GENETIC DISSECTION OF GRAIN YIELD, AGRONOMIC TRAITS AND END-USE QUALITY IN TEXAS WHEAT USING LINKAGE AND ASSOCIATION STUDY

A Dissertation

by

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ABSTRACT

Quantitative trait loci (QTL) study opens the door to marker-assisted selection by dissecting loci into individual component loci, their genetic effects and interactions. The objectives of this study were to find stable marker-trait association and to map QTL associated with grain yield, agronomic traits and end-use quality traits. An association mapping panel consisting of 298 synthetic derived lines from nine environments were phenotyped for end-use quality traits and genotyped with 76K genotype-by-sequencing (GBS) to find marker-trait association. Another population of 124 $F_{5:7}$ recombinant inbred lines were phenotyped for end-use quality in seven environments and for grain yield and agronomic traits in 28 environments. With the use of 90K single nucleotide polymorphism (SNP) and GBS, QTLs for grain yield, agronomic traits and end-use quality traits were determined. Association analysis revealed two sub-population structures originating from maternal parents of the backcross and slight relatedness among lines. Loci on the short arm of chromosome 1B (17.2-30.4 Mb) were significantly associated with mixograph parameters explaining up to 13.0% of the R^2. Hardness loci on the short arm of chromosome 5D (0.3-9.3 Mb) also affected hardness index and flour yield, explaining up to 27% and 33%, respectively. *Glu-D1* loci had strong influence on dough rheology of bi-parental population explaining up to 54.6% of the variation in midline peak time, with favorable allele coming from TAM 112. From multi-trait QTL analysis, homologue group 1 QTLs were strongly linked to mixograph traits from linkage analysis as well. Phenological development gene dependent QTLs were identified on chromosome 1A, 3B for grain yield, and 2B, 4B and 5B for test weight. Phonological development gene independent QTLs were also identified on chromosome 6D, 7D for grain yield, and on 4D, 6B for test weight. We found five genomic regions on chromosome 1D, 4B, 4D and 7D that are related to more than a single trait analyzed. This study unveiled previously identified loci linked to major genes as well as some newly identified QTLs. It will be necessary to validate these QTLs in different wheat backgrounds evaluated under similar growth conditions before developing markers for marker-assisted selection.

DEDICATION

To my lovely wife

Ashmita Bogati

And

My brother Ichchhuk Dhakal and my parents, Indra B. Dhakal and Nirmala Dhakal

They are the source of inspiration in my life!

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NOMENCLATURE

AA	QTL-by-QTL Interaction/Additive-by-Additive Interaction
AAE	QTL-by-QTL-by-Environment Interaction
ANOVA	Analysis of variance
BLUP	Best Linear Unbiased Estimate
CTAB	Cetyltrimethylammonium Bromide
DNA	Deoxyribonucleic Acid
FYLD	Flour Yield (%)
GEI	Genotype-by-Environment Interaction
GLM	General Linear Model
GY	Grain yield
HARD	Hardness index
HD	Heading date
HMW-GS	High Molecular Weight Glutenin Sub-units
HT	Plant Height
HVA	High Value Allele
ICIM	Inclusive Composite Interval Mapping
LMW-GS	Low Molecular Weight Glutenin Sub-units
MAS	Marker-Assisted Selection
MLM	Mixed Linear Model
MLPH	Midline Peak Height

MLPT	Midline Peak Time
MLRS	Midline Right Slope
MLRW	Midline Right Width
MLTW	Midline Tail Width
PCR	Polymerase Chain Reaction
QTL	Quantitative Trait Loci
RIL	Recombinant Inbred Lines
SKCS	Single Kernel Characterization System
SNP	Single Nucleotide Polymorphism

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CHAPTER I

INTRODUCTION

Wheat (*Triticum aestivum* L.) is a major crop in terms of area planted and nourishment of humankind. It provides nearly 20% calories and protein diet to global population (Shiferaw et al., 2013). A wide array of end products such as bread, noodles, cookies are made from wheat flour. With the expected population of 9 billion by 2050, annual genetic gain in crops must increase to 2-3% to meet food and feed demands (Hawkesford et al., 2013). However, current annual genetic gain in wheat is about 1%. In most part of the world, wheat yield is stagnant. Additionally, because of domestication and intensive selection pressure by nature and human kind, wheat has lost more than 69% of the genetic diversity that is present in the wheat genome (Haudry et al., 2007). Furthermore, most of the wheat breeding programs utilize elite-by-elite cross to create new genetic variability, which is the main bottleneck for increasing yield potential (Hao et al., 2010). In this context, selection of plants with desirable traits for increased yield, biotic and abiotic stress should be a major focus of plant breeders (Parry, 2012).

The primary challenge of wheat production in Texas is drought and heat stress which occurs frequently and with increasing intensity. Drought is one of the major factors limiting wheat production in the Southern Great Plains of the U.S. and other parts of the world. The Texas Panhandle area receives an average annual precipitation of 480 mm (Xue et al., 2014). Most of the cultivars grown in Texas are also susceptible to heat stress (Mason et al., 2010). From consumption point of view, awareness about daily diet and demand for diverse wheat food products is increasing in public. Breeding for end-use quality is equally important as breeding for grain yield to any breeding program. Thus, high yielding and drought tolerant wheat varieties without yield penalty and good end-use quality are desirable in Texas and other parts of the world.

In the past several decades, concerted efforts involving Texas A&M University's wheat breeding, genetics, physiology, pathology and entomology have developed widely adapted germplasm and cultivars for the U.S. Great Plains. These germplasm and cultivars possess novel alleles for high grain yield, drought tolerance, disease resistance and better end-use quality traits. Hard red winter wheat (HRWW) cultivar TAM 112 and TAM 111 developed by TAMU wheat breeding program were planted in millions of acers due to their drought tolerance and high grain yield potential (Lazar et al., 2004; Rudd et al., 2014). TAM 112 and TAM 111 rank among the top drought tolerant cultivars in the Southern Great Plains of the U.S. (NASS, 2012, http://www.nass.usda.gov). Advanced breeding line TX05A001822 was high yielding and excellent for end use quality in yield trials (HWWQC, 2010). Synthetic derived wheat was encompassed by TAMU wheat breeding program to increased genetic diversity as well as to break the yield plateau.

Genotypic variation already exists in wheat to make it possible to breed for improved grain yield and end-use quality traits. However, genetic basis and possible candidate genes for these traits are needed before they can be deployed in crop development. With few exceptions, grain yield, agronomic traits and end-use quality traits have continuous phenotype distributions i.e. these traits are controlled by multiple genes termed quantitative trait loci (QTL). QTL study via classical linkage mapping and association mapping provides the starting point to dissect complicated traits into the component alleles, their relative effects on a specific trait and genomic regions responsible for the marker-trait association for traits of interest (Doerge, 2002). It also provides a foundation for marker-assisted selection (MAS), that expedite the breeding process given the proper estimation of position and effects of QTLs.

In this dissertation, single nucleotide polymorphism (SNPs) is used for genetic mapping and detecting QTL for yield, yield components, agronomic traits, and end-use quality. Chapter II studied the major marker-trait association for end-use quality traits in synthetic derived wheat with TAM 112 and TAM 111 in the genetic background. We associated double digest restriction site associated DNA sequencing (ddRAD-Seq) SNPs with important kernel texture, flour characteristics and dough mixing parameters across whole genome (Poland et al., 2012). Chapter III covers mapping and identification of QTLs for end-use quality in bi-parental population from the cross of TAM 112/TAM 111. In chapter IV, linkage mapping for grain yield and agronomic traits is covered on data collected from 28 environments.

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CHAPTER II

ASSOCIATION ANALYSIS OF END-USE QUALITY IN SYNTHETIC DERIVED WHEAT

INTRODUCTION

Bread wheat (*Triticum aestivum* L., 2n=6x=42, AABBDD) is most widely grown in the world and second in terms of production (FAO, 2016). It provides 20% of the daily protein and food calories to the world as well as other minerals and micro-nutrients (Shiferaw et al., 2013). Bread wheat originated from two consecutive hybridization events of three ancestral grass species. First natural hybridization between wild einkorn (*Triticum Urartu*, 2n=2x=14, AA) and a close relative of goat grass (*Aegilops speltoides* 2n=2x=14, BB) gave rise to wild emmer wheat (*Triticum turgidum*, 2n=4x=21, AABB) nearly 0.82 million years ago (Petersen et al., 2006). The second natural hybridization between wild emmer wheat and goat grass (*Aegilops tauschii* ,2n=2x=14, DD) produced today's bread wheat about 0.43 million years ago near the Tigris and Euphrates rivers in the fertile-crescent region (Dubcovsky and Dvorak, 2007; International Wheat Genome Sequencing, 2014; Petersen et al., 2006).

A wide array of end products such as bread, noodles, and cookies, can be made from wheat flour depending upon functional properties of wheat seed, flour, and protein. With changing food preference of increasing population, demand for diverse food products is also increasing. Flour end product's fate is predicted by the kernel characteristics, milling, near infra-red parameters of flour, and dough rheology. These characteristics are collectively called as end-use quality traits (Finney et al., 1987). Gluten protein, comprised of glutenin and gliadin, is responsible for elasticity and extensibility properties of dough, one of the must traits for bread making (Gianibelli et al., 2001). Glutenin gives dough elasticity and gliadins give dough extensibility. Millers demands uniform kernel, high flour yield, and milling efficiency, while bakers require bright white flour with high gluten quantity and strength (Gaines et al., 1997; Simons et al., 2012).

However, because of domestication and intensive selection pressure by nature and humankind, wheat has lost more than 69% of the genetic diversity that is present in the wheat genome and increased the non-random association of alleles between loci (linked or unlinked) i.e. linkage disequilibrium (LD) (Haudry et al., 2007). *Glu-Ay* genes in the short arm of chromosome 1A is expressed in A-genome species, *Triticum dicoccoides*. During the domestication process, *Glu-1Ay* subunit for glutenin remains unexpressed in bread wheat (Waines and Payne, 1987). Interspecific hybridization between tetraploid *Triticum turdigum* and diploid *Aegilops tauschii* accessions were carried out to create synthetic hexaploidy wheat (SHW) in 1987 at CIMMYT, Mexico (Mujeeb-Kazi, 2003a; Mujeeb-Kazi, 2003b). Synthetic hexaploid wheat is useful for introducing novel genes for disease and insect-pest resistance as well as drought tolerance, end-use quality traits and yield and yield-related components (Aktaş et al., 2017).

Many of end-use quality traits are correlated and help us predict the bread making quality (Huang et al., 2006), but its measurement in early generation material is technically demanding. As a result, several predictive indirect assays have been developed, including sodium dodecyl sulfate (SDS) sedimentation volume (SSD), grain protein content (GPC), grain hardness (GH) and various mixograph parameters, and these are widely used in breeding programs to evaluate processing quality (AACC, 2010). These protocols are tedious and time consuming therefore relegating quality testing in earlier generations when there is significantly increasing number of lines to be tested. Moreover, the amount of seed available for extensive quality analysis is limited. Even though amount of seed available in later generation of breeding cycle is no longer an issue, we would loss many genetic resources by pushing end-use quality test towards advanced breeding generation. However, use of molecular signatures as a proxy for end-use quality makes it feasible to test large number of genotypes in advanced generation.

Synthetic hexaploid wheat (SHW) is undoubtedly an excellent source of genetic variation. However, SHW usually shows overall poor agronomic performance. These SHW lines are often backcrossed with elite wheat lines to develop synthetic derived wheat (SDW) lines. SDW bring diversity back without losing much of adapted gene pool in a wheat breeding program. SDW lines were extensively studied for yield, yield components, heat, drought tolerance, greenbug and other biotic stresses in Texas A&M wheat breeding program (Cooper et al., 2013; Cooper et al., 2012; Reddy, 2015). To meet the needs of millers, food processors and consumers, it is necessary to bred for end-use quality traits. However, genetic variability for end-use traits in the SDW lines remained unexplored. Understanding genetic architecture, individual components, and alleles linked to quantitative traits like end-use quality traits are necessary to improve wheat breeding. Genome-wide association study (GWAS) utilizes ancestral recombination present to uncover a significant association between the trait and a gene or molecular marker base on the LD (Zhang et al., 2007). The objectives of this study are 1) to understand the genetic basis of end-use traits using an association mapping approach, 2) to determine the population structure so that the best model can be chose for association analysis, 3) to identify the chromosomal regions affecting end-use quality traits in synthetic derived wheat.

MATERIALS & METHODS

Populations and trials

In the current study, a population of 298 synthetic derived wheat lines was used for association mapping, thus called as association mapping panel of synthetic wheat (AMPSY). This population was created from the back-cross of TAM 111 or TAM 112 with 21 primary synthetic wheat from CIMMYT (International Center for Maize and Wheat Improvement). TAM 111 and TAM 112 are both well adapted hard red winter wheat in the Southern Great Plains of the United States, developed by Texas A&M AgriLife Research (Lazar et al., 2004; Rudd et al., 2014). Multi-environment trails were conducted in more than nine environments to explore genetic variability for end-use quality traits. Backcross population (BC1F5:9) along with TAM 111 and TAM 112 were planted in Etter, TX (35° 51' N, 101° 58' W), Bushland, TX (35° 06' N, 102° 27' W), Chillicothe, TX (34° 15' N, 99° 30' W), and Clovis, NM (34° 24' N, 103° 12' W) in crop year 2014, 2015 and 2016. A total of nine environments (Year-location) were planted: 2014 Chillicothe dry (14CH), 2014 Etter 75% of Evapo-transpiration (ET) demand

(14EP4), 2014 Etter 100% ET (14EP5), 2015 Etter 60% ET (15EP3), 2015 Etter 75% ET (15EP4), 2015 Etter 100% ET (15EP5), 2016 Bushland dry (16BD), 2016 Bushland irrigated (16BI), and 2016 Clovis irrigated (16CLI). Dry environment consisted of 14CH, 15EP3, and 16BD, while irrigated environment consisted of 14EP4, 14EP5, 15EP4, 15EP5, 16BI, and 16CLI. All traits were replicated twice in alpha-lattice design with plot dimension of 15 feet long and 5 feet wide on the dry environments and 10 feet long and 5 feet wide on the irrigated environments with 0.3 meter between plots. Standard agronomic practices were carried out for each environment.

Grain quality evaluation

From each line in all the environments under study, 80 g and 30 g of clean samples were drawn from a single replication. The for milling, near infra-red, and dough rheological studies and the latter being used for single kernel characterization, both conducted at Texas A&M Cereal Quality Lab, College Station, TX.

Single Kernel Characterization System (SKCS)

Kernel properties were determined using 30 g of samples in SCKS 4100 instrument (Perten Instruments, Hagersten, Sweden). It measured the hardness index (HARD), single kernel diameter (DIAM), single kernel weight (SKW) and kernel moisture (GMOIST). Hardness index is measured on 0-100 scale, 0 being the soft kernel and 100 being the hard kernel. DIAM, SKW, and GMOIST were expressed in mm, mg, and %, respectively.

Flour Milling

Based on grain moisture content from SKCS 4100, 80 g of clean seeds were tempered for 24 hours to 14 % moisture content. Samples were soaked in a flask and kept on a shaker for 60 mins. Soaked samples were kept overnight and milled using the Barbender Quadramat Jr. Precision laboratory roller mill (Barbender Instruments, South Hackensack, NJ, USA). Flour weight (FWT) (g) and percentage flour extraction (FYLD) were recorded for each line.

