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ORIGINAL ARTICLE

Major genomic regions responsible for wheat yield and its components as revealed by meta-QTL and genotype–phenotype association analyses

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Abstract

Main conclusion **Meta-QTL (MQTL) analysis was done for yield-related traits in wheat. Candidate genes were identified within the refined MQTL and further validated by genotype–phenotype association analysis.**

Abstract Extensive studies have been undertaken on quantitative trait locus/loci (QTL) for wheat yield and its component traits. This study conducted a meta-analysis of 381 QTL related to wheat yield under various environments, including irrigated, drought- and/or heat-stressed conditions. Markers flanking meta-QTL (MQTL) were mapped on the wheat reference genome for their physical positions. Putative candidate genes were examined for MQTL with a physical interval of less than 20 Mbp. A total of 86 MQTL were identified as responsible for yield, of which 34 were for irrigated environments, 39 for drought-stressed environments, 36 for heat-stressed environments, and 23 for both drought- and heat-stressed environments. The high-confidence genes within the physical positions of the MQTL flanking markers were screened in the reference genome RefSeq V1.0, which identified 210 putative candidate genes. The phenotypic data for 14 contrasting genotypes with either high or low yield performance—according to the Australian National Variety Trials—were associated with their genotypic data obtained through ddRAD sequencing, which validated 18 genes or gene clusters associated with MQTL that had important roles for wheat yield. The detected and refined MQTL and candidate genes will be useful for marker-assisted selection of high yield in wheat breeding.

Keywords Wheat · Meta-QTL · Yield · Candidate genes · Genotype–phenotype association

Introduction

Improved yield with high quality and adaptability is the primary goal of wheat breeding programs to address global food security and sustainability. Wheat yield is a complex quantitative trait controlled by quantitative trait locus/loci (QTL) and affected by environmental factors. A large

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number of QTL have been detected for wheat yield under different environments, including irrigated, drought- and/or heat-stressed conditions. However, few have been successfully adopted for marker-assisted selection (MAS) in breeding. One reason lies in the low map resolutions in many studies, resulting in large QTL intervals with loose marker-gene linkages. Another reason is that many of these QTL have not been validated, as validation or fine mapping of the loci requires substantial effort and investment. Meta-analysis provides a good alternative for validating QTL and narrowing the QTL intervals, as it can detect consistent QTL by integrating QTL from studies using various environmental and genetic backgrounds, and reduce their genetic intervals, leading to the identification of candidate genes (Wu et al. 2016).

Genome-wide QTL meta-analysis approach has been applied for many traits in wheat. A meta-QTL (MQTL) analysis, based on a consensus map of major and consistent QTL for yield and yield-related traits, identified 12 significant MQTL on chromosomes 1A, 1B, 2A, 2D, 3B, 4A, 4B, 4D, and 5A, some of which contained important known genes such as *Rht* and *Vrn* (Zhang et al. 2010). However, candidate genes underlying the meta-QTL were not investigated due to the limited knowledge of the reference genome sequence at the time. Tyagi et al. (2015) conducted an MQTL analysis of grain morphological traits, including grain weight, and identified 17 reliable MQTL on chromosomes 1B, 2A, 2D, 3B, 4A, 6A, and 6B, with 16 of which related to grain weight. Again, no candidate genes were suggested in this study. Acuña-Galindo et al. (2015) conducted a meta-analysis of wheat QTL associated with drought and heat tolerance. They identified 66 MQTL distributed throughout the genome, many of which were co-localized with the yield MQTL identified by Zhang et al. (2010). The authors identified 41 candidate genes through SNP-gene association, including those involved in sugar metabolism, reactive oxygen species (ROS) scavenging, and abscisic acid-induced stomatal closure. Apart from yield-related traits, MQTL analyses have been undertaken for other traits in wheat, including flowering date (Hanocq et al. 2007) and preharvest sprouting tolerance (Tyagi and Gupta 2012). These MQTL studies surveyed relevant QTL studies and refined the positions of some major QTL. However, none investigated how the identified MQTL are distributed in a wide range of wheat genotypes or how they contribute to trait performance.

Reports identifying new yield-related QTL in wheat using high-resolution markers have increased in the past few years (Cabral et al. 2018; Su et al. 2018; Tura et al. 2020). An MQTL analysis incorporating these new studies is needed. Publication of the reference genome sequence in wheat (Appels et al. 2018) paved the way for more efficient gene identification and marker development. Many yield-related genes have also been identified in other cereal crops, including rice and barley (Huang et al. 2018; Nadolska-Orczyk et al. 2017), with some explaining a significant proportion of the phenotypic variation in their traits, such as *OsGS3* in rice for grain weight (Fan et al. 2006). This newly available information will facilitate MQTL analysis on gene predictions and marker development.

As wheat requires significant local adaptation to succeed, breeders need to develop high-yielding cultivars adapted to their target environment. Contributions of genomic regions to yield may vary according to the target environment. Therefore, assessments of the major genomic regions responsible for wheat should be undertaken in the targeted region. This study assessed the MQTL of selected cultivars with extreme expressions of yield traits using association analyses of genotypic data obtained via ddRAD sequencing and phenotypic data from 2012 to 2016 Australian National Variety Trials (NVT) (https://www.nvtonline.com.au). Since Australian wheat cultivation mostly takes place under rainfed conditions, where drought and/or heat stress often occur, the QTL responsible for yield in drought- and/or heat-stressed environments were included in the MQTL analysis, as well as those in irrigated environments.

By integrating and summarizing the results from separate QTL mapping studies, this study aims to locate consistent QTL regions associated with wheat yield and its component traits. We reviewed the genomic regions involved in the control of wheat yield and its related traits and refined the positions of yield-related QTL. While many genes for small effects may contribute to yield, this study only focused on consistent or major QTL to identify MQTL and refine their chromosomal positions to improve MAS efficiency for yield-related traits in wheat.

Materials and methods

Dataset development for yield-related QTL

As Zhang et al. (2010) conducted an MQTL analysis on wheat yield for studies pre-2010, we reviewed and summarized 24 QTL studies published from 2010 to 2020 related to yield and yield components under different environments, including irrigated, drought- and/or heat-stressed conditions (Supplementary Table S1). We identified 381 QTL for inclusion in our meta-analysis, being major QTL with > 10% of the phenotype variation explained (PVE), and those that were consistent within each study. The MQTL analysis required the

R^2 (percentage PVE) and confidence interval (CI) for each QTL (Zhang et al. 2010). The most recent published study (Tura et al. 2020) did not provide PVE values, so the QTL were excluded from the MQTL analysis. However, the QTL were included as a separate reference for comparison on the MQTL map as the study used 3502 high-resolution markers and identified consistent yield QTL, with significant yet small main effects, across 10 environments on three continents over six seasons.

Projection of QTL on a consensus map and MQTL analysis

The major markers used for constructing genetic linkage maps in QTL mapping studies include simple sequence repeat (SSR), diversity arrays technology (DArT), and single nucleotide polymorphism (SNP) markers. A highly saturated consensus map—containing 52,607 markers, including 51,655 SNP, 667 SSR, 266 DArT, and 19 other markers—was simplified for use as a reference map (Wen et al. 2017). Simplification reduces the computer processing time for QTL projection, as it only retains selected markers and reduces the number of markers for the same chromosome positions. The selected markers included those that: (1) overlapped, at least once, with the markers used in the collected QTL studies; and (2) had different chromosome positions to the markers in (1), but only one marker was retained for each chromosome position. The simplification step did not reduce genetic distance on the consensus map because we retained at least one marker for every original map position. In addition, the removed markers were not used in the 24 QTL publications collected for this MQTL study, so their removal will not affect the MQTL results. The simplified consensus map contained 22,664 markers, including 21,909 SNP, 534 SSR, 214 DArT, and seven other markers, and was used as the reference map for QTL projection.

BioMercator V4.2 (https://urgi.versailles.inra.fr/Tools/BioMercator-V4) (Arcade et al. 2004) was used to project QTL from different populations in the collected studies onto the reference consensus map. The QTL projection was based on LOD scores, PVEs, CIs, and QTL positions. For those QTL lacking flanking markers and CIs, a 95% CI was calculated as $530/(N \times R^2)$, where N is the population size, and R^2 is the proportion of phenotypic variance (Zhang et al. 2017); the positions of the closest markers to these intervals were selected as the QTL positions on the reference map. We eliminated QTL that did not have a tightly linked consensus marker from further analysis. Meta-analysis was performed on the QTL clusters for each chromosome using algorithms from the BioMercator software (Goffinet and Gerber 2000; Veyrieras et al. 2007). The lowest Akaike information criterion (AIC) value was used to select the best QTL model for identifying the number of MQTL on each chromosome (Lu et al. 2018).

Searching for putative candidate genes within the MQTL confidence intervals

The flanking markers of the MQTL were blasted with the reference genome IWGSC RefSeq v1.0 (https://wheat-urgi.versailles.inra.fr/) (Appels et al. 2018). Putative candidate genes for that MQTL with a physical interval of less than 20 Mbp were identified to extract gene information within or around the intervals; their functions were compared to find the best possible candidate genes.

Genotype–phenotype association analysis of Australian cultivars with contrasting yield performance

Field phenotypic data of 109 cultivars were collected from the 2012 to 2016 Australian NVT conducted at 108 trial locations across different environments, including Western Australia, Queensland, New South Wales, Victoria, and South Australia. The soil texture and weather conditions of each trial location are available on the NVT website (https://www.nvtonline.com.au). The mean yield performance of each cultivar across 5 years was compared across environments (Table S2). Phenotypic data from 2015 to 2017 CIMMYT Australia ICARDA Germplasm Evaluation (CAIGE) field trials were collected as a reference check (http://www.caigeproject.org.au/germplasm-evaluation/bread/data-compilations/). Cultivars that consistently (in at least two of the four environments listed in Table S2) fell into the top 10 highest or lowest yielding cultivars were chosen for further investigation. As a result, 14 cultivars were used for genotype–phenotype association analysis, including Cobalt, Tenfour, Beckom, Scepter, Scout, Suntop, and Trojan in the high-yielding group, and Sunvale, Crusader, Dart, Hatchet CL Plus, Impress CL Plus, Tungsten and Lang in the low-yielding group. Differences between the mean yields of the high- and low-yielding groups were analyzed using a t test (Table S2).

