Teulat et al. (2001) and Diab et al. (2004).

Markers associated with more than one trait

Markers on the consensus AD-2005 that was found to be associated with more than one trait should receive more attention, as it could be of a great use to correlate traits that were not reported to be correlated or to support a correlation between traits that was suspected or need

more investigation. For example, the marker HVM36 on chromosome 2H was found to be associated with a QTL for Fusarium head blight resistance (Mesfin et al., 2003) and a QTL for osmotic potential (Diab et al., 2004). Also the marker (Bmaq0125) on the same chromosome was found to be associated with a QTL for Fusarium head blight resistance (Mesfin et al., 2003) and a QTL for water soluble carbohydrates (Diab et al., 2004). Another case of one marker associated with 2 different traits is the locus MWG503 on the same chromosome (2H) that was reported to be associated with a QTL for Fusarium head blight resistance (Mesfin et al., 2003) and a QTL for malting quality (Marguez et al., 2000). There are no reports supporting the correlation between these traits, however, the association of these traits with the same marker suggests a sort of correlation between these traits.

The marker CDO484 on chromosome 5 was found to be associated with QTL for relative water content and water soluble carbohydrates (Diab et al., 2004). The colocation of water soluble carbohydrates and relative water content in this region suggests that the accumulation of water soluble carbohydrates may be important for plants to maintain their relative water content. Teulate et al. (2001) reported a correlation between these two traits as a part of the drought tolerance mechanism in barley.

This study reports the first barley consensus map gathering QTL for *Fusarium* head blight resistance, malting quality, flowering date and QTL related to drought stress. Gathering QTL for agronomic traits and biotic and abiotic stress on the same map provides new tools to align QTL traits between gramenea species and determine the most important regions for saturated mapping. The comparative genome mapping of such QTL may provide new information on shared genetic variation for those traits among cereals, which in turn might be useful for identifying potential candidate genes.

Proof of reliability of the consensus AD-2005 map

Comparative genomic studies of maps between cereal species have shown conservation of genome structure (Devos and Gale, 1993 and 1997; Van Devnze et al., More extensive analysis of genome 1995a,b,c). organization has revealed that the genome of rice can be subdivided into 19 linkage segments, which can be aligned with the genomes of wheat and barley (Moore et al., 1995). Based on previous comparative linkage mapping studies, the rice linkage groups 5 and 10 are known to be syntenic with at least parts of the linkage group 1(1H), while the rice chromosome 1 is syntenic with chromosome 3(3H). Similarly, rice non homologous chromosomes (4 and 7), (3 and 10) and (6 and 8) are 2H, 4H. and syntenic with chromosomes 7H. respectively. Accordingly, the Cornell rice RFLP 2001 map (http://www.gramene.org) was downloaded and

	Marker	Position	Marker	Position	Marker	Position	Marker	Position
Мар	OWB - 1H		KXM - 1H		VXHs - 1H		Consensus AD-2005 -1H	
Rice	0	-	CDO105B	102.8	MWG68	46.5	BCD454	0.16
5							CDO580a	0.244
							CDO105B	0.519
Rice	0	-	0	-	0	-	CDO98	0.26
10							BCD207	0.28
	OWB - 2H		KXM - 2H		VXHs - 2H		Consensus AD-2005 - 2H	
Rice	0	-	JBG282	113.7	0	-	CDO680	0.608
4							CDO36	0.97
OW		3 - 3H	KXM - 3H		VXHs - 3H		Consensus AD-2005 - 3H	
Rice	0	-	MWG110	113.3	0	-	CDO395	0.087
1							BCD828	0.35
							MWG110	1.0
	OWB - 4H		KXM - 4H		VXHs - 4H		Consensus AD-2005 - 4H	
Rice	CDO542	31.2	0	-	0	-	CDO795	0.013
3	CDO122	32.3						
	OWB - 7H		KXM - 7H		VXHs - 7H		Consensus AD-2005 - 7H	
Rice	0	-	0	-	0	-	Glx(Wx)	0.175
6							CDO475	0.295
							Amy2	0.67
Total	2		3		1		14	

Table 3. Comparison of the common markers (anchor loci) found in comparative study between rice and consensus AD-2005, OWB, KXM, and VXHs barley maps.

compared with the constructed barley consensus AD-2005, OWB, KXM and VXHs maps based on common markers (anchor loci). The results obtained from this comparative study are showed in Table 3. The total number of shared markers between rice and barley maps increased from two with OWB map, three with KXM and one with VXHs to 14 when the consensus AD-2005 map was used. These results meet the main objective of constructing an integrated barley consensus map to increase the chance of finding anchor loci between durum wheat, barley and rice.

The construction of consensus map allows scientists to easily compare genetic information from diploid species such as barley to species with more complex genomic structure, such as wheat, and increases the efficiency of molecular marker and gene isolation technologies applied to crop improvement. The objective of this work was to construct a consensus map for barley to be used in molecular breeding, QTL analysis and comparative genome mapping, which in turn will help plant breeders to combine QTL traits with other traits desired by farmers. Although more data are desperately needed, we can now conclude that this consensus map will serve as a useful tool for more precise mapping of cereals, molecular breeding studies in barley and related species, gene isolation based on map-based cloning and a basis for studies of genome organization and evolution.

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