Near infra-red (NIR)

Protein and moisture content of the milled flour were determined by third generation diode array near infra-red spectroscopy (NIR), model DA 7250 (Perten Instruments, Hagersten, Sweden). Flour protein content at 14 % moisture (PROT14) was determined simplicity plus software v2.86, a GUI program attached with NIR instrument. The amount of distilled water added to the flour was determined based on AACC method 54-40.02 (AACC International, 2010). The percent optimum water absorption (WABS) was calculated using the formula $\text{WABS} = 1.5 \times \text{Prot14} + 43.6$, where PROT14 is protein at 14% moisture basis. Flour moisture (FMOIST) were expressed in percentage term.

Dough properties

Dough mixing properties 10-gm flour at 14 % moisture basis were determined by mixogram (National Manufacturing Co. Lincoln, NE) with the aid of MixSmart software v1.0.404, based on AACC method 54-40.02 (AACC International, 2010). Midline variable of the mixograph at peak, two mins after the peak, time_X (8 min) were noted.

Time to reach the midline peak is recorded as midline peak time (MLPT), height of midline peak as midline peak height (MLPT), width of outer and inner envelop at midline peak as midline peak width (MLPW), width of outer and inner envelop at midline two minutes after peak as midline right width (MLRW), width of outer and inner envelop at midline eight minutes after peak as midline tail width (MLTW), and slope of midline between two minutes and eight minutes as midline right slope (MLRS) (Figure A1).

Genotyping

Leaf tissue was collected at the two-leaf stage from each of the 298 lines in Texas A&M AgriLife Research Center, Amarillo, TX. Genomic DNA was isolated using a modified cetyl trimethyl ammonium bromide (CTAB) method (Murray and Thompson, 1980). Extracted DNA was checked for quality and quantity by gel analyses. GBS libraries for 298 lines were prepared as developed by Peterson et al. (2012) with some noted modifications and were sequenced with double digest restriction site associated DNA sequencing (ddRAD-seq) with Illumina HiSeq 2500 platform (2*125 bp paired-end) at the Genomics and Bioinformatics Center, Texas A&M AgriLife Research at College Station.

Raw sequence reads were demultiplexed according to the index reads. Sequences were first quality-filtered using the program FASTX-Toolkit (http://hannonlab.cshl.edu/fastx-toolkit): 1). raw sequencing reads were first trimmed to remove low quality bases with quality score less than 20 on the ends of reads; 2). reads with 30% or more bases showing low quality score ($Q < 15$) were removed.

The reference genome for hexaploid wheat (V1.0) was downloaded from International Wheat Genome Sequencing Consortium (IWGSC) website. Bowtie2 [http://bowtie-bio.sourceforge.net/bowtie2/index.shtml] was used to align quality-filtered reads to the reference with the default parameters. Aligned reads were then processed with SAMtools v1.19 [Li et al., 2009] to generated coordinate sorted binary SAM files (BAM). Reads with mapping quality (MQ) less than 5 were removed. Following the aforementioned steps, the local re-alignment tool in the Genome Analysis Toolkit (GATK, https://software.broadinstitute.org/gatk) was used to perform re-alignment in the Insertion/Deletion regions. Finally, the processed alignment files were fed to the tool UnifiedGenotyper, which is part of the GATK, to call variations and perform genotyping for each sample.

SNPs with less than 5 % minor allele frequency (MAF) are filtered. Meanwhile, SNPs with more than 20 % missing values and heterozygotes more than 10 % were also excluded from the dataset along with all monomorphic SNPs. A final set of 76K SNPs was retained for the subsequent association analysis.

Phenotypic data analysis

Each location-by-year combination was considered as a single environment. All the traits within each environment were analyzed as an individual environment analysis. Best linear unbiased predictor (BLUP) mean of each trait across environments were analyzed as single trait analysis. BLUP mean for all the traits combined across locations were analyzed as combined analysis. The current study had the spatial rep and therefore the analysis of variance (ANOVA) follows a statistical linear model of single environment analysis.

$$\mathrm{Y}_{ilp} = \mu + E_p + I_{l(p)} + G_i + \varepsilon_{ik}$$

Where $\mathrm{Y}_{\mathrm{ilp}}$ is the observed phenotypic value of the i^{th} genotype in lth block in p^{th} repetition, μ is the overall mean, E_{p} is the rep effect, $\mathrm{I}_{\mathrm{l(p)}}$ is the block effect, G_{i} is the genetic effect of i^{th} genotype and $\varepsilon_{ilp}$is the residual term corresponding to a quasi-genotype-by-environment interaction (GEI). Combined analysis of variance (ANOVA) for all the traits was determined for the significance of genetic variance, phenotypic variance and genotype-by-environment interaction (GEI) components in each environment. In this context, the interaction of replication (environment in this case) with genotype (ε_{ilp}) was used as the error term to test the significance of genotypes. Although we cannot separate the GEI component from the error term in this study, we computed the magnitude of variance component due to each source of variation to determine the relative proportionality of each component. The variance components were computed using PROC VARCOMP in SAS 9.4 (SAS Institute Inc., 2015). The entry-mean heritability estimate was calculated according to Fehr et al (1987) using the formula:

$$\mathrm{h}^2 = \frac{\sigma_{\mathrm{g}}^2}{\sigma_{\mathrm{e}}^2/\mathrm{r} + \sigma_{\mathrm{g}}^2}$$

Where r is the number of replication (rep), $\sigma^2{}_{\mathrm{g}}$ is the genotype variance, and $\sigma^2{}_{\mathrm{e}}$ is the residual variance. PROC CORR in SAS was used to compute Pearson correlations (r_{P}) based on the following formula:

$$r_P = \frac{Cov_{x,y}}{(\sigma_x^2 \ \sigma_y^2)^{1/2}}$$

Linkage Disequilibrium

For LD calculation, numerical imputation of SNP data was done in TASSEL v 5.0 (Bradbury et al., 2007) using default setting of five nearest neighbor mean. LD estimate was done as the squared allele frequency correlation (R^2). R^2 was plotted against physical distance for each pair locus located on the same chromosome using nonlinear regression as described in the GAPIT v 2.0 (Lipka et al., 2012). Loci were in significant LD when p-value < 0.01.

Population structure and kinship

A subset of 8922 markers from original 76K markers that had $r^2 < 0.1$ and no missing data were used to determine subpopulation. Subpopulation membership of lines were estimated in STRUCTURE 2.3.4 (Pritchard et al., 2000). Using the admixture model with correlated allele frequencies and without prior information, the membership of each line was determined with a burn-in period equal to 50,000 iterations and a run of 50,000 replication of Monte Carlo Markov Chains (MCMC) for subpopulations (K) numbers ranging from K=1 to K=10. For each run, five independent runs of STRUCTURE were performed for each K value, and the posterior probability was determined for each run. The optimum number of subpopulations, ad hoc criterion deltaK, was determined using STRUCTURE HARVESTER (Earl and Vonholdt, 2012). To avoid stochastic effects of replicated STRUCTURE runs, the results were collated using the program CLUMPP (Jakobsson and Rosenberg, 2007). PCA was also used to see relative dispersion of each lines in two-dimensional space as well as validation for deltaK value from STURCUTRE. A pairwise kinship coefficient matrix (K-matrix) that estimates the probability of recent co-ancestry between lines was determined using SPAGeDi v1.2 (Hardy and Vekemans, 2002). Diagonal values were normalized to two and all the negative values for the kinship matrix was set to zero as described by (Yu et al., 2006).

Marker-Trait Association Model testing

Marker-trait association was tested in TASSEL v 5.0 (Bradbury et al., 2007) using SNP data from ddRAD-seq and the three set of phenotypic means, mean from single environment analysis, mean from single trait across environments analysis, and BLUP mean from traits combined across environments analysis. Three different general linear models (GLMs) and two different mixed-linear models (MLMs) were tested best marker-trait association model that reduces the deviation between observed and predicted probability. For GLMs, we considered marker-trait association was calculated. For GLM, kinship (K), principle component analysis (PCA), and population structure (Q) model were tested. For MLM, PCA as covariate and kinship (PCA + K), and population structure as covariate and kinship (Q + K) were tested with the optimum level of compression and population parameters previously determined (P3D). For each model, all marker p-values were ranked from smallest to largest, and the mean square deviation (MDS) was calculated as (Mamidi et al., 2011)

$$MSD = \frac{\{\sum_{i=1}^{n}[p_i - (i/n)^2]\}}{n}$$

Where i is the rank number, p_i is the probability of the i^{th} ranked p-value, and n is the number of markers. Significant markers were selected only from the model determined to have the lowest MSD value. For each marker, the false discovery rate (FDR) was estimated using the 'qvalue' in R environment (Storey et al., 2015). Bonferroni correction of 0.01 genome-wide significance level was applied to declare significant association. Manhattan plot was used to visualize the distribution of markers associated with the traits across different chromosomes using 'CMplot' package in R (LinLin, 2018).

RESULTS

ANOVA and heritability

Fourteen end-use traits under four broad categories were analyzed in this study. Combined ANOVA showed highly significant differences (< 0.001) among lines for all the 14 traits (Table 2.1). All the environments, treated as pseudo-rep, were also significant except for PROT14. However, most of the variation for NIR related traits was explained by pseudo-rep, except for moisture. Traits with heritability ≤ 0.3 were categorized as lowly heritable, 0.4 – 0.6 as moderately heritable and > 0.6 as highly heritable traits. All the single kernel related traits are with high entry-mean heritability. Mean seed moisture content of lines was 11.3% with an average hardness index of 62.1%, an average diameter of 2.7 mm, and mean single kernel weight of 33.6 mg. Flour yield, expressed in percentage, was highly heritable with mean 69% flour extraction. Except for flour moisture content, other NIR related traits were highly heritable.

Table 2.1. Analysis of variance, heritability and mean performance for end-use quality (combined analysis)

Trait name	Abbreviation	Units	σ^2_{Geno}†	σ^2_{Rep}‡	$\sigma^2_{Iblk\ (Rep)}$§	σ^2_{Res}¶	h^2#	$\bar{X}$±SD
Single kernel characterization system								
Hardness Index	HARD	%	133.03***	93.918*	4.88***	11.88***	0.99	62.1 ± 15.3
Moisture	GMOIST	%	0.01***	1.2*	0.14***	0.16***	0.37	11.3 ± 1.18
Diameter	DIAM	mm	0.004***	0.018*	0.0008***	0.005***	0.90	2.7± 0.16
Single kernel weight	SKW	mg	3.48***	18.2*	0.62***	2.95***	0.91	33.6 ± 4.83
Milling								
Flour yield	FYLD	%	12.7***	2.9*	2.6***	11.5***	0.89	69.0 ± 5.45
Near infra-red								
Protein (14% moisture)	PROT14	%	0.22***	1.3	0.04***	0.32***	0.83	12.8 ± 1.29
Moisture (Flour)	FMOIST	%	0.015***	0.23*	0.21***	0.12***	0.47	13.7 ± 0.73
Water absorption	WABS	%	0.66***	2.52*	0.13***	0.65***	0.88	62.9 ± 1.9
Mixograph								
Midline peak time	MLPT	min	0.6***	0.16*	0.06***	0.31**	0.93	4.00 ± 1.05
Midline peak width	MLPW	%	4.97***	26.88*	13.72***	24.10***	0.59	29.8± 8.16
Midline peak height	MLPH		3.47***	25.15	11.82***	27.68***	0.47	60.1 ± 7.95
Midline right width	MLRW	%	12.77***	13.07	5.54***	16.47***	0.84	18.0 ± 6.82
Midline tail width	MLTW	%	15.55***	10.71	3.84***	14.86***	0.88	14.8 ± 6.67
Mixing tolerance	TOL	% min-1	0.19***	0.17*	0.14***	1.27***	0.52	-3.2± 1.32

† σ^2_{Geno}, Genotypic variance
‡ σ^2_{Rep}, Variance due to replication (environment) in percentage
§ $\sigma^2_{Iblk\ (Rep)}$, Variance due to incomplete block nested within replication (environment) in percentage
¶ σ^2_{Res}, residual variance in percentage
\# h^2, entry-mean heritability
*, **, *** significant at 0.05, 0.01, and 0.001 probability levels, respectively

Mean flour moisture was 13.7% with heritability of 0.47. Protein at 14% moisture was they highly heritable trait with average flour protein of 12.8%. Midline peak time (MLPT), which is average time to the maximum dough consistency, was 4 minutes with heritability of 0.93. At the peak time, midline peak width (MLPW) and midline peak time (MLPT) had the heritability of 0.59 and 0.47, respectively. Average MLPW was 29.8%, and average MLPH was 60.1%. Midline right width (MLRW), which is 2 minutes after peak time, was 18% with heritability of 0.84. Midline tail width eight minutes after the dough development (TAILW) was highly heritable with an average value of 14.8%. Mixing tolerance (TOL) is the right slope after peak time had the mean slope of -3.2 % min-1 and heritability of 0.52.

Pearson correlation

The phenotypic relationship between traits on combined data was determined using Pearson correlation coefficients (Table 2.2). Correlation coefficients ≤ 0.3 between two traits were categorized as low correlation, 0.4 - 0.6 as moderate correlation, and > 0.6 as high correlation. SKW and DIAM showed highly significant (0.84) correlation suggesting line with bigger and plum seed always weigh heavier. Similar significant association (0.72) was found between HARD and FYLD. This implies harder the seed will result in higher flour extraction. Flour protein (PROT14) is nearly perfectly related to WABS and this relationship is significant in the positive direction (0.97). Given WABS is calculated using protein %, this relationship holds true. Most of the dough rheological traits were highly positively significantly related.

Table 2.2. Phenotypic correlation (combined analysis)

Traits†	HARD	GMOIST	DIAM	SKW	FYLD	PROT14	FMOIST	WABS	MLPT	MLPW	MLPH	MLRW	MLTW
HARD													
GMOIST	-0.14*												
DIAM	-0.09	-0.13*											
SKW	-0.11	-0.11	0.84***										
FYLD	0.72***	-0.22***	0.12*	0.17**									
PROT14	0.17**	-0.2***	0.37***	0.28***	0.2***								
FMOIST	-0.04	-0.73***	0.21***	0.20***	0.11*	0.24***							
WABS	0.16**	-0.19**	0.38***	0.27***	0.16**	0.97***	0.23***						
MLPT	0.19***	0.20***	-0.21***	-0.29***	-0.06	-0.07	-0.25***	-0.06					
MLPW	0.004	0.13*	0.11	0.005	0.06	0.15**	-0.10	0.17**	0.33***				
MLPH	0.04	-0.23***	0.15**	0.13*	0.18**	0.35***	0.15*	0.31***	-0.23***	0.19***			
MLRW	0.13*	0.21***	-0.02	-0.12*	-0.01	0.06	-0.18**	0.07	0.7***	0.69***	-0.04		
MLTW	0.17**	0.19**	-0.04	-0.14*	-0.01	0.02	-0.20***	0.05	0.84***	0.58***	-0.11	0.89***	
TOL	0.18**	0.24***	-0.07	-0.1	-0.08	-0.07	-0.19**	-0.06	0.51***	0.09	-0.44***	0.45***	0.53***

† Traits abbreviation, HARD, Hardness index (%); GMOIST, grain moisture (%); DIAM, kernel diameter (mm); SKW, single kernel weight (mg); FYLD, flour yield (%); PROT14, flour protein at 14% moisture basis; FMOIST, flour moisture (%); WABS, water absorption (%); MLPT, midline peak time (min); MLPW, Midline peak width (%); MLPH, midline peak height (%); MLRW, midline right width (%); MLTW, midline tail width (%); TOL, tolerance i.e. midline right slope (% min-1)

*, **, *** significant at 0.05, 0.01, and 0.001 probability levels, respectively

All the midline width traits at the different time (MLPW, MLRW, TAILW) were significantly correlated in the positive side. MLPT was also highly and significantly correlated (0.19-0.69) with MLRW, TAILW, TOL. Grain moisture (GMOIST) was significantly (-0.14) related to hardness (HARD). Kernel characteristics were weakly correlated to mixograph trait, so they are the poor predictor of mixograph traits and cannot be used as a proxy. FYLD is positively correlated with kernel characteristics except for grain moisture, which is negatively correlated. MLPH is negatively correlated with TOL. MLPH was negatively moderately correlated (-0.44) with tolerance.