The 14 cultivars were genotyped using ddRAD sequencing, a two-enzyme genotyping-by-sequencing (GBS) technology. Specifically, genomic DNAs were extracted using leaf tissue from three-leaf stage seedlings using a modified CTAB method (Mia et al. 2019), and their quality examined on 1% agarose gel and a Nanodrop 2000 spectrophotometer (Thermo Fisher Scientific Inc.,

Australia). The samples were sent to the Beijing Genomics Institute (BGI), China, where they were double-digested using a rare-cutting EcoRI-HF and a frequent-cutting MseI enzyme. Sequencing libraries of 150 bp paired-end reads were prepared and sequenced using HiSeq X Ten (Illumina, San Diego, USA) according to the manufacturer's standard protocols. Raw sequencing data were filtered following the procedure described in Mia et al. (2020). Genotyping of SNP and detection of indel markers were performed on the clean data. The GBS markers within the MQTL physical positions were blasted with the wheat reference genome to search for their associated genes.

Results

Identification of MQTL for yield and yield components under different environments

Major ($R^2 > 10\%$) or consistent QTL were selected for the meta-analysis, as the only QTL with these qualities can be used in MAS (Zhang et al. 2017). As such, 381 QTL for wheat yield and yield components were projected on different chromosomes (Table S1; Fig. S1). Chromosome 1B had the most QTL (58), and chromosomes 3D and 5D had the least (3) (Table 1). A total of 86 MQTL—integrated QTL from several experiments—were identified by meta-analysis; of which, 39 were responsible for yield under drought-stressed environments, 36 under heat-stressed environments, 23 under drought- and heat-stressed environments, and 34 under irrigated/non-stressed environments (or environments without a specific stress mentioned). MQTL1B.5 integrated the most (12) initial QTL, followed by MQTL3B.2 (10); both formed a significant peak on the density curves (Fig. S1), suggesting that they are hotspots for improving yield in wheat. Chromosomes 4A, 4B, and 7A had the most MQTL detected (7 each), whereas chromosomes 1A, 3D and 5D had the least MQTL (one each). The meta-analysis reduced the CIs of the original QTL from 12.7 cM on average to 5.2 cM for each MQTL. The CIs of MQTL ranged from 0.03 cM in MQTL1B.7 and MQTL1B.8 to 25.06 cM in MQTL6B.2. Some MQTL directly flanked markers for commonly known genes, including MQTL2D.1 with photoperiod loci *Ppd-D1*, MQTL4B.3 with reduced height loci *Rht1*, and MQTL4D.1 with *Rht2* (Table 1). The physical length of these MQTL ranged from 0.17 to 71.36 Mb (Table 2).

Putative candidate gene identification

Apart from the commonly known genes *Ppd*, *Vrn*, and *Rht*, the annotations of high-confidence genes reported in RefSeq v1.0 were screened for the target MQTL with a physical interval < 20 Mbp. The functions of genes within the physical intervals, or around the intervals if inadequate genes were inside each interval of the MQTL, were scrutinized for putative candidate genes. Those genes with functions previously reported as important for yield and stress tolerance traits, such as sugar transporter, sucrose synthase, ethylene response factor, stress-associated proteins, were considered putative candidate genes for the MQTL. Two hundred and ten putative candidate genes were identified using this method (Table 2), of which several genes with similar functions were identified repeatedly on different chromosomes, including 42 genes for functions as E3 ubiquitin ligases, 21 for heat shock proteins (HSPs), 21 for MYB transcription factors (TFs), 15 for ethylene-responsive genes, 14 for sugar transporters, 10 for NAC TFs, and 10 for WRKY family genes. Many of these genes acted as gene clusters with some consecutively arrayed in MQTL regions, such as consecutive HSPs in MQTL1A.1, MQTL2A.2, MQTL3B.3, MQTL 3D.1, and MQTL6D.1, consecutive MYB TFs in MQTL1B.4, MQTL3B.3, MQTL 3D.1, and MQTL7D.2, consecutive NAC TFs in MQTL2A.3, consecutive defensins in MQTL2B.2, consecutive E3 ubiquitin ligases in MQTL3B.1 and MQTL3B.3, consecutive MADS-box proteins in MQTL6B.4, consecutive WRKY TFs in MQTL7A.1 and MQTL7B.5, consecutive transcription elongation factors in MQTL7A.5, consecutive peroxidase in MQT7A.6, consecutive sugar transporters in MQTL7A.7, and consecutive NBS-LRR disease resistance proteins in MQTL7D.3 (Table 2).

Genotype–phenotype association of 14 cultivars with contrasting yield performance

Around 10 Gb of clean data per cultivar sample were obtained from the ddRAD sequencing for the 14 selected cultivars with contrasting yield performance. A total of 139,657 indel and 1,001,955 SNP markers were generated for genotyping. After filtering out markers with no polymorphism, 73,205 indels and 627,697 SNPs were used for final genotyping (Table S3). Variations in the GBS markers most closely located to the identified MQTL gene regions were compared between the two groups of cultivars (7 high-yielding and 7 low-yielding); the t-test identified a highly significant difference ($p < 0.01$) for group mean yield (Table S2). Markers

Table 1 Yield-related MQTL detected in this study

Chr[a]	MQTL ID	Map position	CI (cM)	Flanking markers	Physical position on RefSeq V1.0	Initial QTL traits	Tolerant to stress	No. of QTL within
1A (9)	MQTL1A.1	181.75	1.41	Kukri_c11595_537–wsnp_Ku_c21356_31093507	481691085–483033425	SN-all; GY-DS; HI-DS	DS	3
1B (58)	MQTL1B.1	263.94	0.39	wsnp_Ex_c7447_12751589–BS00067512_51	543082472–543517652	GN-NS; GN-DS; SPS-HS	DS, HS	3
	MQTL1B.2	282.33	0.06	Tdurum_contig57101_1616–BS00098413_51	561507423–565335030	GN-NS; GN-DS; GY-DS; GY-HS; GN-DH	DS, HS, DS + HS	5
	MQTL1B.3	317.3	11.15	wsnp_Ku_c17017_26019611–Kukri_c20486_255	572532662–582715281	TGW-all; GY-DS	DS	3
	MQTL1B.4	345.31	1.72	Tdurum_contig10362_555–BS00063928_51	614331647–621636718	TGW-all; SN-all; GY-NS		4
	MQTL1B.5	358.6	0.10	BS00022775_51–BS00081749_51	604553114–623762494	SN-all; GN-NS; GY-NS; GN-DS; GN-HS; SPS-HS; TGW-DH; HI-DS	DS, HS, DS + HS	12
	MQTL1B.6	361.87	0.63	wsnp_JD_c1544_2179305–Tdurum_contig67656_58	625571625–626085871	TGW-al; SN-all; GY-NS; GN-DS; TGW-DH; HI-DS	DS, HS, DS + HS	6
	MQTL1B.7	373.31	0.03	BS00096498_51–RAC875_c50684_155	629941996–632001695	GY-all; GN-NS; GN-DS; GN-HS; GY-HS	DS, HS	5
	MQTL1B.8	391.03	0.03	tplb0053e09_1284–Ra_c18630_284	638015656–641199314	GN-all; GN-HS; GY-HS; GY-DH	DS, HS, DS + HS	4
1D (9)	MQTL1D.1	96.7	6.00	GENE-3348_203–GENE-3348_44	27540526–27576726	TGW-all; TGW-DS; GN-DH	DS, DS + HS	3
	MQTL1D.2	329.95	0.89	D_contig32020_138–D_GDEEGVY01DD44S_389	488574348–493026726	GW-all; GYM2-DS; TGW-DS	DS	3
2A (20)	MQTL2A.1	187.7	2.25	BS00065276_51–BS00079036_51	31953248–32864757	TGW-all; GN-NS; TGW-NS		3
	MQTL2A.2	265.57	6.47	RAC875_rep_c71350_1712–wsnp_Ex_c41913_48628389	79751994–84951037	GN-NS; TGW-NS; GY-HS; TGW-HS; GFR-HS	HS	5
	MQTL2A.3	574.16	24.12	Xgwm526-IAAV7742	763873451–771073270	TGW-NS; GN-HS	HS	2
2B (31)	MQTL2B.1	145.36	2.25	wsnp_JD_c23434_20022750–BS00009807_51	44424318–52670041	GY-all; TGW-all; GN-all; GY-all		5
	MQTL2B.2	160.84	8.28	BS00096182_51–wPt-5556	65370433–76489059	SPS-HS; SPS-DH	HS, DS + HS	2
	MQTL2B.3	257	0.42	Xwg996–Xbarc91	263220312–453816238	TGW-all; GN-NS; GN-HS	HS	3

Table 1 (continued)