SNP statistics, population structure and relative kinship

Among 76K SNPs, 32.2% of them were on A genome, 36.8% on B genome, and 31 % on the D genome of synthetic derived wheat lines. In a biparental mapping population derived from both the Texas elite lines, A genome had 43.2%, B genome had 42.5% and D genome had 14 % of the makers (Yang et al., 2018). With the SDW lines, D genome polymorphism was comparable among three sub-genomes had nearly equal polymorphisms. Genetic diversity for the AMPSY population ranged 0.04 to 0.5 with an average of 0.24. The expected heterozygosity was 0.024, which generally low for SNP markers because of their bi-allelic nature and the selfing nature of *T. aestivum*. The markers were polymorphic with PIC values, the genetic diversity measure, ranging from 0.04 to 0.38 with an average of 0.21 (Table 2.3).

Table 2.3. Marker summary for AMPSY population

Parameters †	Average	Minimum	Maximum
Major allele frequency	0.83391952	0.5	0.98
Availability	0.968830444	0.75	1
Gene Diversity	0.244412472	0.039	0.5
Heterozygosity	0.024013573	0	0.48
PIC	0.205494297	0.039	0.375
F	0.902085591	-0.24	1

†Availability is calculated as (1-obs)/n, where *obs* is the number of observations, and *n* is the number of individuals sampled; Gene diversity, the probability that two randomly chosen alleles from the population are different; Heterozygosity, proportion of heterozygous individuals in the population; PIC, polymorphic information content; F, inbreeding coefficient

Using all pair-wise analysis of 76K markers with LD sliding window size of 50 markers, LD parameter square allele frequency correlation (R^2) value was regressed on the physical distance (Figure 2.1).

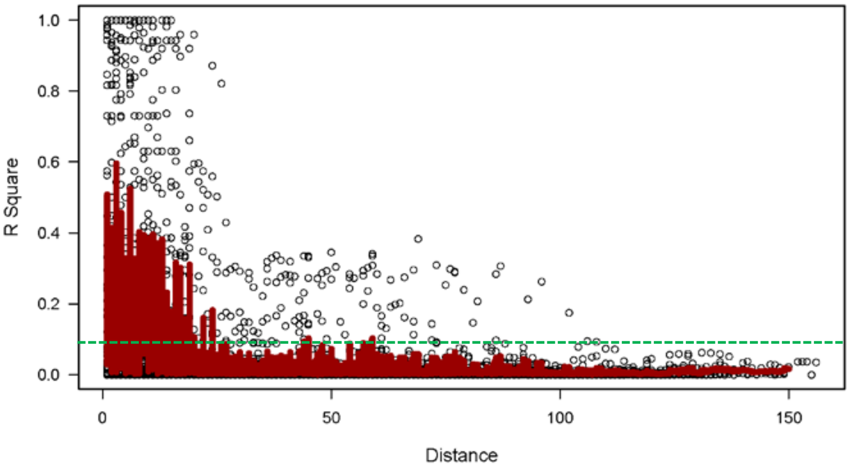

Figure 2.1. Average LD decay in A MPSY population.
X-axis represents the distances in mega base pairs (Mb), and Y-axis represents linkage disequilibrium (LD) value (R^2) on 0 – 1 scale. Green dotted line represents R^2=0.1 threshold line for declaring LD decay.

The average decay of LD in terms of physical distance declined to $R^2 < 0.1$ at 20 Mb. Both 8922 and a subset of 1872 markers without missing data, were used to determine population structure and to calculate relative kinship between pairs of individuals, respectively. The subset of 1872 is the representation of 8922 markers to reduce computational burden. Over 70% of the pair-wise combination had kinship coefficients of 0.05-0.1 and 21 % had kinship coefficients between 0.1-0.15 (Figure 2.2). These values suggest the slight amount of relatedness between lines in the current study.

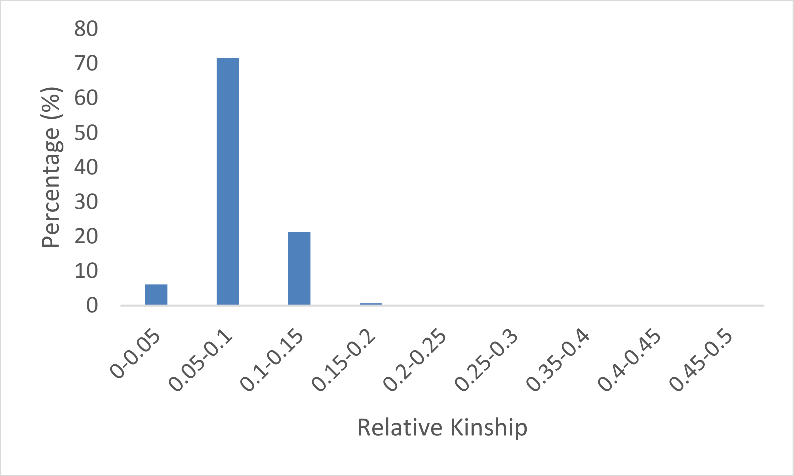

Figure 2.2. Distribution of pair-wise kinship coefficients among AMPSY on 2849 SNP markers.
X-axis represents relatedness on 0-1 scale, 0 being the unrelated and 1 being perfectly related individuals. On Y-axis percentage of individuals in pair.

Based on the posterior probability of the data peak at the two subpopulations, 8922 SNPs can separate the AMPSY into two sub-population (K=2) (Figure 2.3). PCA was also conducted to visualize the relative dispersion of the subpopulation in two-dimensional space (Figure 2.4). First principal component and second principal components explained 27 % and 7 % of the total variance. All the TAM 111 backcrossed SDW lines were grouped together on left side of the cluster along with the TAM 111.

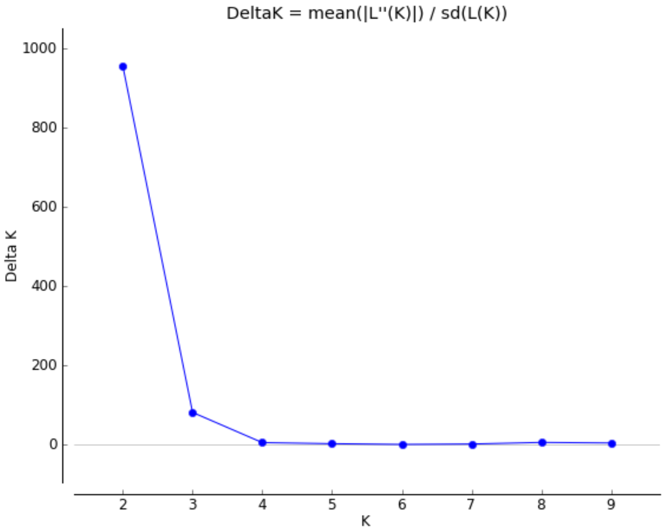

Figure 2.3. Estimation of the number of populations by calculating delta K values. X-axis is subpopulation (K) ranging from 2 to 9, and Y-axis represents the posterior probability (Delta K) for each subpopulation.

TAM 112 backcrossed SDW lines grouped together on the right side of the cluster along with TAM 112 (Figure 2.4). F1 lines from TAM111/primary synthetics were crossed with TAM112 and they also clustered with TAM 112 derived cluster on right. Based on STRUCTURE and PCA, TAM 111 backcrossed subpopulation was different from TAM 112 backcrossed population.

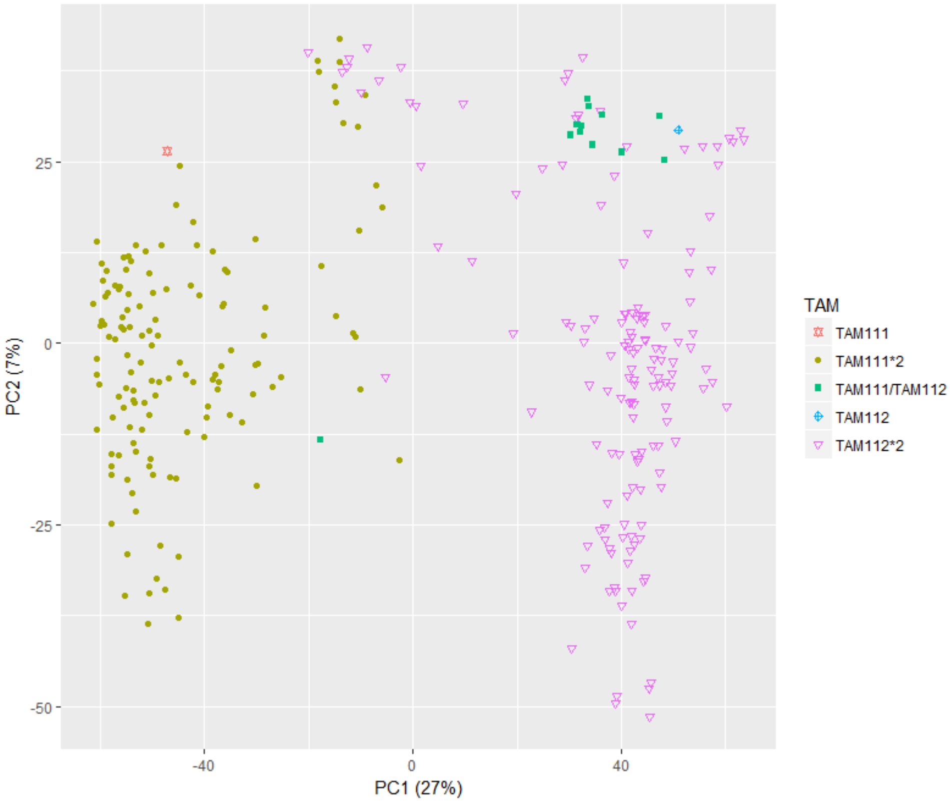

Figure 2.4. Principle component analysis of 295 synthetic derived lines in AMPSY population.
On X-axis is principle component 1 and on Y-axis is principle component 2. Percentage of variation explained by each PC are enclosed in parenthesis.

Association mapping analysis of end-use quality traits

Model testing was performed to determine number of parameters to be included and mode to be run. Five different models were compared to access their usefulness in accounting for population structure and their ability to reduce the inflation of false positive associations (Type I error). (Table 2.4). To observe the degree to which the statistical results for a model deviated from the expected distribution, MSD was calculated. In this study, MLM models that accounted for population structure and relatedness had MSD value of 0.12, whereas MLM model accounting subpopulation from PCA and kinship had 0.16.

Table 2.4. Test statistic for the five models used to discover marker-trait associations

Model†	Percent p-values<0.05	MSD‡
K	8.19	0.1421
PCA	8.47	0.1365
Q	7.33	0.1465
PCA + K	6.43	0.1599
Q + K	10.44	0.1210

† K, kinship matrix; PCA, principle component analysis; Q, population structure matrix
‡ MSD, mean square deviation

The ideal model would exhibit a uniform distribution when cumulative p-values are regressed on observed p-values. This imply Q+K MLM model is the best suited for our population. In most cases controlling for population structure and family relatedness was needed. Association analysis of phenotypic data obtained from individual environment analysis, single trait across environments and combined analysis were conducted using MLM corrected for population structure and kinship i.e. Q+K model.

Based on the IWGSC RefSeq v1.0, QTL within 50 Mb regions was viewed as a unique QTL ID. Three different analysis were performed on phenotypic data; single environment analysis, single trait multi-environment analysis, and combined analysis. For the three analysis, 727, 603, and 44 significant marker-trait association (MTA) corresponding to 132, 123, and 3 unique QTL regions were found, respectively (Table A1, A2, and A3). In individual environmental analysis, significant markers were identified for kernel weight, grain moisture, flour yield, hardness index, protein at 14 % moisture basis, midline peak height, midline right slope, midline right width and midline tail width (Table A1). Markers associated with hardness index (HARD) were detected genome-wide, but majority were on the chromosome 5D. Hardness index decreased by 8.5% or increased up to 7.7% for a locus. These markers explained 10.2% - 32.5 % of the total variation present in the hardness index (Table A1). Marker associated with kernel weight (SKW) were environment specific and expressed only in Etter, TX in 2015 (15EP5). Theses markers were located at 672.1 Mb on the chromosome 4A and explained 10.3% - 12.1% of phenotypic variation of single kernel weight. Grain moisture (GMOIST) associated markers were detected on Clovis, NM in 2016 (16CLI) (Table A1). These markers were identified on the homeolougs group 7 chromosome and 3B explaining 9.7% - 21.3% of the phenotypic variation in the grain moisture. Flour yield (FYLD) related markers were throughout the genome, but majority of the markers were clustered on the chromosome 5D. Phenotypic variation explained by these markers ranged from 9.8% - 27%. Depending upon the marker and alleles, mean FYLD reduced by 2.7% or increased by 1.94% for some locus. Markers associated with protein at 14% moisture basis (PROT14) were detected in mean data from irrigated environments. Chromosomal location of these markers was scattered throughout the genome explaining 10.3% -23.4% of the variation in this trait. Markers on the chromosome 7A from mean of dry environments were associated with water absorption (WABS) explaining 11.8% of the total phenotypic variation. Only one marker was detected for Midline peak height (MLPH) on the chromosome 3B, that explained 11.7% of the total phenotypic variation.

Allele associated with this marker reduced MLPH by 1.7%. Markers associated with midline right slope (MLRS), i.e. tolerance were spread over the genome explaining 11.1% - 17.9% of the variation in this trait. Presence of these markers decreased 0.33 % min-1 and increased the mean phenotypic value up to 0.27 % min-1. Makers associated with midline right width (MLRW) were detected on the chromosome 1B and were very specific to Bushland, TX under irrigation in 2016 (16BI) (Table A1). Presence of these markers increased MLRW by 3.15 % and decreased it up to 3.15%. Chromosomal location of the markers associated with midline tail width (MLTW) were scattered throughout the genome and explained 9.3% -25.1% of the total phenotypic variation. Presence of these markers increased and decreased mean phenotypic value by 2.7% (Table A2).

Among 44 significant association from combined analysis, 15 were associated with FYLD, 22 with HARD, one with PROT14, two with MLRW and four with TAILW (Table A3). Twenty-seven markers were uniquely consistently associated with hardness index, flour yield (%), protein at 14% moisture basis, midline right width and midline tail width parameters across three analyses (Table 2.5, A3). These 27 markers were defined as consistent marker-trait association. Some of these markers were associated with more than one trait. Such marker-traits were defined as clustered marker-trait association.

Table 2.5. Single Nucleotide polymorphism (SNP) marker loci significantly associated with end-use traits

GBS SNP marker	Chromosome	SNP position (bp)	Mb†	Major allele	Minor allele	Minor allele Frequency
3453826_1bs_3023	1B	5923	17.146165	G	C	21.2
3453826_1bs_3043	1B	5926	17.146145	C	T	20.5
3453826_1bs_3226	1B	5932	17.145962	G	T	20.6
3434158_1bs_9081	1B	6314	30.403173	G	A	17.3
4860661_4bs_1872	4B	57492	134.9	T	G	8.3
1477005_5ds_2010	5D	75878	0.344579	T	C	22.2
2770151_5ds_4035	5D	75899	7.257066	C	A	9.5
2765676_5ds_2839	5D	75901	1.344429	T	C	6.3
2773392_5ds_1206	5D	75906	2.22108	T	C	12.24
2773392_5ds_1238	5D	75910	2.221048	A	G	14.28
2773392_5ds_1412	5D	75911	2.220874	T	C	12.24
2736392_5ds_5233	5D	75917	0.934031	T	G	10.6
2739337_5ds_2304	5D	75953	7.485266	G	T	37.4
2745573_5ds_3677	5D	75978	0.55498	A	G	14.23
2781671_5ds_9157	5D	75986	9.332315	A	C	7.8
2781671_5ds_9179	5D	75987	9.332293	A	G	7.1
2781671_5ds_9219	5D	75989	9.332253	T	G	7.1
2781671_5ds_9223	5D	75990	9.332249	G	C	7.8
2781671_5ds_9235	5D	75991	9.332237	C	G	7.1
2781671_5ds_9443	5D	75992	9.332029	A	C	7.1
2781671_5ds_9461	5D	75993	9.332011	C	T	7.1
2781671_5ds_9472	5D	75997	9.332	G	C	7.45
2781025_5ds_24421	5D	76005	8.018756	C	T	5.4
2781025_5ds_24425	5D	76006	8.018752	C	T	5.4
2774182_5ds_7304	5D	76010	8.613963	A	C	7.8
2745020_5ds_15344	5D	76053	8.419265	A	C	10.3
2745020_5ds_15346	5D	76054	8.419267	A	C	10.3

† Physical position of the corresponding markers in IWGSC RefSeq v1.0

Two markers, 3453826_1bs_3043, and 3453826_1bs_3226 were significantly associated with both MLRW and TAILW on chromosome 1B (Figure 2.5, Table 2.6). All the 17 markers that were significantly associated with FYLD were also associated with HARD on chromosome 5D at 0-9.3 Mb (Figure 2.5, Table 2.6, Table A3).

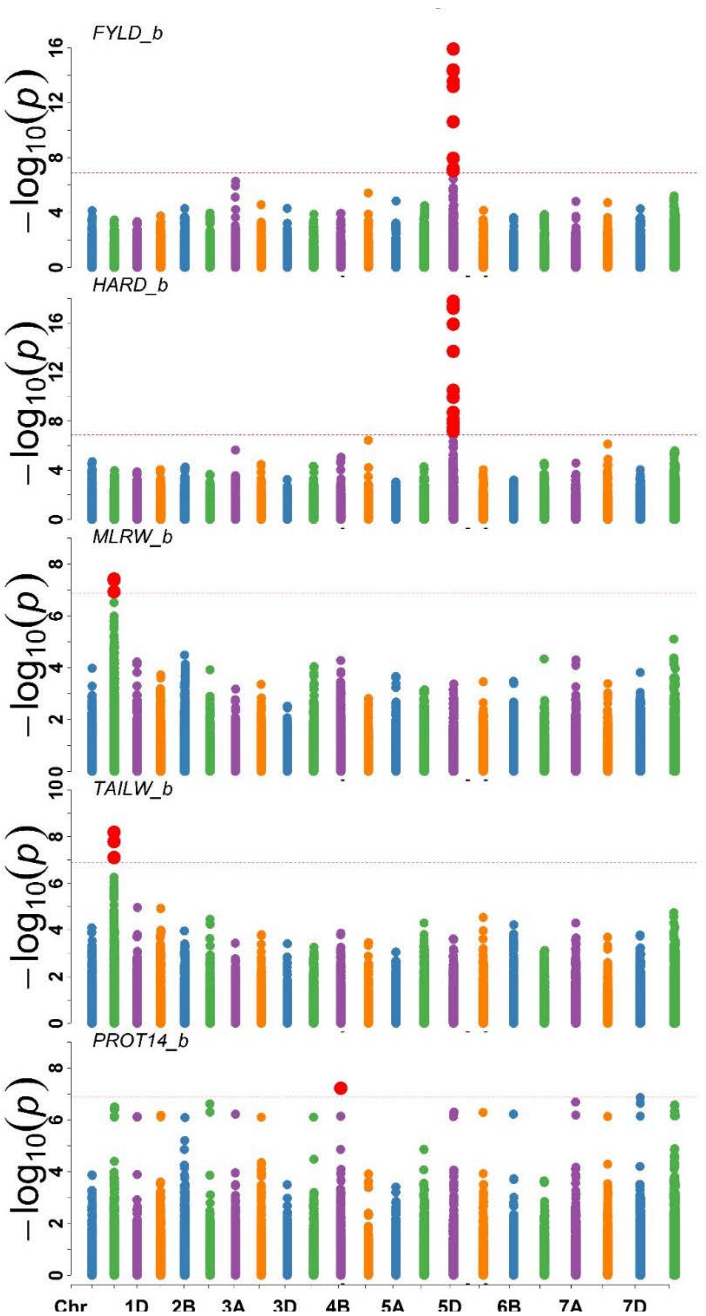

Figure 2.5. Manhattan Plot of significant markers and traits from combined analysis. Abbreviation: FYLD, Flour yield (%); HARD, Hardness index (%); MLRW, Midline right width (%); MLTW, Midline tail width (%); PROT14, Protein at 14% moisture basis (%). On X-axis is chromosome names, and on Y-axis is associated -log10(p) value. Red dotted line (y = -log10(p) = 7.0) is threshold limit for declaring significant marker-trait association.

Table 2.6. QTL associated with end-use quality from combined environment data

Traits / Chrom †	Position (bp)	Markers	-log10(p) ‡	R^2 (%) §	Effect ¶	Env#
MLRW						
1B	5926	3453826_1bs_3043	7.42 - 7.71	0.12 - 0.13	C > t > CT: -1.1 > 2.07	**IRR**, COMB
1B	5932	3453826_1bs_3226	7.38 - 7.57	0.12 - 0.12	G > t > GT: -1.02 > 2.1	**IRR**, COMB
TAILW						
1B	5923	3453826_1bs_3023	7.1 - 8.01	0.11 - 0.12	c > G > CG: 2.3 > -0.9	**16BI**, COMB
1B	5926	3453826_1bs_3043	7.70 - 7.78	0.11 - 0.12	C > t > CT: -0.9 > 2.6	16BI, **COMB**
1B	5932	3453826_1bs_3226	8.02 - 8.19	0.13 - 0.13	G > t > GT: -0.8 > 2.9	16BI, **COMB**
1B	6314	3434158_1bs_9081	7.1 - 8.25	0.09 - 0.12	a > G: 2.8	**16BD**, COMB
PROT14						
4B	57492	4860661_4bs_1872	7.21 - 10.50	0.12 - 0.18	g > T > GT: 2.5 > 2.4	**IRR**, COMB
FYLD						
5D	75878	1477005_5ds_2010	7.69-14.32	0.11 - 0.23	c > T: -3.27	14EP4, 14EP5, 15EP3, 15EP5, 16BD, 16BI, DRY, IRR, **COMB**
5D	75899	2770151_5ds_4035	7.03-7.98	0.1 - 0.11	a > C: -2.96	**14EP4**, COMB
5D	75906	2773392_5ds_1206	9.32-15.04	0.14 - 0.24	c > T: -4	14EP4, **14EP5**, 15EP3, 15EP5, DRY, IRR, COMB
5D	75910	2773392_5ds_1238	7.63-15.78	0.11 - 0.26	A > g: 3.91	14EP4, **14EP5**, 15EP3, 15EP5, 16BD, 16BI, DRY, IRR, COMB
5D	75911	2773392_5ds_1412	9.32-15.05	0.14 - 0.24	c > T: -4	14EP4, **14EP5**, 15EP3, 15EP5, DRY, IRR, COMB
5D	75917	2736392_5ds_5233	8.9-16.44	0.13 - 0.27	g > T: -4.7	14EP4, 14EP5, 15EP3, 16BI, 16CLI, DRY, **IRR**, COMB
5D	75953	2739337_5ds_2304	7.11-7.95	0.11 - 0.12	G > t: -2.47	14EP5, **COMB**
5D	75978	2745573_5ds_3677	7.37-14.13	0.11-0.22	A > g: 3.73	**14EP4**, 14EP5, 15EP3, **16BI**, 16CLI, DRY, IRR, COMB
5D	75987	2781671_5ds_9179	7.03-7.21	0.09-0.1	A > g: 3.68	14EP4, IRR, **COMB**
5D	75989	2781671_5ds_9219	7.03-7.21	0.09-0.1	g > T: -3.68	14EP4, IRR, **COMB**
5D	75991	2781671_5ds_9235	7.03-7.21	0.09-0.1	C > g: 3.68	14EP4, IRR, **COMB**
5D	75992	2781671_5ds_9443	7.03-7.21	0.09-0.1	A > c: 3.68	14EP4, IRR, **COMB**
5D	75993	2781671_5ds_9461	7.03-7.21	0.09-0.1	C > t: 3.68	14EP4, IRR, **COMB**
5D	75997	2781671_5ds_9472	7.18-7.33	0.1-0.11	c > G: -3.6	**IRR**, COMB
5D	76010	2774182_5ds_7304	7.23 - 10.6	0.1 - 0.16	A > c: 4.32	14EP4, 14EP5, 15EP3, 15EP5, 16CLI, DRY, IRR, **COMB**
HARD						
5D	75878	1477005_5ds_2010	10.4 - 15.2	0.16 - 0.25	c > T: -12.95	14CH, 14EP4, **15EP4**, 14EP5, 15EP3, 15EP5, 16BD, 16BI, 16CLI, DRY, IRR, COMB
5D	75899	2770151_5ds_4035	7.66 - 8.1	0.11 - 0.12	a > C: -12.27	15EP3, DRY, **COMB**
5D	75901	2765676_5ds_2839	7.46 - 7.86	0.12 - 0.13	c > T > CT: -22.4> -7.4	**15EP3**, COMB
5D	75906	2773392_5ds_1206	12.43 - 16.92	0.19 - 0.28	c > T: -17.8	14CH, 14EP4, 15EP4, 14EP5, **15EP3**, 15EP5, 16BD, 16BI, 16CLI, DRY, IRR, COMB
5D	75910	2773392_5ds_1238	13.02 - 17.84	0.2 - 0.3	A > g: 17.68	14CH, 14EP4, 15EP4, 14EP5, **15EP3**, 15EP5, 16BD, 16BI, 16CLI, DRY, COMB
5D	75911	2773392_5ds_1412	12.43 - 16.92	0.19 - 0.28	c > T: -17.8	14CH, 14EP4, 15EP4, 14EP5, **15EP3**, 15EP5, 16BD, 16BI, 16CLI, DRY, IRR, COMB
5D	75917	2736392_5ds_5233	13.82 - 18.23	0.22 - 0.32	g > T: -21.2	14CH, 14EP4, **15EP4**, 14EP5, 15EP3, 15EP5, 16BD, 16BI, 16CLI, DRY, IRR, COMB
5D	75953	2739337_5ds_2304	7.1 - 9.6	0.1 - 0.15	G > t: -9.2	14EP4, 15EP4, 15EP3, 15EP5, 16BD, 16BI, 16CLI, DRY, **IRR**, COMB

Table 2.6 Continued

5D	75978	2745573_5ds_3677	11.78 - 18.9	0.18 - 0.33	A > g: 18.5	14CH, 14EP4, **15EP4**, 14EP5, 15EP3, 15EP4, 15EP5, 16BD, 16BI, 16CLI, DRY, IRR, COMB
5D	75986	2781671_5ds_9157	7.23 - 8.41	0.11 - 0.13	A > c: 15.7	14EP4, 15EP3, **15EP4**, 15EP5, 16CLI, IRR, COMB
5D	75987	2781671_5ds_9179	7.34 - 9.3	0.11 - 0.14	A > g: 17.5	14CH, 14EP4, 14EP5, 15EP3, 15EP4, **15EP5**, 16BD, 16BI, 16CLI, DRY, IRR, COMB
5D	75989	2781671_5ds_9219	7.34 - 9.3	0.11 - 0.14	g > T: -17.5	14CH, 14EP4, 14EP5, 15EP3, 15EP4, **15EP5**, 16BD, 16BI, 16CLI, DRY, IRR, COMB
5D	75990	2781671_5ds_9223	7.23 - 8.41	0.11 - 0.13	c > G: -15.7	14EP4, 15EP3, **15EP4**, 15EP5, 16CLI, IRR, COMB
5D	75991	2781671_5ds_9235	7.34 - 9.3	0.11 - 0.14	C > g: 17.5	14CH, 14EP4, 14EP5, 15EP3, 15EP4, **15EP5**, 16BD, 16BI, 16CLI, DRY, IRR, COMB
5D	75992	2781671_5ds_9443	7.34 - 9.3	0.11 - 0.14	C > g: 17.5	14CH, 14EP4, 14EP5, 15EP3, 15EP4, **15EP5**, 16BD, 16BI, 16CLI, DRY, IRR, COMB
5D	75993	2781671_5ds_9461	7.34 - 9.3	0.11 - 0.14	C > g: 17.5	14CH, 14EP4, 14EP5, 15EP3, 15EP4, **15EP5**, 16BD, 16BI, 16CLI, DRY, IRR, COMB
5D	75997	2781671_5ds_9472	7.33 - 8.93	0.11 - 0.13	c > G: -16.4	14EP4, 15EP3, 15EP4, **15EP5**, IRR, 16CLI, COMB
5D	76005	2781025_5ds_24421	8.19 - 11.85	0.12 - 0.18	C > t: 20.6	14CH, 14EP4, 14EP5, 15EP3, 15EP4, **15EP5**, 16BD, 16BI, 16CLI, DRY, IRR, COMB
5D	76006	2781025_5ds_24425	8.19 - 11.85	0.12 - 0.18	C > t: 20.6	14CH, 14EP4, 14EP5, 15EP3, 15EP4, **15EP5**, 16BD, 16BI, 16CLI, DRY, IRR, COMB
5D	76010	2774182_5ds_7304	7.3 - 11.8	0.11 - 0.19	A > c: 18.2	14CH, 14EP4, 14EP5, 15EP3, 15EP4, **15EP5**, 16BD, 16BI, 16CLI, DRY, IRR, COMB
5D	76053	2745020_5ds_15344	7.16 - 8.01	0.12 - 0.13	A > c > AC: 20.4 > 6.8	14EP4, 14EP5, 15EP3, **15EP4**, 16BD, DRY, COMB
5D	76054	2745020_5ds_15346	7.16 - 8.01	0.12 - 0.13	A > c > AC: 20.4 > 6.8	14EP4, 14EP5, 15EP3, **15EP4**, 16BD, DRY, COMB

†Trait and chromosome abbreviation, FYLD, flour yield (%); HARD, hardness index (%); MLRW, midline right width (%); PROT14, flour protein at 14% moisture basis; TAILW, midline tail width (%)

‡ range of -log10(p) value across multiple environments. When a single value is present, the marker for corresponding trait is expressed only in single environments

§ range of R^2 (%) across multiple environments. When a single value is present, the marker for corresponding trait is expressed only in single environments

¶Genotypic effects of alleles at that loci are based on combined environment analysis; lower case represents minor allele, upper case allele represents major allele, negative value means reduction in trait value, positive value means enhancement of the trait. A class with lowest frequency is set to zero effect, then the other genotype effects are given as deviations between their estimated values and the lowest frequency class after correcting for population structure and relationship matrix. For example, c > G > CG: 1.9 > -1.02, heterozygous class has the lowest frequency, GG class has value 1.02 less than heterozygous class, CC class has value 1.9 higher than heterozygous class. So, class GG has 1.9- (-1.02) less than CC class.

Environment abbreviation, 14CH, 2014 Chillicothe, TX; 14EP4, 2014 Etter pivot (75% ET), TX; 14EP5, 2014 Etter pivot (100% ET), TX; 15EP3, 2015 Etter pivot (60% ET), TX; 15EP4, 2015 Etter pivot (75% ET), TX; 15EP5, 2015 Etter pivot (100% ET), TX; 16BD, 2016 Bushland Dry, TX; 16BI, 2016 Bushland Irrigated, TX; 16CLI, 2016 Clovis Irrigated, NM; DRY, data averaged over dry environments (i.e. 14CH, 15EP3, 16BD); IRR, data averaged over irrigated environments (i.e. 14EP4, 14EP5, 15EP4, 15EP5, 16BI, 16CLI); COMB, data averaged over all the locations.