Chr[a]	MQTL ID	Map position	CI (cM)	Flanking markers	Physical position on RefSeq V1.0	Initial QTL traits	Tolerant to stress	No. of QTL within
	MQTL2B.4	260.06	1.00	Ku_c46339_317–Xbarc1064	408194756–443966122	TGW-all; HI-DS	DS	3
	MQTL2B.5	297.73	17.00	wPt-7506–wsnp_Ex_c47157_52450090	683043641–779229586	GY-all; GY-NS		2
	MQTL2B.6	328.35	1.64	wsnp_Ex_c26818_36041748–wsnp_BG274584B_Ta_2_3	657791845–710281768	GY-all; TGW-all		2
2D (16)	MQTL2D.1	80.68	6.39	wsnp_CAP12_c812_428290–Ppd-D1	32792768–36204134	GY-all; TGW-all		2
	MQTL2D.2	92.66	12.81	D_contig29912_428–D_GBB-4FNX01DJHXL_88	29715676–50941419	GY-all; TGW-all; GN-DS	DS	4
	MQTL2D.3	108.53	15.29	wsnp_Ex_c29666_38670435–Tdurum_contig5311_112	62288723–75506740	GY-all; GN; HSI(TGW)	HS	5
	MQTL2D.4	122.94	0.82	Kukri_rep_c71152_906–BS00046890_51	75393708–79941414	GYM2-all; TGW-all; GN-all		3
3A (12)	MQTL3A.1	113.94	1.79	BS00057445_51–Excalibur_c55624_86	25387970–26194886	TGW-NS; TGW-DH	DS + HS	3
	MQTL3A.2	168.67	1.61	Kukri_c23388_695–CAP8_c359_95	64788455–74365042	GN-all; GY-DS; TGW-DS	DS	4
	MQTL3A.3	202.18	3.86	BobWhite_c47722_613–Kukri_rep_c104383_1216	302928129–480147815	GN-all		2
3B (38)	MQTL3B.1	48.04	0.54	BS00017635_51–BS00058861_51	5673703–8814393	TGW-all; GY-NS; TGW-DS	DS	4
	MQTL3B.2	118.97	4.52	BS00027346_51–Kukri_c13830_487	21343759–23600280	TGW-all; GN-DS; GY-DS; TGW-DS; SN-DS; HI-DS	DS	10
	MQTL3B.3	140.83	14.09	TA001229-0435–RAC875_c5799_170	24943474–31813797	HI-DS; DSI(GY)	DS	2
	MQTL3B.4	227.59	6.93	Kukri_c4345_83–Tdurum_contig10426_280	140851970–257841306	GY-all; TGW-all		2
	MQTL3B.5	260.84	6.52	BobWhite_c634_420–BobWhite_c16847_99	242168620–414186365	GN-HS; GY-HS	HS	2
	MQTL3B.6	533	8.44	RFL_Contig2578_862–RAC875_c7158_687	779535677–783472564	GY-all; TGW-all; GN-HS	HS	4
3D (3)	MQTL3D.1	196.54	12.70	IAAV2729–GENE-1919_120	51042786–86353210	GY-DS; GN-DH; HI-DS	DS, DS + HS	3
4A (26)	MQTL4A.1	85.86	15.26	RAC875_c9110_331–BS00066739_51	717297782–722909098	GY-all; SN-all		2
	MQTL4A.2	210	3.08	wsnp_Ex_c3988_7221220–Excalibur_c7034_234	660988814–666149150	TGW-all; TGW-DS; TGW-DH	DS, DS + HS	3
	MQTL4A.3	224.89	0.54	Excalibur_c53864_331–CAP11_c18_238	673446685–684269347	GN-all; TGW-all; TGW-DS; TGW-HS; TGW-DH	DS, HS, DS + HS	6
	MQTL4A.4	238.61	1.36	RAC875_c17197_504–RAC875_c49370_327	629917641–705760459	GN-all; TGW-DS; TGW-HS; TGW-DH	DS, HS, DS + HS	4
	MQTL4A.5	292.15	1.50	BS00022839_51–wPt-6303	602875611–603053087	GN-all; GY-DS	DS	2

Table 1 (continued)

Chr[a]	MQTL ID	Map position	CI (cM)	Flanking markers	Physical position on RefSeq V1.0	Initial QTL traits	Tolerant to stress	No. of QTL within
	MQTL4A.6	300.33	1.86	BobWhite_c19919_572–BobWhite_rep_c49931_364	600898972–601279774	GY-all; GY-DS; GN-HS	DS, HS	3
	MQTL4A.7	381.69	2.92	wsnp_Ex_c10390_17007929–wsnp_BE591195A_Ta_1_1	68565243–71250948	GY-NS; SN-all		2
4B (29)	MQTL4B.1	122.25	3.50	Excalibur_c24115_858–BS00022431_51	23657287–24554785	GN-all; SN-all; TGW-all		4
	MQTL4B.2	129.81	0.49	wsnp_BE442666B_Ta_2_2–GENE_4933_1085	27396703–28954608	GY-all; GN-all; SN-all; TGW-all		5
	MQTL4B.3	138.57	5.04	BS00084070_51–Rht1	33613374–35515028	GY-all; GN-all; SN-all; TGW-all		5
	MQTL4B.4	166.94	4.45	BS00030842_51–D_contig26957_307	132334183–409740551	SN-all; TGW-NS; TGW-all		3
	MQTL4B.5	171.91	0.98	BS00049907_51–BS00089409_51	139570212–171618747	SN-all; TGW-all		4
	MQTL4B.6	174.38	0.29	Xcsu25–Xbcd1262	201085859–351338556	SN-all; TGW-all		2
	MQTL4B.7	208.71	6.75	BS00020575_51–RFL_Contig3363_1294	519257662–531053980	GN-DS; TGW-all	DS	3
4D (13)	MQTL4D.1	73.3	3.94	Rht2–GENE-3024_59	19189381–19301407	SN-all; TGW-all		3
	MQTL4D.2	102.22	1.78	Xwmc48–BS00094770_51	335782060–361802106	GN-all; TGW-all; SN-all		3
	MQTL4D.3	121.64	0.80	BobWhite_c4264_200–RAC875_c40619_130	121181572–348798389	HI-all; SN-all; GY-HS	HS	3
	MQTL4D.4	123.8	0.04	BS00065818_51–Xcfd23	126644126–281881023	GY-all; HI-all		2
5A (18)	MQTL5A.1	83.91	5.54	Xbarc232–wsnp_BG607308A_Ta_2_2	617352363–625177133	GY-all; GN		3
	MQTL5A.2	108.34	11.48	Tdurum_contig10843_745–wsnp_Ku_c6977_12078885	592280059–594962156	GY-all; GN-all		3
	MQTL5A.3	286.84	5.40	GENE-3493_612–wsnp_Ex_c19647_28632894	461519115–470033346	GY-all; GN-DH	DS + HS	2
	MQTL5A.4	302.06	0.37	RFL_Contig5137_602–wsnp_Ex_rep_c67292_65834396	456608086–457076459	GY-all; TGW-all		2
	MQTL5A.5	304.51	3.38	Kukri_c40919_372–BS00109052_51	445287898–504759564	GY-all; GN-DH	DS + HS	3
	MQTL5A.6	376.15	5.05	Kukri_rep_c107435_940–BobWhite_c5917_529	46621851–47459518	GY-DS; GN-HS; GN-DH; GY-DH	DS, HS, DS + HS	4
5B (13)	MQTL5B.1	539.65	4.00	wPt-2041–Xwmc682	37278118–78551199	TGW-all; GN-NS; GN-HS	HS	3
	MQTL5B.2	543.55	0.99	wsnp_Ex_c5915_10378807–Xbarc1032	63363312–6464906	TGW-all; GY-DS		3
5D (3)	MQTL5D.1	221.31	17.57	tplb0041f21_972- Xgdm63	520727140–528416210	SN-NS; SN-HS	HS	2
6A (14)	MQTL6A.1	224.58	21.28	Tdurum_contig67686_1149–wsnp_Ku_c38215_46911010	49110182–65655647	GY-all; TGW-all		2

Table 1 (continued)

Chr[a]	MQTL ID	Map position	CI (cM)	Flanking markers	Physical position on RefSeq V1.0	Initial QTL traits	Tolerant to stress	No. of QTL within
	MQTL6A.2	361.68	3.44	BS00065082_51–wsnp_JD_c22766_19622512	562931571–563378468	TGW-all; GN-all; TGW-DS; TGW-HS	DS, HS	4
6B (16)	MQTL6B.1	91.54	4.48	Tdurum_contig62941_85–Excalibur_c61792_51	39339041–40283335	GN-all; TGW-all; GN-HS		3
	MQTL6B.2	122.98	25.06	Tdurum_contig9612_971–RFL_Contig2024_316	40456055–77011442	GY-all; GN-HS; SN-DH	HS, DS + HS	3
	MQTL6B.3	320.65	6.43	wsnp_BQ171182B_Ta_1_1–BS00011479_51	652640002–661857003	GN-all; HI-all; TGW-all		4
	MQTL6B.4	333.7	0.09	wPt-4924–RAC875_rep_c69963_514	652630361–668776797	HI-all; GN-DH	DS + HS	2
6D (13)	MQTL6D.1	113.18	19.52	D_F5XZDLF02HW3JD_131–wsnp_RFL_Contig3793_4087750	426983697–437167247	GN-NS; GN-DS	DS	2
	MQTL6D.2	287.66	2.91	Xcfd190–Xgwm325	101436794–172798554	TGW-all; GY-all		2
	MQTL6D.3	303.54	7.13	Ku_c13130_1319–CAP11_c4727_205	27421606–32870850	GN-all; GN-NS; GY-NS; TGW-NS; GFR-NS		5
	MQTL6D.4	334.48	2.58	Xgwm469–BS00021970_51	17257264–24003436	GY-all; GN-all		2
7A (25)	MQTL7A.1	191.91	3.37	Kukri_c16695_51–BS00022076_51	54997908–61816857	TGW-all; DSI(TGW)	DS	2
	MQTL7A.2	328.42	1.25	BobWhite_c8366_563–Ra_c8985_557	138157853–611804564	TGW-NS; GN-DS	DS	2
	MQTL7A.3	414.33	3.58	wsnp_Ku_c10202_16937059–Kukri_rep_c105157_460	581349401–611333731	GY-all; HI-all; GN-all; SCC-HS	HS	5
	MQTL7A.4	422.21	0.40	wsnp_CAP11_c2211_1157166–wsnp_Ex_c5448_9619922	612975347–615340591	GY-all; GY-NS		3
	MQTL7A.5	431.2	1.46	BS00084605_51–Xbarc29	619886163–634959758	GY-all; GY-DS; SCC-HS	HS	3
	MQTL7A.6	446.47	2.48	BS00022202_51–wsnp_Ra_c8394_14242442	645082804–646956340	GY-all; GY-DS	DS	3
	MQTL7A.7	523.75	2.17	Xgwm332–Kukri_c62757_198	686003394–692230721	GY-all; HI-all; TGW-all		3
7B (17)	MQTL7B.1	147.7	14.03	Ku_c9561_699–RFL_Contig124_558	86666894–121054087	GY-all		3
	MQTL7B.2	314.63	8.12	wPt-2356–Excalibur_rep_c88230_511	648658065–713633034	GY-all; TGW-all; TGW-DS; GN-HS	HS	4
	MQTL7B.3	324.08	9.81	wPt-3093–Kukri_c16034_113	665678848–719498022	GY-all; TGW-all; TGW-DS; GN-HS	DS, HS	4
	MQTL7B.4	338.22	7.98	Xbarc20–Excalibur_rep_c74778_252	444475000–678635377	GY-all; TGW-all; TGW-DS	DS	3
	MQTL7B.5	351.43	2.05	BS00023023_51–RAC875_c40569_716	683445783–687673177	TGW-all; TGW-DS; HI-DS	DS	3
7D (23)	MQTL7D.1	165.36	0.40	wsnp_CAP11_c2839_1425826–Tdurum_contig11727_274	211406603–380146695	GN-NS; GN-DS; GN-HS	DS, HS	3

Table 1 (continued)

Chr[a]	MQTL ID	Map position	CI (cM)	Flanking markers	Physical position on RefSeq V1.0	Initial QTL traits	Tolerant to stress	No. of QTL within
	MQTL7D.2	218.6	5.87	Xbarc70–Xbarc87	10558719–18054823	SN-NS; SN-DS; GN-HS; GY-all; GY-HS; TGW-all; TGW-DS; TGW-DH	DS, HS, DS + HS	9
	MQTL7D.3	228.38	0.07	Excalibur_c22419_460–D_GDS7LZN02IKCKF_139	59091469–63444566	GY-all; GY-NS; TGW-NS; GY-DS; TGW-DS; GY-HS:; TGW-HS; GY-DH	DS, HS, DS + HS	8

Chr chromosome, *CI* confidence interval, *SN* spike number per unit (square meter or plant), *GN* grain number per unit (square meter, spike or plant), *GY* grain yield per unit (square meter or plant), *TGW* thousand-grain weight or grain weight per grain, *SPS* spikelet per spike, *GFR* grain filling rate, *SCC* SPAD chlorophyll content, *HI* harvest index, *DSI* drought susceptibility index, *HSI* heat susceptibility index, *DS* drought stress, *HS* heat stress, *DH* drought plus heat stress, *NS* non-stress, *all* all environments with no specific stress description

[a]Number in the brackets indicates the initial number of QTL on the chromosome

with distinctive variations only in the high-yielding group were considered positive alleles for yield, while those only in the low-yielding group were considered negative alleles for yield. Table 3 lists the positive alleles, and some of the negative alleles if they fell inside the target genes. Generally, only the closest marker is shown for each candidate gene; however, markers showing additional variations, or significant variations between the two groups—which could be useful for MAS—were included in the list, even if they were not the closest marker to the gene. Examples of such markers are: (1) an indel marker on chromosome 2A showing variations in five of the 14 cultivars, 0.74 Mbp away from genes *TraesCS2A01G136700* and *TraesCS2A01G136800*; and (2) an indel marker on chromosome 2B with distinctive positive and negative alleles for yield, 2.67 Mbp away from *TraesCS2B01G110000* and *TraesCS2B01G110100*. Notably, an SNP marker on chromosome 2B, 0.01 Mbp away from the target gene *TraesCS2B01G087400*, showed a distinctive negative allele for yield in the low-yielding group, and a positive allele mostly in the high-yielding group (5 of 7 cultivars).

Putative candidate genes with distinctive positive alleles in the high-yielding group in at least two cultivars were deemed validated for their important role for wheat yield. Eighteen genes or gene clusters were validated, of which two were located in MQTL2A.2 (*TraesCS2A01G136700* and *TraesCS2A01G138100*), two in MQTL2B.1 (*TraesCS2B01G087400* and *TraesCS2B01G089700*), four in MQTL2B.2 (*TraesCS2B01G105100*, *TraesCS2B01G105300*, *TraesCS2B01G110000*, and *TraesCS2B01G112600*), three in MQTL7A.1 (*TraesCS7A01G090700*, *TraesCS7A01G095100*, and *TraesCS7A01G096200*), and one each in MQTL1D.1, MQTL2A.1, MQTL3A.2, MQTL3D.1, MQTL4A.7, MQTL6A.1, and MQTL7D.3 (Table 3).

Discussion

Key MQTL and associated genes can be target regions for improving yield in wheat

Although wheat yield has increased over time as a direct result of new varieties produced by breeders, there is substantial room to improve, compared to other major cereal crops, such as rice and barley. Genes or genomic regions responsible for high yield potential, adaptability, and stability are desirable. Meta-analysis can map QTL from different mapping populations in different experiments on the same linkage group and lower the QTL CIs for more effective identification of candidate genes (Goffinet and Gerber 2000). In this study, 381 QTL were integrated into 86 MQTL responsible for yield-related traits under irrigated, drought- and/or heat-stressed conditions in wheat. All of the MQTL

Table 2 Putative candidate genes of MQTL

Chr	MQTL ID	Interval size (bp)	No. of genes[a]	Putative candidate gene ID	Gene function annotation	Gene cluster
1A	MQTL1A.1	1,342,340	24	TraesCS1A01G284000	MYB-like protein	
				TraesCS1A01G285000	70 kDa heat shock protein	2 consecutive
1B	MQTL1B.1	435,180	9	TraesCS1B01G318800	MYB transcription factor	
	MQTL1B.2	3,827,607	35	TraesCS1B01G334800	Phosphoenolpyruvate carboxylase	
	MQTL1B.3	10,182,619	79	TraesCS1B01G344300	E3 ubiquitin-protein ligase	
				TraesCS1B01G346300	TCP family transcription factor containing protein	
				TraesCS1B01G350000	14 kDa proline-rich protein DC2.15, putative	
				TraesCS1B01G350600 and 351600	Trehalose-6-phosphate synthase	
				TraesCS1B01G350900	Ethylene-responsive transcription factor	
	MQTL1B.4	7,305,071	59	TraesCS1B01G383600–384000	MYB transcription factors	5 consecutive
				TraesCS1B01G384100	Chaperone protein dnaJ	
				TraesCS1B01G385600 and 385800	NAD(P)H-quinone oxidoreductase subunit	
	MQTL1B.6	514,246	5	TraesCS1B01G392600	MYB transcription factor-like	
	MQTL1B.7	2,059,699	30	TraesCS1B01G399800	Defensin	
				TraesCS1B01G401700	MYB transcription factor	
	MQTL1B.8	3,183,658	42	TraesCS1B01G414500	Stress up-regulated Nod 19 protein	
				TraesCS1B01G416200	Disease resistance protein (NBS-LRR class) family	
1D	MQTL1D.1	321,361	7	TraesCS1D01G047800	Major heat shock 70 kDa protein Ab	
	MQTL1D.2	4,452,378	52	TraesCS1D01G448300	Early-responsive to dehydration stress protein (ERD4)	
				TraesCS1D01G450900	E3 ubiquitin-protein ligase RNF14	
2A	MQTL2A.1	911,509	27	TraesCS2A01G073900	Photosystem II CP43 reaction center protein	
	MQTL2A.2	5,199,043	72	TraesCS2A01G136700 and 136800	Chaperone protein dnaJ-related	2 consecutive
				TraesCS2A01G138100	E3 Ubiquitin ligase family protein	
	MQTL2A.3	7,199,819	141	TraesCS2A01G564000	E3 ubiquitin-protein ligase	
				TraesCS2A01G565900–566400	NAC domain-containing protein, putative	6 consecutive
				TraesCS2A01G576600	Chaperone protein DnaJ	
2B	MQTL2B.1	8,245,723	114	TraesCS2B01G082400	MYB-related transcription factor	
				TraesCS2B01G087400	Peroxidase family protein	
				TraesCS2B01G089700	E3 ubiquitin-protein ligase SINA-like 10	
	MQTL2B.2	11,118,626	81	Ppd-B1	Photoperiod response	
				TraesCS2B01G105100	Heat shock transcription factor	
				TraesCS2B01G105300	Abscisic acid receptor	
				TraesCS2B01G110000 and 110100	Defensin	2 consecutive

Table 2 (continued)