BOLD environments represent environments with maximum -log(p) value and R^2 (%). UNDERLINDED environments represents minimum -log(p) value and R^2(%).

Significant marker-trait association were expressed in all the environments from individual environment analysis. Variance explained by markers ranged from 9.33 % in 16BI for TAILW to 32.5 % in 15EP4 for HARD in individual environment analysis (Table A1 & A2). From single trait analysis, association were significant for FYLD, HARD, MLRW, GMOIST, PROTdb, SKW, TAILW, TOL, WABS (Table A2). In combined analysis, similar variation range was found with 9.5 % variation for HARD to 31 % for TAILW (Table 2.6). In this analysis, only five traits, FYLD, HARD, MLRW, TAILW, and PROT14 were significantly present above threshold limit. Markers for FYLD, HARD, MLRW, TAILW, and PROT14 explained up to 27 %, 33 %, 13 %, 13% and 18 % variation, respectively. Minor allele a single locus normally reduced the flour yield up to 4.7 % and hardness index up to 22.4. Major allele at a single locus increased FYLD up to 4.32 % and HARD up to 20.6. Similar pattern for allele effect was found for MLRW. Positive effect was imparted by major allele, up to 2.1 % for MLRW.

DISCUSSION

Genetic variability that were present in the ancient wheat gene pools are lost due to domestication as well as selection process that skyrocketed after green revolution. Heavy reliance on elite-by-elite cross to create new germplasm has led to a genetic pool with reduced diversity (Hao et al., 2011). These factors have contributed up to 69 % loss in genetic diversity in wheat (Haudry et al., 2007). To overcome the narrow genetic base, and continued pressure from biotic and abiotic stress, breeders are constantly looking for new source of genetic variation in wheat germplasm. Synthetic wheat is a promising source for improving qualitative and quantitative traits in wheat (Ogbonnaya et al., 2013). In CIMMYT huge task of bringing back lost genetic diversity was carried out in 1980's (Mujeeb-Kazi et al., 1996; Warburton et al., 2006). Durum wheat were crossed with Ae. tauschii to create synthetic hexaploid wheat (SHW) or primary synthetics (PS). Primary synthetics are characterized by higher grain yield than elite varieties primarily due to improvement in yield components (Warburton et al., 2006). However, SHW are low yielding and have poor agronomic and quality traits (Trethowan and Ginkel, 2009). Backcrossing of primary synthetics with elite lines is reported to have better agronomic performance and end-use quality traits (Lopes and Reynolds, 2011).

Evaluating QTL across several environments conditions is essentials to achieve consistent and validated QTL, which is the important basis for dissecting the candidate genes further. In the present study we explored SDW from end-use quality traits perspective. Combined ANOVA shows significant genotypic difference present for all the traits analyzed. Genetic diversity of primary synthetics and this population was accessed across three sub-genomes. SDW had 32.2%, 36.8%, and 31% marker polymorphism compared to biparental population of the two TAM elite cultivars where 43.2%, 42.5% and 14.4% marker polymorphisms were present. Molecular analysis of these SDW lines has indicated improvement in the genetic diversity of bread wheat genome (Dreisigacker et al., 2008).

Synthetic derived wheat has bigger kernel diameter and increased kernel weight (Cooper et al., 2012; Reddy, 2015). Uniformly large, plump and vitreous seed is one the quality requirement for millers and bakers. Kernel weight and kernel width both are positively related to flour yield. Larger kernel tends to be associated with a higher flour yield than kernel dimension (Breseghello and Sorrells, 2006). We found significantly positive but weaker relationship between KW and KD with FYLD using combined data. Kernel diameter and weight has significantly stronger correlation and both the traits are also highly heritable. High, significant correlation between hardness index and flour yield is also observed and both the traits are highly heritable. It is easier to select these traits phenotypically and simultaneous improvement of correlated traits is possible. Significant markers that are associated with flour yield are also associated with hardness index. High heritability of these traits means significant shift in the mean performance of these traits can be achieved through selection. Mixograph traits were highly correlated, this could be because all these traits explain gluten strength and mostly controlled by same locus.

A careful choice of the biometrical model is pivotal in association mapping and greatly depends on the underlying population structure and relatedness of the germplasm used in the study (Stich et al., 2008; Zhao et al., 2007). Because population structure and kinship matrix are estimated with marker data, overcorrection for population stratification can result in a low power to detect QTL (Wurschum et al., 2011). Inability to account for population structure and genetic relatedness may result in spurious marker-trait associations (Gupta et al., 2010). Population structure, kinship and PCA varies with populations, traits, or both (Sun et al., 2010). Mean significant deviation (MSD) helps to select best model and parameters in the given model. One effective strategy to address this problem is the mixed linear model (MLM) suggested by Yu et al. (2006) based on the chosen Q-matrix derived from STRUCTURE and the kinship-matrix from SPAGeDi. Our analysis also supports the choice of population structure and kinship while doing marker-trait association. Determining number of subpopulations is not explicitly understood. Principle component analysis is classic way of figuring number of clusters. PCA of the AMPSY population revealed two subpopulations. Since percentage of variance explained by PC1 and PC2 were 27 % and 7%, these higher percentage suggest major population structure present in our population. PC1 captured variation due to maternal pedigree, while PC2 captured the variation created due to backcross i.e. percentage of in the final product. Kinship coefficient K_{ij} of two individuals i and j are the probability of two alleles, one drawn from i and the other drawn from j are identical-by-descent (IBD). The slight K_{ij} values observed between several pairs of wheat lines in this study clearly point to the presence of family structures. Accounting for population structure and kinship does not avoid false positives due to pleiotropy, multiple casual factors or epistasis.

End-use quality trait is must-have traits to any wheat breeding. End products from wheat flour ranges from noodles, cookies, cake, bread and so on. Increasing population is relying on wheat for their daily diet. Increasing urban population means increased demand for variety of wheat products. Increasing awareness among people and significantly higher rural population in Indian subcontinent is depending on wheat flour for chapati (flat bread). Hardness index is an essential measurement for breeders, producers, millers, and bakers and is used primarily to determine the suitability of different wheat varieties for various end-use products. Hard wheat is mainly used for bread whereas soft wheat is used for cookies. Hardness is controlled by a single locus Ha on distal part of chromosome 5DS that controls puroindoline (*Pina* and *Pinb*) and grain softness protein (*Gsp-1*) genes (Gautier et al., 1994; Giroux and Morris, 1998). Wild type *Pina* and *Pinb* i.e. *Pina-D1a* and *Pinb-D1a* gives soft grain texture. Point mutation of *Pina-D1a* gives *Pina-D1b*, and mis-sense mutation of *Pinb-D1a* give rise *Pinab-D1b*. Mutation in one of the wild alleles or both gives hard grain texture. Durum wheat do not have D genome and is hardest wheat of all. Different mutation has been reported to cause different degree of kernel hardness in wheat. *Pina-D1b*/*Pinb-D1b* > *Pina-D1b*/*Pinb-D1a* > *Pina-D1a*/*PinbD1b* > *Pina-D1a*/*Pinb-D1a* imparts hardness in declining order; left being the hard and the right most being the soft kernel (Rasheed et al., 2016). We identified 22 markers significantly associated with hardness index. Physical location of these markers was very close to *Pina* and *Pinb* on Ha locus on the short arm of chromosome 5D. *Pina-D1* and *Pinb-D1* are at 3.5 Mb on IWGSC RefSeq v1.0, which is very close to 2773392_5ds_1206, one of the markers associated with hardness index at 2.2 Mb (Rasheed et al., 2016). Interclass hybridization between soft and hard wheat demonstrated that the hardness locus *Pinb* on 5D chromosome had a strong influence on flour yield (Campbell et al., 2001). Flour yield, or the percentage of flour from a given quantity of grain, is of great importance to flour milling companies. It can be increased through either enhancement of techniques in the milling process or through the development of varieties with higher flour yield. We identified 17 markers significantly associated with flour yield on chromosome 5D. These markers are mapped in 0.34-9.33 Mb region on IWGSC RefSeq v1.0. Since location of these markers are close to *Pina* and *Pinb* gene, it could be the effect from these loci. *Pinb-D1b* increase flour yield, higher loaf volume and lower ash (Hogg et al., 2005). In spring wheat RIL genotyped with 116 DArT markers, QTL for HARD was detected on chromosome 5D (Tsilo et al., 2011). Arbelbide and Bernardo (2006) reported QTL for HARD on chromosome 5D. Crepieux et al. (2005) detected significant QTL for HARD on chromosome 5D.

Mixograph tells protein quality, which is predictive of baking quality. Longer Midline peak times (how longer it took to develop dough) and wider midline peak width indicates stronger dough. Midline right width is indicative of dough tolerance to overmixing (Miles et al., 2013). Wider MRLW means tolerance to gluten overmixing even after peak. The ascending and descending slopes are critical parameter in the interpretation of the mixograph as they indicate mixing tolerance or stability (MMST). Gentler slope is favorable as it implies greater resistance to overmixing. The majority (90%) of the wheat kernel protein is composed of gluten. Which is further composed of polymeric, insoluble glutenins (40-50%) and monomeric, soluble gliadins (30-40%) (Lindsay and Skerritt, 1999). Glutenin is further classified into high molecular weight glutenins sub-unit (HMW-GS) and low molecular weight glutenins sub-unit (LMW-GS). HMW-GS encoded by the *Glu-A1, Glu-B1* and *Glu-D1* loci on chromosome 1A, 1B, and 1D respectively. LMW-GS are encoded by *Glu-A3, Glu-B3,* and *Glu-D3* loci on the short arm of chromosome 1A, 1B and 1D, respectively (Payne, 1987). Gliadins are encoded by *Gli-A1, Gli-B1,* and *Gli-D1* loci on the short arm of chromosome 1A, 1B, and 1D, respectively. The allelic variability at these loci impacts the protein functionality and defines the end-use quality traits of wheat. We identified three common markers, 3453826_1bs_3023, 3453826_1bs_3043, 3453826_1bs_3226 for MLRW and TAILW within 20 bp interval on the short arm of chromosome 1B. These markers are at 17.1 Mb region and 3434158_1bs_9081 marker uniquely associated with TAILW, is at 30.4 Mb region. Reif et al. (2011) mapped wmc419 on chromosome 1B at 31.8 cM for protein content and sedimentation volume. This marker was mapped very closely to the chromosomal regions of glutenin and gliadin-related genes at 52.3 Mb region on IWGSC RefSeq v1.0. Mann et al. (2009) mapped QTLs for grain protein content, Bx subunit of *Glu-B1*, MLPT, MLPW, LMW-GS on chromosome 1BS using Australian wheat population. Suprayogi et al. (2009) identified GPS QTL on 1BS on durum DH population. Li et al. (2009) found SSD QTL on chromosome 1BS, region like Reif (2009). QTL for MLPT was detected on chromosome 1B, with significant additive genetic effects (Ocheya, 2016). Crepieux et al. (2005) reported significant QTL for dough strength on homoeologous region of chromosome 1A, 1B and 1D near the high molecular weight glutenin loci. QTL for curve widths were mapped on chromosome 1A and 1D (Ocheya, 2016). Although there is no direct match of QTL position for studies using different population and markers, genomic regions on chromosome 1 seem to be important for dough strength. In addition, the MTXW QTL on chromosome 1A was detected in all the individual environments which further support environment non-specificity for this QTL. The QTL linked to mixing tolerance was detected only in a multi-trait model on chromosome 1D.1, consistent with previous studies although the QTL position could be different (Huang et al., 2006; Sun et al., 2008). The magnitude of the R^2 and the effect size were relatively low. QTL collocated on 1B include MMST, MPV, MPW, and MRW ((Ocheya, 2016).

CONCLUSION

In the present work, use of synthetic derived wheat line increased the overall diversity and especially maintained D-genome diversity. Two population structure were identified with the help of a set of unlinked markers. Twenty-seven markers were uniquely associated with flour yield, hardness index, flour protein, and mixograph trait after accounting for population structure and relatedness. From association analysis, genomic regions on chromosome 1B and 5D are important for end-use quality traits in wheat. Chromosome 1B is associated with mixograph traits like MLRW and TAILW, and chromosome 5D is associated with HARD and FYLD. The SNP associated with FYLD, HARD, MLRW, TAILW and PROT14 could be targeted in MAS for end-use quality traits and for future wheat breeding work.

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CHAPTER III

LINKAGE MAPPING OF END-USE QUALITY IN TAM WHEAT

INTRODUCTION

Successfulness of a breeding program is governed by the development of cultivars with higher yield, superior end-use quality and better adaptability to wider range of growing environments. Wheat grown in the Southern High Plains is under continuous threat of drought stress and adversely affecting end-use quality (Bekes et al., 2001). End-use quality test is now an inseparable part of selection process besides grain yield. End-use quality traits referred here imply characteristics of the wheat-flour derived food products. Different methods are used to quantify end-use quality traits depending on wheat classes. Based on kernel texture, wheat is categorized into hard and soft classes. Hard wheat is characterized by strong gluten, extensive starch damage during milling, and high-water absorption, while soft wheat tends to have weaker gluten and low starch damage and water absorption (Breseghello and Sorrells, 2006). In general, end-use quality traits are evaluated by physical, functional, biochemical and rheological assays.

Several characteristics are measured to predict bread making quality. These include hardness index, flour protein content, water absorption, flour paste viscosity, and dough resistance. Kernel properties including single kernel weight, diameter, moisture, and hardness are needed beforehand while setting milling machine. Flour properties are needed for determining the amount of water to be added to dough. Millers and bakers use mixograph to determine the suitability of dough to bread-making (Primard et al., 1991). To reproduce the similar results as millers and bakers, breeding programs utilized small-scale testing equipment to quantify the end-use quality traits of breeding lines. The US wheat breeding programs also rely heavily on 10g-mixograph to discriminate end-use performance of breeding lines since this method requires 8 min or less for relatively a small amount of flour (Liang et al., 2010)

End-use quality traits are primarily under genetic control. Major wheat storage protein gluten is classified into glutenin and gliadins based on solubility and peptide structure. The glutenin is further composed of high molecular weight glutenin subunit (HMW-GS) and low molecular glutenin subunit (LMW-GS) (Payne, 1987). HMW-GS is encoded by *Glu-1* orthologous genes on the long arm of chromosome 1A, 1B, and 1D (Payne, 1987). LMW-GS is encoded by *Glu-3* orthologous genes on the short arm of chromosome 1A, 1B, and 1D (Gupta et al., 1989). Gliadin protein is encoded by the Gli-1 and Gli-2 gene on the short arm of chromosome 1A, 1B, and 1D, and Gli3 on the short arm of chromosome 6A, 6B, and 6D (Payne, 1987). However, almost half the phenotypic variation in dough resistance is explained by the main and two-way interaction effects of the *Glu-1* and *Glu-3* orthologous genes (Eagles et al., 2002). In addition to glutenin protein-encoding regions, Ha locus on the short arm of chromosome 5D is important for bread-making quality of hard red winter wheat (HRWW). Two genes *Pina-D1* and *Pinb-D1* at Ha locus encodes the puroindoline (Pin) protein *Pina* and *Pinb* (Giroux and Morris, 1998), with wildtype (*Pina-D1a* and *Pinb-D1a*) resulting in softer wheat. While null mutation and mis-sense mutation (*Pina-D1b*, and *Pinb-D1b*) impart harder texture in hard wheat (Rasheed et al., 2016).