Chr	MQTL ID	Interval size (bp)	No. of genes[a]	Putative candidate gene ID	Gene function annotation	Gene cluster
				TraesCS2B01G112100	DELLA protein	
				TraesCS2B01G112600	MYB transcription factor	
2D	MQTL2D.1	3,411,366	72	Ppd-D1	Photoperiod response	
				TraesCS2D01G081100	Carbon storage regulator homolog	
				TraesCS2D01G077700	DNAJ heat shock N-terminal domain-containing protein-like	
				TraesCS2D01G077900 and 078000	DnaJ domain containing protein	
				TraesCS2D01G080000	Ascorbate peroxidase	
				TraesCS2D01G082800	Chaperone protein dnaJ	
				TraesCS2D01G083700	NAC domain protein	
	MQTL2D.4	4,547,706	66	TraesCS2D01G131800	Auxin-induced in root cultures protein 12	
				TraesCS2D01G131900	NAD(P)-binding Rossmann-fold superfamily protein	
3A	MQTL3A.1	806,916	16	TraesCS3A01G048300	E3 ubiquitin-protein ligase	
				TraesCS3A01G048600	Disease resistance protein (TIR-NBS class)	
	MQTL3A.2	9,576,587	87	TraesCS3A01G101400	E3 ubiquitin-protein ligase	
				TraesCS3A01G102800	Sugar transporter, putative	
				TraesCS3A01G105500	MYB-like transcription factor family protein	
				TraesCS3A01G107100	Bidirectional sugar transporter SWEET	
3B	MQTL3B.1	3,140,690	87	TraesCS3B01G018000–018200, and 019600	E3 ubiquitin-protein ligase	3 consecutive
				TraesCS3B01G019700 and 020600	Myb/SANT-like DNA-binding domain protein	
				TraesCS3B01G019000	Disease resistance protein (NBS-LRR class) family	
	MQTL3B.2	2,256,521	41	TraesCS3B01G042900	Heat stress transcription factor A-9	
	MQTL3B.3	6,870,323	105	TraesCS3B01G049800 and 049900	Heat shock protein	2 consecutive
				TraesCS3B01G050100, 050200, 050700, 050900, 052300, 052400, 054000, 052700, 052800, 053000, 01G053300–01G053500, 054000, 01G054200–01G054400, and 054800–055300	E3 ubiquitin-protein ligase	22 (up to 6 consecutive)
	MQTL3B.6	3,936,887	73	TraesCS3B01G541300	Proline synthase co-transcribed bacterial	
				TraesCS3B01G541500	ERD (early-responsive to dehydration stress) family protein	
				TraesCS3B01G541800	Heat-inducible transcription repressor (DUF639)	
3D	MQTL3D.1	35,310,424[b]	291	TraesCS3D01G114700–115400	Heat shock protein	8 consecutive
4A	MQTL4A.1			TraesCS4A01G452600	MYB-related transcription factor	

Table 2 (continued)

Chr	MQTL ID	Interval size (bp)	No. of genes[a]	Putative candidate gene ID	Gene function annotation	Gene cluster
				TraesCS4A01G456000	DnaJ domain-containing protein	
	MQTL4A.2	5,160,336	56	TraesCS4A01G384900	Sugar transporter, putative	
				TraesCS4A01G387200	E3 ubiquitin-protein ligase SINA-like 10	
	MQTL4A.3	10,822,662	143	TraesCS4A01G403600	MADS-box transcription factor family protein	
				TraesCS4A01G411900	MYB transcription factor	
				TraesCS4A01G412200	Ethylene-responsive transcription factor	
	MQTL4A.5	177,476	8	TraesCS4A01G309600	NBS-LRR-like resistance protein	
				TraesCS4A01G310200	Disease resistance protein (NBS-LRR class) family	
	MQTL4A.6	1,214,475	31	TraesCS4A01G308300	NBS-LRR disease resistance protein-like protein	
	MQTL4A.7	2,685,705	18	TraesCS4A01G072100	Senescence/dehydration-associated protein-like protein	
				TraesCS4A01G072400	Stress inducible protein coi6.1	
4B	MQTL4B.1	897,498	13	TraesCS4B01G031700	Core-2/I-branching beta-1,6-*N*-acetylglucosaminyltransferase family protein	
	MQTL4B.2	1,557,905	46	TraesCS4B01G038300	E3 ubiquitin-protein ligase SINA-like 10	
				TraesCS4B01G039200	Transcription elongation factor (TFIIS) family protein	
				TraesCS4B01G039300	Ethylene receptor	
				TraesCS4B01G040800	Nucleotide-sugar transporter family protein	
	MQTL4B.3	1,901,654	15	Rht1		
	MQTL4B.7	11,796,318	87	TraesCS4B01G261300	E3 ubiquitin-protein ligase	
				TraesCS4B01G261900	DnaJ domain-containing protein	
4D	MQTL4D.1	112,026	3	Rht2		
5A	MQTL5A.1	7,824,770	112	Vrn-A1		
				TraesCS5A01G435500	E3 ubiquitin-protein ligase	
				TraesCS5A01G437900	Heat shock transcription factor	
				TraesCS5A01G440100	Mannitol transporter, putative, expressed	
				TraesCS5A01G440200	MYB domain protein 65	
				TraesCS5A01G443000	E3 ubiquitin-protein ligase DRIP2	
				TraesCS5A01G443600	WRKY transcription factor, putative	
				TraesCS5A01G445300	Protein REVERSION-TO-ETHYLENE SENSITIVITY1	
	MQTL5A.2	2,682,097	40	Vrn-A1		
	MQTL5A.3	8,514,231	69	TraesCS5A01G249200	Peroxidase	

Table 2 (continued)

Chr	MQTL ID	Interval size (bp)	No. of genes[a]	Putative candidate gene ID	Gene function annotation	Gene cluster
				TraesCS5A01G250900	Disease resistance protein (TIR-NBS-LRR class) family	
	MQTL5A.4	468,373	8	TraesCS5A01G240700	Chaperone DnaJ	
	MQTL5A.6	837,667	9	TraesCS5A01G052300	Salt stress response/anti-fungal	
5D	MQTL5D.1	7,689,070	143	TraesCS5D01G485700	E3 ubiquitin-protein ligase SINA-like 10	
				TraesCS5D01G486600	Ethylene-responsive transcription factor	
				TraesCS5D01G492900	70 kDa heat shock protein	
				TraesCS5D01G495200	Phosphoenolpyruvate carboxylase 2	
				TraesCS5D01G497200	Chaperone DnaJ	
				TraesCS5D01G498200	Sugar transporter family protein, putative, expressed	
6A	MQTL6A.1	16,545,465	184	TraesCS6A01G080500	WRKY transcription factor, putative	
				TraesCS6A01G084400	E3 ubiquitin-protein ligase BOI	
				TraesCS6A01G086800	E3 ubiquitin-protein ligase	
				TraesCS6A01G087000	Chaperone protein dnaJ	
				TraesCS6A01G087600	Heat-shock protein	
				TraesCS6A01G096200	E3 ubiquitin-protein ligase MARCH8	
				TraesCS6A01G097500	Ethylene-responsive transcription factor	
				TraesCS6A01G097700	Ethylene-responsive transcription factor	
	MQTL6A.2	446,897	10	TraesCS6A01G330500	Ethylene-responsive transcription factor	
6B	MQTL6B.1	944,294	11	TraesCS6B01G060200	NAD(P)-binding Rossmann-fold superfamily protein	
	MQTL6B.3 and MQTL6B.4	16,146,436	165	TraesCS6B01G377400	MYB-related transcription factor	
				TraesCS6B01G384500	Trehalose-6-phosphate synthase	
				TraesCS6B01G380300	Sugar transporter family protein, expressed	
				TraesCS6B01G384700	Sugar transporter, putative	
				TraesCS6B01G384800	heat-inducible transcription repressor (DUF639)	
				TraesCS6B01G391600–391800	AGAMOUS-like MADS-box protein	3 consecutive
				TraesCS6B01G392600	MADS-box transcription factor family protein	
				TraesCS6B01G393200	Ethylene-responsive transcription factor	
6D	MQTL6D.1	10,183,550	178	TraesCS6D01G319100	MADS-box transcription factor	
				TraesCS6D01G320700	Ethylene-responsive transcription factor	

Table 2 (continued)

Chr	MQTL ID	Interval size (bp)	No. of genes[a]	Putative candidate gene ID	Gene function annotation	Gene cluster
				TraesCS6D01G322200	Chaperone protein dnaJ	2 consecutive
				TraesCS6D01G322300	Heat-shock protein, putative	
				TraesCS6D01G322700 and 322800	70 kDa heat shock protein	2 consecutive
				TraesCS6D01G324200	Ethylene-responsive transcription factor	
				TraesCS6D01G324500	E3 ubiquitin-protein ligase	
				TraesCS6D01G326600	Protein ETHYLENE INSENSITIVE 3	
				TraesCS6D01G327300	MYB-related transcription factor	
				TraesCS6D01G329700	Sugar transporter family protein, expressed	
				TraesCS6D01G330100	Early-responsive to dehydration stress protein (ERD4)	
				TraesCS6D01G334000	Trehalose-6-phosphate synthase	
	MQTL6D.2	71,361,760[b]	430	Grain Weight 2 gene: GW2-D		
	MQTL6D.3	5,449,244	94	TraesCS6D01G059300	NAC domain-containing protein, putative	
	MQTL6D.4	6,746,172	75	TraesCS6D01G043600	MYB transcription factor	
				TraesCS6D01G049100	Heat shock 70 kDa protein	
7A	MQTL7A.1	6,818,949	105	TraesCS7A01G090700	Sucrose transporter	
				TraesCS7A01G095100	AP2-like ethylene-responsive transcription factor	
				TraesCS7A01G096200–096500	WRKY family transcription factor	4 consecutive
	MQTL7A.4	2,365,244	13	TraesCS7A01G422600	NBS-LRR-like resistance protein	
	MQTL7A.5	15,073,595	137	TraesCS7A01G430500	Sugar transporter family protein	
				TraesCS7A01G43060	Heat shock 70 kDa protein	
				TraesCS7A01G431700, 436800, 437400 and 437500	Transcription elongation factor (TFIIS) family protein	2 consecutive
				TraesCS7A01G436400	Ethylene-responsive transcription factor, putative	
	MQTL7A.6	1,873,536	7	TraesCS7A01G452900 and 453000	Peroxidase	2 consecutive
	MQTL7A.7	6,227,327	77	TraesCS7A01G495800	AP2-like ethylene-responsive transcription factor	
				TraesCS7A01G498300	WRKY DNA-binding protein 39	
				TraesCS7A01G503100–503300	Bidirectional sugar transporter SWEET	3 consecutive
7B	MQTL7B.5	4,227,394	31	TraesCS7B01G416600, 417100 and 417300	Disease resistance protein (NBS-LRR class) family	
				TraesCS7B01G416100	Transcription elongation factor (TFIIS) family protein, putative	
				TraesCS7B01G418100	Stress responsive protein	
				TraesCS7B01G418400–418600	WRKY transcription factor	3 consecutive