End-use quality traits are influenced by genotypic, environmental and genotypic-by-environmental (G×E) factors. Environmental factors affect most of the end-use quality traits than genotypic factors (Rozbicki et al., 2015b). The strong effect of year and location on water absorption, and dough development respectively is documented, certain quality traits like hardness, flour yield, Zeleny sedimentation value are highly influenced by the genotype (Carson and Edwards, 2009; Rozbicki et al., 2015a; Yong et al., 2004). Multi-environment trials enable us to partition phenotypic variation in end-use quality traits into genotypic, environmental and G×E terms.

Even though breeding program utilizes these small-scale assessment methods, it can still be expensive, laborious and require quantities of grain more than that available at the early stages of a breeding cycle. Which pushes end-use quality trait testing down towards advanced generation in breeding pipeline. Due to the greater influence of environmental variable (field and lab) on end-use quality traits, it may reduce the heritability of phenotypic quality selection, making it further inefficient. With the aid of diagnostic molecular markers, we can test end-use quality trait in the early generation of breeding cycles as well as avoid the environmental influence. In the present study, we used molecular markers from 90K Illumina Infinium array single nucleotide polymorphism (SNP) and double digest restriction-site associated DNA sequencing (ddRADSeq) to genotype 124 RIL lines derived from TAM 112/TAM 111. The objective of this study was to understand and identify the genetic components controlling end-use quality trait of wheat. In the multi-environment trials of winter wheat in crop year 2013 and 2014, 16 traits were investigated that characterize grain, flour and dough quality. The complex genetic basis of wheat end-use quality trait was analyzed using QTL IciMapping software with inclusive composite interval mapping (ICIM) mapping function.

MATERIALS AND METHODS

Populations and trials

A recombinant inbred line (RIL) population of 124 F5:7 lines from the cross of TAM 112 and TAM 111 was generated to map end-use quality traits. TAM 111 and TAM 112 are both well adapted HRWW in the Southern Great Plains of the United States, developed by Texas A&M AgriLife Research (Lazar et al., 2004; Rudd et al., 2014). Both parents are identical in terms of glutenin-gliadin ratio, high molecular weight glutenin subunit (HMW-GS) to low molecular weight glutenin subunit (LMW-GS) ratio. Overall, TAM112 with *Glu-D1* subunit 5x+10y, has better milling and baking quality than that of TAM 111 with *Glu-D1* subunit 2x+12y (Jondiko et al., 2016). The RIL plus parents were planted in Etter, TX (35° 51' N, 101° 58' W), and Chillicothe, TX (34° 15' N, 99° 30' W) in the year 2013, and 2014. A total of seven environments (year-location) were planted: 2013 Etter 40% of evapotranspiration (ET) demand (13EP2), 2013 Etter 60% ET demand (13EP3), 2013 Etter 75% ET demand (13EP4), 2013 Etter 100% ET demand (13EP5), 2014 Chillicothe dry (14CH), 2014 Etter 75% ET demand (14EP4), 2014 Etter 100% ET demand (14EP5). Dry environment consisted of 13EP2, 13EP3, and 14CH while irrigated environment consisted of 13EP4, 13EP5, 14EP4, and

14EP5. All trails were replicated twice in alpha-lattice design, and three occurrences of each parent in a replication. Plot dimension was 15 feet long and 5 feet wide on the dry environments and 10 feet long and 5 feet wide on the irrigated environments with 0.3 meter between plots. Standard agronomic practices were carried out for each environment.

Grain quality evaluation

End-use quality trait phenotyping was performed on sample from a single replication form each environment at Texas A&M Cereal Quality Lab, College Station, TX. From each genotype, 30g and 80g of clean samples was drawn. The former was for single kernel characterization, and the latter for milling, near infra-red, and dough rheological studies.

Single Kernel Characterization System (SKCS)

Kernel properties were determined using 30g of samples in SCKS 4100 instrument (Perten Instruments, Hagersten, Sweden). It measured the hardness index (HARD), single kernel diameter (DIAM), single kernel weight (SKW) and kernel moisture (GMOIST). Hardness index is measured on 0-100 scale, 0 being the soft kernel and 100 being the hard kernel. DIAM, SKW, and GMOIST were expressed in mm, mg, and %, respectively.

Flour Milling

Based on grain moisture content from SKCS 4100, 80g of clean seeds was tempered for 24 hours to 14 % moisture content. Samples were soaked in a flask and kept on a shaker for 60 mins. Soaked samples were kept overnight and milled using the

Barbender Quadramat Jr. Precision laboratory roller mill (Barbender Instruments, South Hackensack, NJ, USA). Flour weight (FWT) (g) and flour yield (FYLD) (%) were recorded for each genotype.

Near infra-red (NIR)

Protein and moisture content of the milled flour were determined by third generation diode array near infra-red spectroscopy (NIR), model DA 7250 (Perten Instruments, Hagersten, Sweden). Flour protein content at 14 % moisture (PROT14) was determined simplicity plus software v2.86, a GUI program attached with NIR instrument. Flour moisture (FMOIST) were expressed in percentage term. The amount of distilled water added to the flour was determined based on AACC method 54-40.02 (AACC International, 2010). The percent optimum water absorption (WABS) was calculated using the formula WABS = 1.5 × Prot14 + 43.6, where PROT14 is protein at 14% moisture basis.

Dough properties

Dough mixing properties of flour at 14 % moisture basis were determined by mixogram (National Manufacturing Co. Lincoln, NE) with the aid of MixSmart software v1.0.404, based on AACC method 54-40.02 (AACC International, 2010). Midline variable of the mixograph at peak, two mins after the peak, eight minutes after the peak were noted. Time to reach the midline peak is recorded as midline peak time (MLPT), width of outer and inner envelop at midline peak as midline peak width (MLPW), height of the midline at peak as midline peak value (MLPV), area under the midline curve until peak time as midline peak integral (MLPI), width of outer and inner envelop at midline two minutes after peak as midline right width (MLRW), width of outer and inner envelop at midline eight minutes after peak as midline tail width (MLTW), and slope of midline between two minutes and eight minutes as midline right slope (MLRS) (Table 3.1). All mixing characteristics except mixing time are reported on a 100-mixograph unit scale (% height). Mixing time is measure on the minute scale and MLPI is expressed as %torque (TQ) x min.

Phenotypic data analysis

Descriptive statistics including means, minimum, maximum, standard deviation, and coefficient of variation were calculated to evaluate the variability of the examined traits. Each location-by-year combination was considered as a single environment. Raw data for all the traits within each environment were analyzed as an individual environment analysis. The phenotypic mean of a trait across environments was analyzed as single trait analysis. Best linear unbiassed predictor (BLUP) mean for all the traits combined across locations were analyzed as combined analysis. BLUP was calculated using a restricted maximum likelihood (REML) approach implemented in 'lme4' package on META-R (Alvarado et al., 2018). The current study had the spatial rep and therefore the analysis of variance (ANOVA) follows a statistical linear model of single environment analysis.

$$\mathrm{Y}_{ilp} = \mu + E_p + I_{l(p)} + G_i + \varepsilon_{ilp}$$

Where Y_{ilp} is the observed phenotypic value of the ith genotype in lth block in pth repetition, μ is the overall mean, E_p is the rep effect, $I_{l(p)}$ is the block effect, G_i is the genetic effect of ith genotype and $\varepsilon_{ilp}$is the residual term corresponding to a quasi-genotype-by-environment interaction (GEI). Combined analysis of variance (ANOVA) for all the traits was determined for the significance of genetic variance, phenotypic variance and genotype-by-environment interaction (GEI) components in each environment. In this context, the interaction of replication (environment in this case) with genotype (ε_{ilp}) was used as the error term to test the significance of genotypes. The ANOVA and significance were calculated using PROC MIXED with replication and incomplete block as random effect in SAS 9.4 (SAS Institute Inc., 2015). The variance components were calculated to estimate the share of the factors and their interaction in the total variability of the examined traits. The variance components were computed using PROC VARCOMP in SAS 9.4 (SAS Institute Inc., 2015). The entry-mean heritability estimate was calculated according to Fehr et al (1987) using the formula:

$$h^2 = \frac{\sigma_g^2}{\sigma_e^2/r + \sigma_g^2}$$

Where r is the number of replication (rep), σ2g is the genotype variance, and σ2e is the residual variance. PROC CORR in SAS was used to compute Pearson correlations (rP) based on the following formula:

$$r_P = \frac{Cov_{x,y}}{(\sigma_x^2\ \sigma_y^2)^{1/2}}$$

Genotyping and linkage map construction

DNA was isolated from young leaf tissue of each RIL using the cetyl trimethylammonium bromide (CTAB) method with modifications (Doyle and Doyle, 1990; Liu et al., 2013). DNA purification and quantification were conducted in the wheat genetics lab at Texas A&M AgriLife Research, Amarillo, TX. RIL lines along with parental DNA were genotyped with Illumina Infinium iSelect 90K array SNP. This population was also genotyped with double digest restriction-site associated DNA sequencing (ddRADSeq) method developed by Peterson et al (2012) with slight modification in Texas A&M AgriLife Research's Genomics and bioinformatics center, College Station, TX (Wang et al., 2014). SNP with significant segregation distortion and similarity index of one were eliminated. A total of 5948 polymorphic SNP, and GBS markers were mapped into 25 linkage groups covering 21 chromosomes using maximum likelihood (ML) algorithm, and minimum LOD score for linkage of 3 in JoinMap v4.0 software (Van Ooijen, 2006).

QTL analysis

One-dimensional scanning for mapping additive QTL, and two-dimensional scanning for mapping epistasis were undertaken using both the adjusted for multi-environment analysis and unadjusted data for single environmental analysis in the QTL IciMapping software (Wang et al., 2016). Unadjusted data from individual environment were ran as individual environment QTL analysis. Raw data for a trait across multiple environments were analyzed as multi-environment QTL analysis. The genetic position and effects of QTL were determined by integrated composite interval mapping (ICIM) function in QTL IciMapping for additive effect (ICIM-ADD) and epistasis effect (ICIM-EPI). Stepwise regression with a walking speed of 1cM for additive mapping (ICIM-ADD) and 5cM for epistasis mapping (ICIM-EPI) was set. Two flanking markers for ICIM-ADD and two pairs of flanking markers for ICIM-EPI were selected automatically to control for genetic background in additive and epistasis mapping. The probability for entering variables in stepwise regression of residual phenotype on marker variables was set at 0.001 for ICIM-ADD, and 0.0001 for ICIM-EPI. Threshold for declaring the presence of a QTL was determined through permutation analysis (n=1000) for each trait in each environment to obtain a 0.05 genome-wide probability level of Type I error. The QTL position was estimated as the point on the LOD curve with a peak score greater than the threshold. The QTL were designated according to guidelines in McIntosh et al. (2003) with a slight change as *QX.tamu.Y.N*, where x is a trait, tamu is Texas A&M University, Y is chromosome on which the QTL is located, and N is the unique QTL identifier given to genomic regions within 50 Mb of the QTL.

RESULTS

ANOVA and heritability

Sixteen end-use quality traits under four broad categories were analyzed in this study. Combined ANOVA showed highly significant differences (< 0.001) among lines for all the 16 traits except for midline peak integral (MLPI) (Table 3.1). All the environments, treated as pseudo-rep, were not significant even though it explained most of the variation for most of the traits. Traits with heritability ≤ 0.3 were categorized as lowly heritable, 0.4 – 0.6 as moderately heritable and > 0.6 as highly heritable traits. All the end-use quality traits were highly heritable (0.69- 0.95) except flour moisture (FMOIST) and midline right width (MRLW), which are moderately heritable (0.4-0.5). Hardness index (HARD) was highly heritable (0.93) with the mean of 64.7 %. Mean seed moisture content (GMOIST) of lines was 11.6% with heritability of 0.91.

Table 3.1. Analysis of variance, heritability and mean performance of end-use quality in linkage population (combined analysis)

Traits	Units	σ^2_{Geno}†	σ^2_{Rep}‡	$\sigma^2_{Iblk\ (Rep)}$§	σ^2_{Res}¶	$h^{2\#}$	$\bar{X}$±SD	TAM 112	TAM 111
Single kernel characterization system									
Hardness Index (HARD)	%	23.81**	75.52	0.89	11.60**	0.93	64.66 ± 9.97	68.15	63.17
Moisture (GMOIST)	%	0.016**	0.07	0.011**	0.011**	0.91	11.63 ± 0.32	11.74	11.61
Diameter (DIAM)	mm	0.002**	0.05	0.00	0.002**	0.84	2.44 ± 0.21	2.42	2.48
Single kernel weight (SKW)	mg	0.99**	28.39	0.35**	1.42**	0.84	26.15 ± 5.19	25.95	27.51
Milling									
Flour yield (FYLD)	%	2.06**	4.13	0.76**	2.96**	0.83	68.44 ± 3.08	68.76	69.15
Near infra-red									
Flour moisture (FMOIST)	%	0.002**	0.05	0.02**	0.015**	0.50	13.6 ± 0.29	11.74	11.61
Protein (14% moisture) (PROT14)	%	0.09**	2.60	0.09**	0.22**	0.75	14.29 ± 1.66	14.63	14.04
Ash (14% moisture) (ASH14)	%	0.00017**	0.00	0.0002**	0.0003**	0.77	0.45 ± 0.04	0.47	0.45
Water absorption (WABS)	%	0.17**	5.84	0.18**	0.54**	0.69	65.015 ± 2.49	65.38	64.72
Mixograph									
Midline peak time (MLPT)	min	0.77**	0.36	0.00	0.26**	0.95	3.92 ± 1.15	4.74	3.3
Midline peak width (MLPW)	%	4.74**	17.27	5.11**	20.78**	0.65	24.89 ± 6.86	23.21	25.18
Midline peak value (MLPV)	%	6.74**	36.32	8.07**	18.09**	0.71	59.46 ±8.5	60.77	62.37
Midline peak integral (MLPI)	%TQ x min	4.00	1138.80	12.42	634.29**	0.95	160.81 ± 49.79	197.96	137.02
Midline right slop (MLRS)	% min-1	0.55**	0.49	0.18	1.38**	0.71	-3.14 ± 1.59	-2.43	-3.6
Midline right width (MLRW)	%	2.99	26.41	28.92**	31.33**	0.40	16.32 ± 9.34	15.76	13.67
Midline tail width (MLTW)	%	7.05**	10.80	3.62**	9.71**	0.84	10.56 ± 5.18	13.82	8.64

† σ^2_{Geno}, genotypic variance

‡ σ^2_{Rep}, variance due to replication (environment) in percentage

§ $\sigma^2_{Iblk\ (Rep)}$, variance due to incomplete block nested within replication (environment) in percentage

¶ σ^2_{Res}, residual variance in percentage

\# h^2, entry-mean heritability

*, **, significant at 0.05, and 0.01 probability levels, respectively

On average kernel of RIL population was 2.4 mm, and heritability of 0.84. Similarly, the heritability of single kernel weight (SKW) was 0.84 with mean kernel weight of 26.15 mg. Flour yield (FYLD), expressed in percentage, was highly heritable (0.83) with mean 68.4% flour extraction. All near infrared (NIR) related traits were highly heritable except flour moisture. Protein at 14% moisture (PROT14) was highly heritable (0.75) with average flour protein of 14.3%. Midline peak time (MLPT), which is average time to the maximum dough consistency, was 3.92 minutes with heritability of 0.95. At the peak time, midline peak width (MLPW) had the heritability of 0.65 with an average width of 24.9%. Midline peak value (MLPV), which is the height of the midline at peak, was also highly heritable (0.71) with the average midline peak height of 59.5%. Midline tail width eight minutes after the dough development (MLTW) was highly heritable (0.84) with an average value of 10.6%. Mixing tolerance or midline right slope (MLRS) is the right slope after peak time had the mean slope of -3.1 % min-1 and heritability of 0.71. Mean flour moisture (FMOIST) was 13.6% with heritability of 0.5. Midline right width (MLRW), which is 2 minutes after peak time, was 16.3% with heritability of 0.40. Two parents were significantly differing for hardness index (HARD), flour moisture (FMOIST), protein at 14% moisture (PROT14), ash content at 14% moisture (ASH14), midline peak time (MLPT), midline peak integral (MLPI), and midline tail width (MLTW) (Table A4). Hardness index for the population ranged from 39.5% to 87.5%. Midline peak integral (MLPI) showed greatest variability from 62.92 – 294.8 % TQ x min-1. Transgressive segregation was observed for hardness index (HARD) towards TAM112, flour yield (FYLD) towards TAM 112, midline peak width

(MLPW) towards TAM 111, Midline right width (MLRW) towards TAM 112 and midline tail width (MLTW) towards TAM 112 (Table A4).

Pearson correlation

The phenotypic relationship between traits on combined data was determined using Pearson correlation coefficients (Table 3.2). Correlation coefficients ≤ 0.3 between two traits were categorized as low correlation, 0.4 - 0.6 as moderate correlation, and > 0.6 as high correlation. Single kernel weight (SKW) and kernel diameter (DIAM) showed highly significant (0.71) correlation suggesting line with bigger and plum seed always weigh heavier. Flour protein (PROT14) is nearly perfectly related to WABS and this relationship is significant in the positive direction (0.96). Given WABS is calculated using protein %, this relationship holds true. Midline peak time (MLPT) and midline peak value (MLPV) were also almost perfectly and significantly correlated (0.97). MLPT is also highly correlated with midline right slope (MLRS) (0.58), and midline tail width (MLTW) (0.77). Midline tail width (MLTW) showed positive and high correlation with midline peak integral (MLPI) (0.77) and midline right width (MLRW) (0.65). Most of the dough rheological traits were highly positively significantly related (Table 3.2). All the midline width traits at the different time (MLPW, MLRW, TAILW) were significantly correlated in the positive direction. Moderate and negative correlation was found between flour moisture (FMOIST) and ash content at 14% moisture (ASH14) (-0.43), hardness index (HARD) and midline peak width (MLPW) (-0.44), and midline peak value (MLPV) and midline right slope (MLRS) (-0.49).

Table 3.2. Correlation matrix for end-use quality traits for predicted means (BLUP) across environments

Traits [†]	HARD	GMOIST	DIAM	SKW	FYLD	FMOIST	PROT14	ASH14	WABS	MLPT	MLPW	MLPV	MLPI	MLRS	MLRW
GMOIST	0.13														
DIAM	-0.12	-0.02													
SKW	-0.29**	-0.13	0.71**												
FYLD	-0.09	-0.02	0.18*	0.12											
FMOIST	-0.28**	-0.36**	-0.01	0	0.23*										
PROT14	0.07	-0.37**	-0.09	-0.16	0.26**	0.35**									
ASH14	-0.13	0.03	0.02	-0.01	-0.06	-0.43**	0.02								
WABS	0.11	-0.38**	-0.11	-0.18*	0.24**	0.33**	0.96**	0.02							
MLPT	0.01	0.14	0.02	0.02	0.11	0.02	-0.07	0.07	-0.12						
MLPW	-0.44**	-0.13	0.06	-0.02	0.2*	0.2*	0.27**	0.07	0.24**	0.06					
MLPV	-0.31**	-0.09	0.05	-0.12	0.13	0.16	0.4**	0.15	0.41**	-0.15	0.53**				
MLPI	-0.06	0.08	0.03	0.02	0.13	0.07	-0.02	0.07	-0.06	0.97**	0.18*	-0.02			
MLRS	0.32**	-0.03	-0.06	-0.01	-0.12	-0.16	-0.16	0.04	-0.18*	0.58**	-0.2*	-0.49**	0.51**		
MLRW	-0.13	-0.1	0.06	0.07	0.05	0.05	-0.01	-0.01	-0.04	0.34**	0.61**	0.03	0.42**	0.3**	
MLTW	0.08	0.02	-0.01	0.01	-0.01	-0.07	0	0.02	-0.05	0.77**	0.31**	-0.08	0.77**	0.58**	0.65**

[†] HARD, hardness index; GMOIST, grain moisture; DIAM, kernel diameter; SKW, single kernel weight; FYLD, flour yield %; FMOIST, flour moisture; PROT14, flour protein at 14% moisture basis; ASH14, flour ash content at 14% moisture; WABS, water absorption; MLPT, midline peak time; MLPW, midline peak width; MLPV, midline peak value; MLPI, midline peak integral; MLRS, midline right slope; MLRW, midline right width; MLTW, midline tail width

*, **, significant at 0.05, and 0.01 probability levels, respectively

Positive and moderate correlation (r = 0.4-0.58) was found for PROT14 and MLPV, WABS and MLPV, MLPW and MLPV, MLRS and MLPI, MLRW and MLPI, and MLRS and MLTW.

QTL for Kernel Characteristics

The QTL for hardness index (HARD) were detected on chromosome 1A (*Qhard.tamu.1A*, at 13.8, 393.8 and 474.6 Mb), 1B (*Qhard.tamu.1B* at 7.2 Mb), 2D (*Qhard.tamu.2D* at 1.7 Mb), 4D (*Qhard.tamu.4D* at 62.8 Mb), and 7D (*Qhard.tamu.7D* at 72 Mb) both in individual environment (Table 3.3) and multi-environment trial analysis (Table 3.4). Additional QTLs were detected on chromosome 3A (*Qhard.tamu.3A* at 702.6 Mb) in 14CH, and on chromosome 7D (*Qhard.tamu.7D* at 175.9 Mb) in 13EP5 from individual environment analysis (Table 3.3). Similarly, two additional QTL was detected on chromosome 2B (*Qhard.tamu.2B* at 16.9 and 578.7 Mb), one on chromosome 5A (*Qhard.tamu.5A* at 688.3 Mb) from multi-trait environment analysis. All the QTLs on chromosome 1A at 13.8, 399.2 and 475.6 Mb explained 7.8%-33.9% of the variation in hardness index. High value allele (HVA) came from TAM 112 for QTLs in chromosome 1A, 1B, 2D, 4D, and from TAM 111 for QTLs in chromosome 3A, 5A, and 7D (Table 3.3). All the QTLs for hardness index showed significant QTL × Env (AE) interactions accounting for 2.44%-43.1%, and their effect ranged from 0.01 – 6.67 depending on environment and QTLs (Table A5)

Table 3.3. Significant end-use quality trait QTLs, additive effects detected in Individual environment analysis

Traits[†]	Envs [‡]	QTL name	QTL ID	Peak (cM)	LeftCI[§]	RightCI[¶]	Mb[#]	Peak SNP	LOD[††]	R^2[‡‡]	A[§§]	M-E[¶¶]
HARD	14EP4	*Qhard.tamu.1A.1*	1	10	9.5	11	13.8	IWB55537	15.60	31.33	3.73	Y
HARD	14EP5	*Qhard.tamu.1A.1*	1	10	9.5	11	13.8	IWB55537	14.72	29.32	4.03	Y
HARD	13EP4	*Qhard.tamu.1A.4*	4	55	53.5	56	393.8	3928641_1al_1202	9.22	14.90	1.75	Y
HARD	13EP3	*Qhard.tamu.1A.4*	4	56	55.5	57	399.2	3920586_1al_9412	4.46	11.16	1.65	Y
HARD	13EP2	*Qhard.tamu.1A.5*	5	61	60.5	62	474.6	IWB44485	3.62	7.76	1.29	Y
HARD	14CH	*Qhard.tamu.1A.5*	5	62	61.5	63	475.6	3974856_1al_3401	13.60	26.09	4.54	Y
HARD	13EP2	*Qhard.tamu.1B.7*	7	3	1.5	4.5	0.6	3473141_1bs_756	6.86	15.49	1.82	Y
HARD	13EP3	*Qhard.tamu.1B.7*	7	6	5.5	14	7.2	3285535_1bs_1678	7.07	19.75	2.18	Y
HARD	13EP4	*Qhard.tamu.1B.7*	7	6	5.5	11	7.2	3285535_1bs_1678	17.03	33.94	2.63	Y
HARD	13EP5	*Qhard.tamu.1B.7*	7	9	5.5	16	7.2	3285535_1bs_1678	9.50	25.16	2.84	Y
HARD	14EP4	*Qhard.tamu.1B.7*	7	6	5.5	14	7.2	3285535_1bs_1678	11.90	17.90	2.82	Y
HARD	14EP5	*Qhard.tamu.1B.7*	7	6	5.5	14	7.2	3285535_1bs_1678	8.60	14.37	2.82	Y
HARD	14EP4	*Qhard.tamu.2D.22*	22	20	11.5	23	1.7	IWB34642	3.79	5.15	1.51	Y
HARD	14CH	*Qhard.tamu.3A.27*	27	109	107.5	112	702.6	4365353_3al_191	4.61	7.81	-2.49	N
HARD	13EP2	*Qhard.tamu.4D.39*	39	11	8.5	12	62.8	2305880_4ds_1018	8.36	19.30	2.03	Y
HARD	14EP5	*Qhard.tamu.7D.72*	72	90	86.5	96	78.5	IWB44453	6.77	11.15	-2.49	Y
HARD	13EP4	*Qhard.tamu.7D.72*	72	97	93.5	100	84.3	3938880_7ds_2029	7.01	11.35	-1.52	Y
HARD	14CH	*Qhard.tamu.7D.72*	72	96	92.5	99	84.3	3938880_7ds_2029	7.17	12.95	-3.20	Y
HARD	14EP4	*Qhard.tamu.7D.72*	72	94	86.5	98	84.3	3938880_7ds_2029	4.06	5.36	-1.54	Y
HARD	13EP2	*Qhard.tamu.7D.72*	72	100	97.5	102	91.1	3891967_7ds_1529	4.24	9.10	-1.40	Y
HARD	13EP5	*Qhard.tamu.7D.73*	73	128	127.5	133	175.9	IWB27602	3.96	7.02	-1.54	N
GMOIST	13EP5	*Qgmoist.tamu.1B.7*	7	3	0	4.5	0.6	3473141_1bs_756	3.38	8.16	-0.05	Y
GMOIST	14CH	*Qgmoist.tamu.4B.37*	37	45	44.5	53	404.0	7040005_4bl_5774	3.34	7.25	0.06	N
GMOIST	13EP5	*Qgmoist.tamu.4D.39*	39	8	5.5	8.5	29.0	IWB30733	11.27	31.85	0.09	Y
GMOIST	14EP5	*Qgmoist.tamu.4D.39*	39	8	4.5	8.5	29.0	IWB30733	7.10	17.59	0.10	Y
GMOIST	14EP4	*Qgmoist.tamu.4D.39*	39	9	8.5	11	35.4	2305190_4ds_510	6.05	17.70	0.08	Y
GMOIST	14CH	*Qgmoist.tamu.4D.39*	39	10	8.5	12	62.8	2305880_4ds_1018	12.51	32.17	0.13	Y
GMOIST	13EP2	*Qgmoist.tamu.4D.42*	42	20	19.5	21	312.7	14410083_4dl_v2_5128	3.92	13.67	0.07	N
GMOIST	13EP4	*Qgmoist.tamu.4D.43*	43	27	24.5	29	408.8	IWA5751	4.02	13.77	0.07	N
GMOIST	14EP4	*Qgmoist.tamu.7D.72*	72	79	77.5	81	60.6	IWB35446	4.16	11.81	-0.06	Y
GMOIST	14EP5	*Qgmoist.tamu.7D.72*	72	79	77.5	81	60.6	IWB35446	3.66	8.76	-0.07	Y
DIAM	13EP2	*Qdiam.tamu.2D.24*	24	114	111.5	115	531.4	9852937_2dl_2983	5.14	17.46	0.03	Y
DIAM	13EP4	*Qdiam.tamu.2D.24*	24	113	111.5	115	531.4	9852937_2dl_2983	4.56	15.25	0.03	Y
DIAM	13EP5	*Qdiam.tamu.2D.24*	24	113	111.5	115	531.4	9852937_2dl_2983	4.28	14.63	0.03	Y
DIAM	13EP3	*Qdiam.tamu.5D.52*	52	21	18.5	21	385.6	4522185_5dl_458	4.94	12.40	-0.02	Y
DIAM	13EP3	*Qdiam.tamu.6A.54*	54	87	84.5	91	104.4	IWB23452	4.15	10.29	-0.02	Y
DIAM	14EP5	*Qdiam.tamu.7D.72*	72	85	84.5	90	72.9	IWA1247	4.26	14.43	0.03	N
SKW	14CH	*Qskw.tamu.1D.11*	11	12	10.5	14	8.6	IWA1788	3.79	10.06	0.56	N
SKW	13EP2	*Qskw.tamu.2D.24*	24	114	111.5	115	531.4	9852937_2dl_2983	3.50	10.79	0.35	Y
SKW	13EP4	*Qskw.tamu.2D.24*	24	113	111.5	115	531.4	9852937_2dl_2983	4.52	15.02	0.49	Y
SKW	13EP5	*Qskw.tamu.2D.24*	24	113	111.5	115	531.4	9852937_2dl_2983	4.95	12.81	0.81	Y