Table 2 (continued)

Chr	MQTL ID	Interval size (bp)	No. of genes[a]	Putative candidate gene ID	Gene function annotation	Gene cluster
7D	MQTL7D.2	7,496,104	128	TraesCS7D01G026800–027000	MYB transcription factor	3 consecutive
				TraesCS7D01G034000	NAC domain	
				TraesCS7D01G035000	NBS-LRR disease resistance protein	
	MQTL7D.3	4,353,097	55	TraesCS7D01G099800 and 099900	NBS-LRR-like resistance protein	2 consecutive
				TraesCS7D01G100400	NAC domain-containing protein	
				TraesCS7D01G102700 and 103100	Fatty acid hydroxylase superfamily protein	
				TraesCS7D01G103800	Transcription elongation factor 1	

[a]Indicates that the genes within or around the MQTL were screened

[b]Indicates those MQTL with > 20 Mbp interval but having noteworthy characters

had narrower CIs (95%) than the mean values for the original QTL. Six MQTL spanned a physical interval of < 0.5 Mbp each—MQTL1B.1, MQTL1D.1, MQTL4A.5, MQTL4D.1, MQTL5A.4, and MQTL6A.2. Two hundred and ten candidate genes were identified for the MQTL—those with small genetic and physical intervals or with candidate genes or gene clusters having robust effects on yield and stress tolerance (Table 2) are important regions for MAS, pyramiding, fine mapping, positional cloning, and functional analysis.

Wheat yield is controlled by many genes with small effects and significantly affected by environmental factors. Contributions of genomic regions to yield will vary according to the target environment; therefore, breeding strategies will differ for individual environments. Identification of major or consistent genes within a targeted environment is crucial for successful gene-stacking practices. In this study, phenotypic data of 14 cultivars were collected from 5-year Australian NVT in key wheat production areas. Genotype–phenotype association analysis between the different cultivar groups (high- or low-yielding) enabled us to detect the genomic regions responsible for high yield in Australian environments. Eighteen genes or gene clusters were validated and can be used as main targets for wheat breeding in these areas.

Drought and heat stress are major limiting factors to wheat yield, especially in rainfed farming areas. Breeding stress-tolerant varieties remain the best approach for increasing crop production (Zhang et al. 2017). This study identified major chromosome regions responsible for yield and yield components under drought and/or heat stress. The MQTL contained validated genes and showed combined drought and heat stress tolerance for MQT1D.1, MQTL2B.2, MQTL3D.1, and MQTL7D.3. These regions and their validated genes can act as favorable locus/gene combinations for pyramiding to create highly adaptable high-yielding cultivars.

The MQTL identified in this study were compared with the QTL detected in a recent QTL mapping study on wheat yield under drought and heat stress (Tura et al. 2020). The study was based on a linkage map containing 3502 markers and phenotypic data collected from 32 field experiments at 10 locations over six seasons. Two of the QTL were co-localized with MQTL with matching traits—QTgw.aww-7B.2 overlapped MQTL7B.3, and QYld.aww-7DS.2 overlapped MQTL7D.3. Tura et al. (2020) fine mapped the 1B QTL QYld.aww-1B.2 to a 2.2 Mbp physical interval of 659,988,745–662,154,351 bp, which was close (18,789,404 bp away) to MQTL1B.8 at an interval of 638,015,656–641,199,314 bp. Two other QTL were closely located to the MQTL—QTgw.aww-6B to MQTL6B.1 (5.95 Mbp away), and QYld.aww-7A.3 to MQTL7A.7 (1.09 Mbp away). These five MQTL are important for future breeding of wheat yield.

The MQTL associated with commonly known genes, such as *Ppd*, *Vrn,* and *Rht*, were further explored in this study to detect other genes that might be co-located in the genomic regions. No candidate mutation was found for *Ppd-B1* alleles and *Vrn-A1* alleles in Chinese Spring wheat (Díaz et al. 2012), so the search of putative candidate genes excluded these gene regions on RefSeq V1.0. Studies have suggested that other yield-related genes could co-exist in these regions; for example, Kadam et al. (2012) identified a

Table 3 Variations in gene-linking GBS markers among the 14 wheat cultivars contrasting in yield performance

No.	Gene ID[1] TraesCS	Function	Marker-gene distance (bp)	Marker physical position	Call "0"	Call "1" to "5"	Cob (H)	Ten (H)	Bec (H)	Sce (H)	Sco (H)	Sunt (H)	Tro (H)	Sunv (L)	Lan (L)	Cru (L)	Dar (L)	Hat (L)	Imp (L)	Tun (L)	T-test p value[2]
1	**1D01G047800**	HSP	80,387	27941959	GTTT	GTTTT,G	0/0	0/0	0/0	1/1	1/1	0/0	0/0	0/0	-	-	0/0	0/0	0/0	0/1	0.1466
2	**2A01G073900**	PSII	1,040	32525738	GA	G	-	-	0/0	1/1	-	0/0	1/1	-	-	-	-	-	1/1	-	0.1721
3	**2A01G136700, 136800**	HSP	Marker 1: 743,758	83098529	ACCC	ACCCCC,ACCCCC,ACC,AC,A	0/3	0/0	0/3	0/0	3/3	1/1	2/2	0/0	-	0/0	4/4	0/0	0/5	5/5	0.0145*
4			Marker 2: 18,427	82373198	C	G	0/0	0/0	1/1	0/0	1/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0.1222
5	**2A01G138100**	E3 ligase	2,784	83816418	C	T	1/1	1/1	0/0	1/1	0/0	1/1	1/1	1/1	-	1/1	1/1	1/1	1/1	1/1	0.1222
6	2B01G082400	MYB	96,654	45833568	T	C	0/0	1/1	0/0	0/0	0/0	0/0	0/0	0/0	-	0/0	0/1	0/0	0/0	0/0	0.0330*
7	**2B01G087400**	Peroxidase	Marker 1: 26,553	49411020	C	G,T	-	1/1	2/2	2/2	2/2	2/2	2/2	1/1	-	1/1	0/0	0/0	2/2	-	0.0541
8			Marker 2: 17,707	49402174	G	A	0/0	-	0/0	0/0	1/1	1/1	0/0	-	-	-	0/0	0/0	0/0	0/0	0.3504
9	**2B01G089700**	E3 ligase	Inside the gene	50593509	A	C	0/0	0/0	1/1	0/0	0/0	1/1	0/0	0/0	-	0/0	0/0	0/0	0/0	0/0	0.0596
10	Ppd-B1	Ppd	8,592	63375142	G	A	0/0	0/0	1/1	-	-	0/0	0/0	0/0	-	0/0	-	-	-	-	0.0596
11	**2B01G105100**	HS-TF	55,737	65431219	C	CA	0/0	0/0	0/0	0/0	0/0	1/1	1/1	0/0	-	0/0	0/0	0/0	0/0	0/0	0.2483
12	**2B01G105300**	ABA receptor	5,120	65888807	A	C	0/0	0/0	0/0	0/0	0/0	1/1	1/1	0/0	-	0/0	0/0	0/0	0/0	0/0	0.2483
13	**2B01G110000, 110100**	Defensin	Marker 1: 2,673,314	68694266	CGG	CGGGG,CGGG,CG,C	1/1	-	4/4	0/2	4/4	4/4	3/4	-	-	-	2/2	0/2	0/2	0/2	0.0144*
14			Marker 2: 72,496	71295084	TA	T	1/1	-	0/0	0/0	0/0	0/0	0/0	-	-	-	0/0	0/0	0/0	0/0	0.0695
15	**2B01G112100**	DELLA	Marker 1: 1,708,385	73126505	GC	G	0/0	0/0	1/1	0/0	1/1	1/1	-	0/0	-	0/0	0/0	0/0	0/0	0/0	0.1832
16			Marker 2: 25,826	74809064	C	A	0/0	0/0	1/1	0/0	1/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0.1222
17	**2B01G112600**	MYB	18,080	75829312	G	GA	0/0	0/0	1/1	-	1/1	-	-	0/0	0/0	0/0	-	0/0	-	0/0	0.1222
18	2D01G077900, 078000	HSP	Marker 1: 23,143	33390738	CT	CTT, C	0/0	0/0	0/2	0/0	0/0	2/2	0/0	0/0	-	0/0	0/0	0/2	0/0	0/0	0.4487
19			Marker 2: Inside the gene	33354015	T	A	0/0	0/0	0/0	1/1	0/1	-	0/0	0/1	-	0/0	0/0	0/0	0/0	0/0	0.0878
20	2D01G080000	Peroxidase	169,153	34400629	G	A	0/0	0/0	0/0	0/0	0/0	0/0	1/1	0/0	-	0/0	0/0	0/0	0/0	0/0	0.1379
21	2D01G082800	HSP	73,674	35705007	A	G	0/0	0/0	0/0	0/0	0/0	0/0	1/1	0/0	-	0/0	0/0	0/0	0/0	0/0	0.1379
22	2D01G131800	AIR12	1,734	76804423	GT	G	0/0	1/1	0/0	0/0	0/0	0/0	0/0	0/0	-	0/0	0/0	0/1	0/0	0/0	0.0330*
23	2D01G131900	NADP	5,607	76853507	C	T	0/0	1/1	0/0	0/0	0/0	0/0	0/0	0/0	-	0/0	0/0	0/0	0/0	0/0	0.0330*
24	3A01G048600	TIR-NBS	4,548	25916138	T	C	-	1/1	1/1	1/1	1/1	0/0	1/1	1/1	-	1/1	1/1	-	1/1	1/1	0.0695
25	3A01G101400	E3 ligase	29,204	65923611	A	G	1/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	-	0/0	0/0	0/0	0/0	0/0	0.1379
26	**3A01G102800**	Sugar transport	52,683	66407986	AT	A	0/0	0/0	0/0	0/0	1/1	0/0	1/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0.1853
27	3A01G105500	MYB	5,128	69503935	CTG	C	0/0	1/1	1/1	1/1	1/1	1/1	1/1	1/1	-	1/1	1/1	1/1	1/1	1/1	0.0695
28	3B01G019700, 020600	MYB	Marker 1: 45,497	8551945	T	C	1/1	0/0	-	1/1	1/1	1/1	1/1	-	-	1/1	-	1/1	1/1	1/1	0.0330*
29			Marker 2: Inside the gene	8786333	G	T	1/1	1/1	1/1	1/1	1/1	1/1	1/1	0/1	-	1/1	1/1	0/0	1/1	1/1	0.1570
30	3B01G019000	NBS-LRR	105,356	7934599	G	GA	1/1	0/0	-	1/1	1/1	1/1	1/1	-	-	1/1	-	1/1	1/1	1/1	0.0330*
31	3B01G050100 ... 055300	E3 ligase	In between the genes	27939068	AG	A	1/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	-	0/0	0/0	-	0/0	0/0	0.0695
32	**3D01G114700 - 115400**	HSP	Marker 1: between genes	68697367	TCCC	TCC, TC,T	1/1	1/2	2/2	2/2	2/2	2/2	1/1	2/2	2/2	2/2	2/2	2/2	2/2	2/2	0.0364*

Table 3 (continued)

No.	Gene ID[1]	TraesCS	Function	Marker-gene distance (bp)	Marker physical position	Call "0"	Call "1" to "5"	Cob (H)	Ten (H)	Bec (H)	Sce (H)	Sco (H)	Sunt (H)	Tro (H)	Sunv (L)	Lan (L)	Cru (L)	Dar (L)	Hat (L)	Imp (L)	Tun (L)	T-test p value[2]
33				Marker 2: between genes	69404427	CGGGG	C,CGGG,CGG,CG	3/3	3/3	1/1	1/1	1/1	3/3	2/2	3/4	0/2	2/3	0/0	0/0	3/4	4/4	0.0186*
34	**4A01G072100**		Dehydration related	113,816	69948297	AATG	A	1/1	0/0	0/0	1/1	-	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0.0866
35				123,158	69707955	C	T	1/1	0/0	0/0	1/1	1/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0.0878
36	4B01G031700		Branching	85,360	23749825	C	T	0/0	0/0	0/0	1/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0.0695
37	4B01G039300		Ethylene receptor	12,850	28056525	T	TA	1/1	1/1	1/1	0/0	1/1	1/1	1/1	1/1	1/1	1/1	0/1	1/1	1/1	1/1	0.0487*
38	4B01G040800		Sugar transport	193,148	28596762	G	A	1/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0.0695
39	Rht1		Rht1	Marker 1: 371,915	33992347	G	GCC,GCCC,GC	2/2	1/2	2/2	1/2	0/0	0/0	3/3	1/2	0/0	1/2	1/2	0/0	1/2	0/0	0.0487*
40				Marker 2: 1,609,175	35229607	CGG	CGGGG,CAGG,CGGG,CG,C	1/1	0/0	0/0	1/3	0/5	5/5	2/2	1/3	5/5	1/3	3/3	5/5	0/4	5/5	0.0228*
41	Rht2		Rht2	Inside the gene?	19298590	T	G	0/0	0/0	0/0	1/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0.0878
42	**6A01G084400**		E3 ligase	Marker 1: 277,151	52795305	GCC	GCCCC,GCCC,GC,G	0/2	1/1	1/1	3/3	0/0	0/0	0/3	1/2	3/4	1/2	0/3	0/2	0/3	0/3	0.0499*
43				Marker 2: 34,376	53038080	C	T	1/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	-	0.0695
44	6A01G097500		Ethylenersponsive TF	1,245	64677474	C	T	1/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0.0695
45				72,508	64606211	G	A	0/0	0/0	0/0	1/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0.0878
46	6A01G097700		Ethylenersponsive TF	102,979	64804489	TG	TGGG,TGGGG,TGG,T	0/3	0/3	0/3	1/3	1/3	2/2	1/1	0/3	3/3	0/3	1/3	0/3	1/2	2/2	0.1379
47	GW2-D		GW2	336,962	196922173	C	CA	-	0/1	0/0	1/1	0/0	0/0	0/0	0/0	0/1	0/0	0/0	0/1	0/0	0/0	0.0878
48	6D01G059300		NAC	163,748	27984266	T	A	1/1	0/1	0/1	0/1	0/0	0/1	0/0	0/1	0/1	0/1	0/1	0/1	0/1	0/1	0.0695
49	6D01G043600		MYB	22,043	18040578	G	A	0/0	0/0	1/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0.0596
50	6D01G049100		HSP	73,679	23910138	C	T	1/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0.0695
51	**7A01G090700**		Sugar transporter	21,489	55367660	T	G	1/1	-	0/0	0/0	1/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0.1330
52	**7A01G095100**		Ethylenersponsive TF	Marker 1: 35,180	58016619	CACA	C	1/1	0/0	0/0	0/0	1/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0.1330
53				Marker 2: 3,823	57985262	C	T	-	0/0	0/0	1/1	-	-	-	0/0	0/0	0/0	0/0	-	-	-	0.0878
54	**7A01G096200 - 096500**		WRKY	79,262	59122592	A	AG	0/0	1/1	1/1	1/1	0/0	1/1	1/1	1/1	1/1	1/1	1/1	1/1	1/1	1/1	0.1330
55	7D01G034000		NAC	67,476	17329110	C	G	1/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0.0695
56	7D01G035000		NBS-LRR	55,586	18059657	G	C	0/0	0/0	0/0	0/0	0/0	0/0	1/1	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0.1379
57	**7D01G100400**		NAC	55,586	60159590	G	T	-	0/0	0/0	1/1	0/0	1/1	1/1	0/0	0/0	0/0	0/0	0/0	0/0	-	0.1483

Calls highlighted in yellow are positive alleles and calls highlighted in blue are negative alleles

Cob Cobalt, *Ten* Tenfour, *Bec* Beckom, *Sce* Scepter, *Sco* Scout, *Sunt* Suntop, *Tro* Trojan, *Sunv* Sunvale, *Lan* Lang, *Cru* Crusader, *Dar* Dart, *Hat* Hatchet CL Plus, *Imp* Impress CL Plus, *Tun* Tungsten, *H* high-yielding group, *L* low-yielding group

[1]Genes in bold indicate those with positive alleles in at least two cultivars of the high-yielding group

[2]*p*-value from *t* test of mean yield data between the groups with positive-alleles and negative/other-alleles. Yield data from the agricultural area "NSW-S and VIC-N" (Table S2) are used for the analysis. *Indicates significantly different at $p < 0.05$

4BS QTL for grain yield under drought stress that explained up to 22% of the phenotypic variation, and its contributor was a tall cultivar C306. Although the QTL, flanked by markers Xbarc20 and Xgwm368, is only 27 Mbp away from chromosome 4B's *Rht1* gene (responsible for reduced height), it is a large-effect locus independent of *Rht1*. Fine mapping of QTL/genes with low Q×E effects, independent of phenology, should be focused on to identify the causal gene(s) controlling yield. Therefore, more genes in the major MQTL regions need to be identified, excluding known yield-related genes such as plant height (*Rht*) or phenology (*Ppd* or *Vrn*).

Orchestrated networks of gene families and gene clusters play important roles in determining yield performance in wheat

The genes associated with the MQTL could be classified into yield-related and stress-related genes. The most yield-related genes functioned as E3 ubiquitin ligases, which also underlie the known *Grain Weight 2* (*GW2*) gene on chromosome 6D (Su et al. 2011). Nadolska-Orczyk et al. (2017) reviewed that the major genes determining yield-related traits in wheat often had functions in four categories, including TFs, carbohydrate metabolism, or signaling of growth regulators, cell division and proliferation, and floral regulators. They summarized some yield-determining genes in wheat with known orthologues in rice, maize, and barley, including cytokinin dehydrogenase (*CKX*), transcript elongation factor (*TEF*), *GW2*, thousand-grain weight 6 (*TGW6*), grain size (*GS5* and *GS-D1*), sucrose synthase (*Sus1* and *Sus2*), Nuclear Factor Y (*NFYAs*, *NFYBs,* and *NFYCs*), NAC TFs, and cell wall invertase (*CWI*). The TCP family genes also affect the development of spike and grain development (Zhao et al. 2018) and showed high frequencies in the MQTL regions identified in this study, which were considered putative candidate genes related to yield. The C4 enzymes genes, such as phosphoenolpyruvate carboxylase (*PEPC*), located in MQTL1B.2 and MQTL5D.1 in this study, are important for increasing yield in C3 plants like wheat. Over-expression of C4 enzyme genes *PEPC* and *PPDK* (pyruvate orthophosphate dikinase) increased yield and photosynthesis rate in wheat (Häusler et al. 2002; Khan et al. 2019; Zhang et al. 2014).

Many of the candidate genes identified in the MQTL belong to large gene families responsive to stress, including MYB TFs, NAC TFs, WRKY TFs, ethylene-responsive TFs, HSPs, NADPH family gens, and MADS-box genes. These genes have been found responsible for tolerances to various stresses in wheat (Dey and Corina Vlot 2015; Erdayani et al. 2020; Guérin et al. 2019; Hu et al. 2018; Mia et al. 2019, 2020; Schilling et al. 2020; Xue et al. 2011; Yousfi et al. 2017; Zhao et al. 2017, 2018). Kulkarni et al. (2017) reviewed the key genes responsive to drought stress for controlling root system and transpiration in wheat. Later, Khan et al. (2019) summarized the genes responsible for drought tolerance that were used for transgenic improvement in wheat, in which *WRKY*, *NAC*, and *Dehydration Responsive Element Binding* (*DREB*) genes were among the major responsible or targeted genes. Heat shock TFs (*Hsfs*), which modulate the expression of HSPs, are crucial for stress tolerance (Xue et al. 2014; Zhou et al. 2019). Other stress-responsive factors include proline (Mwadzingeni et al. 2016), mannitol (Abebe et al. 2003), trehalose (Ibrahim and Abdellatif 2016), defensin (Stotz et al. 2009), and late embryogenesis abundant (LEA) proteins that act as a molecular chaperone protein by stabilizing the protein or membrane structure (Chen et al. 2019). Chini et al. (2004) reported that some disease resistance proteins, such as NBS-LRR, play crucial roles in drought tolerance. These genes repeatedly appeared in the MQTL regions. The peroxide detoxifying system—antioxidant defense to detoxify ROS—is important for plant stress tolerance, in which ascorbate peroxidase (APX) is a key enzyme for scavenging hydrogen peroxide (H_2O_2) in chloroplasts (Caverzan et al. 2012; Janda et al. 2019). These genes were found in MQTL2B.1, MQTL2D.1, MQTL5A.3, and MQTL7A.6. Other genes occasionally found in the MQTL regions, such as fatty acid hydroxylase superfamily protein, have been related to stress (Kandel et al. 2005; Wang et al. 2016).

A noteworthy phenomenon is that many genes appeared as gene clusters in the MQTL regions. Gene clusters of functionally related genes are common in eukaryotic genomes (Yi et al. 2007). Dixit et al. (2015) hypothesized that gene clusters and multiple intra-QTL genes underpinned large-effect MQTL. Many enzymatic pathways in plants are encoded in gene clusters (Medema et al. 2015), which often locate closely (a few thousand base pairs away to each other) in a small genome region, encode for similar proteins, and collectively share a generalized function. In such cases, we suggest that the transgenic method using a single gene might not be as effective as MAS, where markers can target a much larger region where all the genes in gene clusters underlying the QTL play important roles. The genotype–phenotype association analysis of the 14 contrasting cultivars found that the most suitable markers for MAS may not necessarily be those closest to or only targeting a single gene. The indel marker on chromosome 2A linked to two

genes, *TraesCS2A01G136700* and *TraesCS2A01G136800*, and an indel on chromosome 2B linked to two genes *TraesCS2B01G110000* and *TraesCS2B01G110100*, are such examples, as they showed more variation among the cultivars than those closer to the genes.

Conclusions

The MQTL validated in this study as major genomic regions controlling yield-related traits are MQTL1D.1, MQTL2A.1, MQTL2A.2, MQTL2B.1 MQTL2B.2, MQTL3A.2, MQTL3D.1, MQTL4A.7, MQTL6A.1, MQTL7A.1, and MQTL7D.3 (Table 4; Fig. 1). Of these, MQTL1D.1, MQTL2B.2, MQTL3D.1, and MQTL7D.3 stand out, as they can be used as target regions for improving wheat yield under combined drought and heat stress. MQTL2A.2 is a key region responsible for yield under heat stress, and MQTL3A.2 and MQTL7A.1 are responsible for yield under drought stress and can serve as prime targets for improving stress tolerance in wheat. Future studies, including the development of near-isogenic lines, fine mapping, and functional analyses of these regions, are required to pinpoint the key gene(s) for improving wheat yield and adaptability to stresses.

Table 4 Summary of key MQTL and their associated genes identified in this study

MQTL	Tolerant to stress	Traits controlled	GBS markers	Candidate genes	Gene functions
MQTL1D.1	DS, DS + HS	TGW-all; TGW-DS; GN-DH	27941959 GTTT/GTTTT/G	1D01G047800	HSP
MQTL2A.1		TGW-all; GN-NS; TGW-NS	32525738 GA/G	2A01G073900	PSII
MQTL2A.2	HS	GN-NS; TGW-NS; GY-HS; TGW-HS; GFR-HS	83098529 ACCC/ACCCCC /ACCCC/ACC/AC/A, 83816418 C/T	2A01G136700, 2A01G138100	HSP, E3 ligase
MQTL2B.1			49411020 C/G/T, 50593509 A/C (functional)	2B01G087400, 2B01G089700	Peroxidase, E3 ligase
MQTL2B.2	HS, DS + HS	SPS-HS; SPS-DH	65431219 C/CA, 65888807 A/C, 68694266 CGG/ CGGGG/CGGG/CG/C, 75829312 G/GA	2B01G105100, 2B01G105300, 2B01G110000, 2B01G112600	HS-TF, ABA receptor, defensin, MYB
MQTL3A.2	DS	GN-all; GY-DS; TGW-DS	66407986 AT/A	3A01G102800	Sugar transporter
MQTL3D.1	DS, DS + HS	GY-DS; GN-DH; HI-DS	69404427 CGGG/C/ CGGG/CGG/CG	3D01G114700	HSP
MQTL4A.7		GY-NS; SN-all	69948297 AATG/A	4A01G072100	Dehydration-related
MQTL6A.1		GY-all; TGW-all	52795305 GCC/GCCCC/ GCCC/GC/G	6A01G084400	E3 ligase
MQTL7A.1	DS	TGW-all; DSI(TGW)	55367660 T/G, 58016619 CACA/C, 59122592 A/ AG	7A01G090700, 7A01G095100, 7A01G096200	Sugar transporter, ethylene-responsive TF, WRKY
MQTL7D.3	DS, HS, DS + HS	GY-all; GY-NS; TGW-NS; GY-DS; TGW-DS; GY-HS:; TGW-HS; GY-DH	60159590 G/T	7D01G100400	NAC

Abbreviations in the columns 'Tolerant to stress', 'Traits controlled' and 'Gene functions' are the same as described in Tables 1 and 2

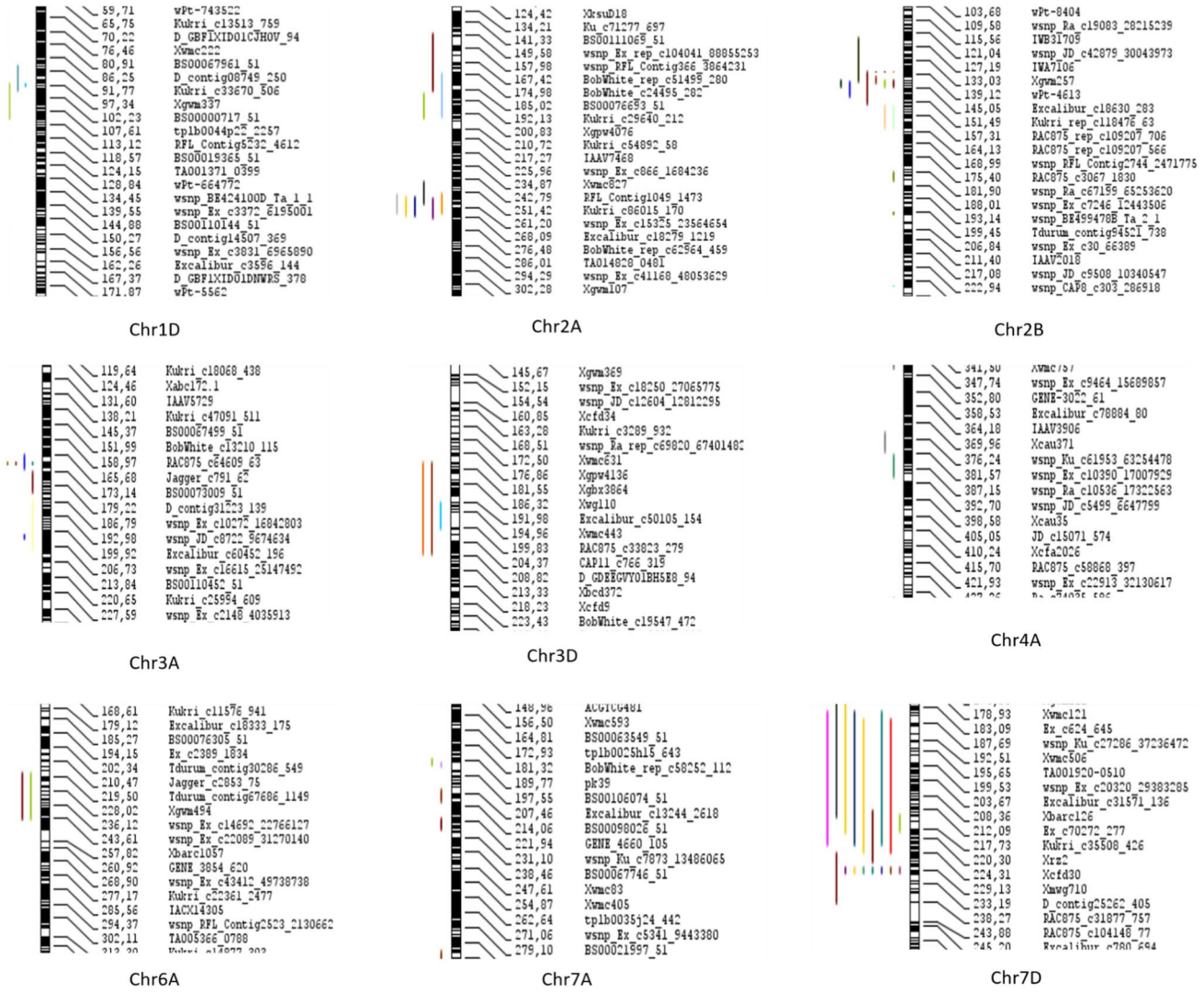

Fig. 1 Key MQTL regions with major or consistent QTL for yield and yield components on the wheat consensus map

Author contribution statement HL and GY designed and conceived the study. DM, CZ, and SZ helped with the phenotypic and genotypic data acquisition. HL performed data analysis and wrote the manuscript. DM, CZ, SZ, XL, AZ, ZL, YW, and GY critically reviewed the article and provided constructive feedback. All authors are participants of the Global Innovation Linkages Project.

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