Table 3.3 Continued

SKW	14EP4	*Qskw.tamu.4D.42*	42	22	21.5	23	366.3	IWB10053	6.28	18.99	-0.91	Y
SKW	14EP5	*Qskw.tamu.4D.42*	42	22	21.5	23	366.3	IWB10053	3.39	11.20	-0.58	Y
SKW	13EP5	*Qskw.tamu.5B.51*	51	152	150.5	156	704.8	IWB53784	4.70	11.59	0.77	Y
SKW	14EP5	*Qskw.tamu.7D.72*	72	89	86.5	93	78.5	IWB44453	5.97	21.42	0.80	Y
FYLD	13EP2	*Qfyld.tamu.1A.5*	5	88	87.5	89	485.2	IWA4536	5.00	12.87	-1.11	N
FYLD	14CH	*Qfyld.tamu.4D.40*	40	13	11.5	14	109.8	2279925_4ds_1008	11.13	11.31	1.87	Y
FYLD	13EP5	*Qfyld.tamu.7D.74*	74	187	186.5	190	596.9	3395780_7dl_1754	4.17	11.78	-0.68	N
FMOIST	13EP3	*Qfmoist.tamu.2A.16*	16	29	28.5	33	36.8	IWB70473	5.14	15.47	-0.10	N
FMOIST	13EP2	*Qfmoist.tamu.2A.17*	17	136	135.5	137	742.1	6290829_2al_337	3.78	9.43	-0.05	N
FMOIST	13EP2	*Qfmoist.tamu.2D.23*	23	103	96.5	106	82.0	5329935_2ds_3804	5.28	13.86	0.06	Y
FMOIST	14CH	*Qfmoist.tamu.4D.39*	39	8	4.5	8.5	29.0	IWB30733	3.82	13.09	-0.07	N
PROT14	14EP4	*Qprot14.tamu.4D.39*	39	5	4.5	7.5	29.0	IWB30733	8.62	23.18	0.33	Y
PROT14	14EP5	*Qprot14.tamu.4D.40*	40	13	12.5	14	109.8	2279925_4ds_1008	34.64	27.26	0.75	Y
PROT14	14EP5	*Qprot14.tamu.4D.41*	41	18	17.5	19	182.6	2273804_4ds_1113	17.14	9.34	-0.44	Y
PROT14	13EP3	*Qprot14.tamu.4D.43*	43	28	25.5	29	445.5	IWB3336	4.38	10.41	-0.20	Y
PROT14	14EP4	*Qprot14.tamu.5B.50*	50	74	60.5	75	588.2	IWB36196	4.32	10.68	-0.23	Y
PROT14	14CH	*Qprot14.tamu.7B.68*	68	58	55.5	65	126.1	7950984_2bl_656	3.42	10.84	0.18	N
ASH14	14CH	*Qash14.tamu.2A.16*	16	93	92.5	94	684.1	6337088_2al_8303	6.21	12.61	-0.01	Y
ASH14	14CH	*Qash14.tamu.2A.17*	17	120	119.5	121	728.8	IWA1960	4.17	8.15	0.01	N
ASH14	14CH	*Qash14.tamu.2B.21*	21	133	130.5	134	730.6	7956824_2bl_4641	3.35	6.47	0.01	N
ASH14	13EP5	*Qash14.tamu.6B.58*	58	20	18.5	21	662.3	3252764_6dl_2803	3.86	17.38	-0.01	Y
ASH14	14EP4	*Qash14.tamu.6B.58*	58	20	17.5	21	662.3	3252764_6dl_2803	4.78	12.30	-0.01	Y
WABS	14EP4	*Qwabs.tamu.4D.39*	39	6	4.5	7.5	29.0	IWB30733	6.66	21.49	0.52	Y
WABS	14EP5	*Qwabs.tamu.4D.40*	40	13	12.5	14	109.8	2279925_4ds_1008	34.62	27.26	1.12	Y
WABS	14EP5	*Qwabs.tamu.4D.41*	41	18	17.5	19	182.6	2273804_4ds_1113	17.11	9.33	-0.66	Y
WABS	13EP3	*Qwabs.tamu.4D.43*	43	28	25.5	29	445.5	IWB3336	5.31	10.31	-0.30	Y
WABS	14CH	*Qwabs.tamu.7B.68*	68	58	55.5	65	126.1	7950984_2bl_656	3.42	10.84	0.27	N
MLPT	14CH	*Qmlpt.tamu.1A.3*	3	43	42.5	44	357.6	3966094_1al_942	5.63	6.31	-0.36	Y
MLPT	13EP2	*Qmlpt.tamu.1B.7*	7	4	3.5	4.5	1.4	3482114_1bs_10487	4.25	6.40	0.25	Y
MLPT	14EP4	*Qmlpt.tamu.1B.7*	7	7	5.5	17	7.2	3285535_1bs_1678	5.96	13.72	0.31	Y
MLPT	14EP4	*Qmlpt.tamu.1D.13*	13	58	57.5	59	412.0	IWB58572	14.99	34.64	0.50	Y
MLPT	13EP2	*Qmlpt.tamu.1D.13*	13	59	58.5	60	412.5	2207179_1dl_2124	23.86	54.60	0.74	Y
MLPT	13EP5	*Qmlpt.tamu.1D.13*	13	59	58.5	60	412.5	2207179_1dl_2124	11.25	37.85	0.72	Y
MLPT	13EP3	*Qmlpt.tamu.1D.13*	13	60	59.5	61	413.2	2236927_1dl_656	18.38	48.27	0.69	Y
MLPT	14EP5	*Qmlpt.tamu.1D.13*	13	60	59.5	61	413.2	2236927_1dl_656	15.31	39.15	0.54	Y
MLPW	14CH	*Qmlpw.tamu.1A.1*	1	6	3.5	6.5	9.2	IWB33789	8.29	24.11	-2.13	Y
MLPW	14EP4	*Qmlpw.tamu.1A.2*	2	21	20.5	22	230.0	3980487_1al_11151	11.51	35.10	-2.83	N
MLPW	13EP2	*Qmlpw.tamu.1A.5*	5	64	63.5	65	485.2	3894604_1al_116	4.76	17.03	-2.38	Y
MLPW	14EP5	*Qmlpw.tamu.1D.11*	11	16	14.5	17	10.4	1884715_1ds_1224	3.99	12.86	1.24	N
MLPV	13EP3	*Qmlpv.tamu.1A.1*	1	12	11.5	13	14.4	IWB10932	3.68	13.67	-2.49	N
MLPI	14EP4	*Qmlpi.tamu.1A.1*	1	10	9.5	11	13.8	IWB55537	25.31	30.65	-26.95	N
MLPI	13EP2	*Qmlpi.tamu.1A.2*	2	20	19.5	21	227.9	3904015_1al_2374	14.13	20.86	21.71	N
MLPI	14CH	*Qmlpi.tamu.1A.3*	3	43	42.5	44	357.6	3966094_1al_942	5.37	6.36	-13.57	Y

Table 3.3 Continued

Traits[†]	Envs [‡]	QTL name	QTL ID	Peak (cM)	LeftCI[§]	RightCI[¶]	Mbp[#]	Peak SNP	LOD[††]	R^2[‡‡]	A[§§]	M-E[¶¶]
MLPI	14EP5	*Qmlpi.tamu.1A.5*	5	61	60.5	62	474.6	IWB44485	5.45	8.29	-9.90	Y
MLPI	13EP3	*Qmlpi.tamu.1A.5*	5	62	61.5	63	475.6	3974856_1al_3401	3.82	4.24	-9.74	Y
MLPI	13EP3	*Qmlpi.tamu.1B.7*	7	4	3.5	4.5	1.4	3482114_1bs_10487	4.82	5.56	11.20	Y
MLPI	14EP4	*Qmlpi.tamu.1B.7*	7	9	5.5	18	7.2	3285535_1bs_1678	6.98	4.80	10.66	Y
MLPI	14EP5	*Qmlpi.tamu.1D.13*	13	58	57.5	59	412.0	IWB58572	19.43	36.98	20.90	Y
MLPI	14EP4	*Qmlpi.tamu.1D.13*	13	59	58.5	60	412.5	2207179_1dl_2124	23.51	17.14	20.13	Y
MLPI	13EP2	*Qmlpi.tamu.1D.13*	13	64	63.5	65	416.1	IWB35348	24.10	40.01	29.93	Y
MLPI	13EP3	*Qmlpi.tamu.1D.13*	13	64	63.5	65	416.1	IWB35348	24.12	42.44	30.81	Y
MLPI	13EP5	*Qmlpi.tamu.1D.13*	13	64	63.5	65	416.1	IWB35348	11.19	36.36	26.78	Y
MLPI	13EP3	*Qmlpi.tamu.3A.26*	26	66	63.5	68	608.4	IWA8374	4.80	5.59	-11.19	Y
MLPI	14EP5	*Qmlpi.tamu.5A.44*	44	25	22.5	26	17.2	1514513_5as_10557	4.98	7.15	9.26	Y
MLRS	13EP2	*Qmlrs.tamu.1B.7*	7	13	5.5	25	7.2	3285535_1bs_1678	4.61	16.32	0.74	Y
MLRS	13EP2	*Qmlrs.tamu.1D.13*	13	60	59.5	61	413.2	2236927_1dl_656	7.62	17.94	0.78	Y
MLRS	13EP3	*Qmlrs.tamu.1D.13*	13	66	65.5	68	418.5	2252364_1dl_16749	5.29	13.82	0.61	N
MLRW	14EP5	*Qmlrw.tamu.1A.1*	1	12	11.5	13	14.4	IWB10932	7.07	14.84	-1.45	Y
MLRW	14EP5	*Qmlrw.tamu.1D.13*	13	58	57.5	59	412.0	IWB58572	4.33	8.45	1.08	Y
MLRW	14EP5	*Qmlrw.tamu.5A.44*	44	25	22.5	26	17.2	1514513_5as_10557	5.88	11.86	1.29	N
MLTW	13EP2	*Qmltw.tamu.1B.7*	7	3	1.5	4.5	0.6	3473141_1bs_756	4.64	15.97	1.74	Y
MLTW	13EP5	*Qmltw.tamu.1B.7*	7	8	5.5	23	7.2	3285535_1bs_1678	4.87	13.66	2.03	Y
MLTW	14CH	*Qmltw.tamu.1B.7*	7	13	5.5	25	7.2	3285535_1bs_1678	3.68	12.39	1.65	Y
MLTW	13EP5	*Qmltw.tamu.1D.13*	13	58	57.5	59	412.0	IWB58572	3.88	8.86	1.63	Y
MLTW	14EP4	*Qmltw.tamu.1D.13*	13	60	59.5	61	413.2	2236927_1dl_656	4.04	11.31	0.92	Y
MLTW	14EP5	*Qmltw.tamu.1D.13*	13	63	62.5	64	414.8	IWB12851	5.10	15.39	0.96	Y
MLTW	14CH	*Qmltw.tamu.1D.13*	13	64	63.5	65	416.1	IWB35348	7.13	14.16	1.76	Y
MLTW	14EP5	*Qmltw.tamu.5A.44*	44	25	22.5	26	17.2	1514513_5as_10557	3.55	10.50	0.80	N
MLTW	13EP3	*Qmltw.tamu.6B.56*	56	1	0	1.5	3.2	2950610_6bs_6372	4.54	8.53	-1.63	N
MLTW	14CH	*Qmltw.tamu.7D.72*	72	78	75.5	79	58.9	IWB6964	5.07	9.67	-1.46	N
MLTW	13EP2	*Qmltw.tamu.7D.74*	74	181	180.5	183	591.2	IWB10006	3.33	11.10	1.45	Y

[†] HARD, hardness index; GMOIST, grain moisture; DIAM, kernel diameter; SKW, single kernel weight; FYLD, flour yield %; FMOIST, flour moisture; PROT14, flour protein at 14% moisture basis; ASH14, flour ash content at 14% moisture; WABS, water absorption; MLPT, midline peak time; MLPW, midline peak width; MLPV, midline peak value; MLPI, midline peak integral; MLRS, midline right slope; MLRW, midline right width; MLTW, midline tail width

[‡] Env, environments; 13EP2, 2013 Etter pivot 2; 13EP3, 2013 Etter pivot 3; 13EP4, 2013 Etter pivot 5; 13EP5, 2013 Etter pivot 5, 14CH, 2014 Chillicothe; 14EP4, 2014 Etter pivot 4; 14EP5, 2014 Etter pivot 5

[§] Left Confidence interval for QTL position

[¶] Right confidence interval for QTL position

[#] IWGSC RefSeq v1.0 pseudomolecule position in mega base pair (Mbp)

[††] Logarithm of odds

Table 3.3 Continued

[‡‡] Phenotypic variance explained by each QTL

[§§] Additive effect of each QTL, negative additive effects indicate high value allele (HAV) from TAM 111, positive values correspond to HVA from TAM 112

[¶¶] M-E, multi-environment QTL analysis; Y, QTL was also detected in multi-environment analysis; N, QTL was detected only in individual environment analysis

Table 3.4. Significant QTLs, additive effects and additive-by-environment interaction effects from single trait-multi environment trials

Traits[†]	QTL Name	QTL ID	Peak (cM)	LeftCI[‡]	RightCI[§]	Mbp[¶]	Peak SNP	LOD[#]	R^{2}[††]	R^2 (A)[‡‡]	R^2 (A×E)[§§]	A[¶¶]	AE[##]	I-E[†††]
HARD	*Qhard.tamu.1A.1*	1	10	9.5	10.5	13.8	IWB55537	30.43	24.89	7.94	16.95	1.17	-0.98, 2.85	Y
HARD	*Qhard.tamu.1A.4*	4	55	53.5	55.5	393.8	3928641_1al_1202	9.40	2.57	0.62	1.95	0.33	-0.12, 1.42	Y
HARD	*Qhard.tamu.1A.5*	5	62	61.5	62.5	475.6	3974856_1al_3401	13.64	16.22	3.31	12.91	0.76	-0.49, 3.66	Y
HARD	*Qhard.tamu.1B.7*	7	3	1.5	4.5	0.6	3473141_1bs_756	8.06	3.72	1.19	2.53	0.45	-0.32, 1.35	Y
HARD	*Qhard.tamu.1B.7*	7	6	5.5	7.5	7.2	3285535_1bs_1678	57.40	27.06	22.34	4.72	1.97	0.12, -1.93	Y
HARD	*Qhard.tamu.2B.18*	18	14	13.5	14.5	16.9	IWA2303	50.45	46.46	3.37	43.08	0.76	-0.76, 6.67	N
HARD	*Qhard.tamu.2B.20*	20	107	106.5	108.5	578.7	8086989_2bl_2189	6.77	3.53	3.08	0.45	0.73	-0.03, 0.56	N
HARD	*Qhard.tamu.2D.22*	22	21	17.5	21.5	1.7	IWB34642	7.34	3.71	2.55	1.16	0.67	-0.08, 0.75	Y
HARD	*Qhard.tamu.4D.39*	39	11	9.5	11.5	62.8	2305880_4ds_1018	13.63	6.05	3.61	2.44	0.79	-0.01, 1.22	Y
HARD	*Qhard.tamu.4D.42*	42	22	21.5	22.5	366.3	IWB10053	9.09	3.89	2.98	0.91	0.72	0.04, -0.74	N
HARD	*Qhard.tamu.5A.48*	48	187	185.5	187.5	688.3	IWA2947	7.45	3.65	3.30	0.35	-0.76	0, -0.38	N
HARD	*Qhard.tamu.7D.72*	72	95	93.5	96.5	84.3	3938880_7ds_2029	25.13	14.71	10.13	4.58	-1.32	-0.11, -1.55	Y
GMOIST	*Qgmoist.tamu.1B.7*	7	3	1.5	4.5	0.6	3473141_1bs_756	7.30	7.48	5.25	2.23	-0.03	0, 0.03	Y
GMOIST	*Qgmoist.tamu.4D.39*	39	10	9.5	10.5	62.8	2305880_4ds_1018	19.59	21.31	8.86	12.45	0.04	0, 0.09	Y
GMOIST	*Qgmoist.tamu.7B.70*	70	2	1.5	2.5	709.6	IWB5306	6.82	6.23	4.94	1.29	-0.03	0, 0.03	N
GMOIST	*Qgmoist.tamu.7D.72*	72	79	78.5	79.5	60.6	IWB35446	15.02	14.42	12.76	1.66	-0.04	0, 0.02	Y
DIAM	*Qdiam.tamu.1A.1*	1	1	0	2.5	3.4	IWB47522	8.45	1.62	1.51	0.11	-0.01	0, 0.01	N
DIAM	*Qdiam.tamu.1A.1*	1	9	8.5	9.5	11.8	IWB46642	8.51	1.67	1.55	0.12	-0.01	0, 0.01	N
DIAM	*Qdiam.tamu.1A.1*	1	11	10.5	11.5	13.8	IWB63611	8.34	1.62	1.51	0.11	-0.01	0, 0.01	N
DIAM	*Qdiam.tamu.1A.2*	2	22	21.5	24.5	232.6	3877153_1al_1567	7.71	1.49	1.37	0.12	-0.01	0, 0.01	N
DIAM	*Qdiam.tamu.1A.2*	2	26	25.5	26.5	263.5	846120_1al_517	8.02	1.56	1.44	0.12	-0.01	0, 0.01	N
DIAM	*Qdiam.tamu.1A.2*	2	28	27.5	29.5	289.2	3968338_1al_936	8.22	1.62	1.50	0.12	-0.01	0, 0.01	N
DIAM	*Qdiam.tamu.1A.3*	3	34	33.5	35.5	304.1	3916820_1al_4455	8.18	1.60	1.48	0.12	-0.01	0, 0.01	N
DIAM	*Qdiam.tamu.1A.3*	3	37	36.5	37.5	316.6	3871107_1al_72	7.17	1.40	1.29	0.10	-0.01	0, 0.01	N
DIAM	*Qdiam.tamu.1A.3*	3	40	39.5	40.5	347.8	3871937_1al_2041	9.97	1.98	1.81	0.17	-0.01	0, 0.01	N
DIAM	*Qdiam.tamu.1A.4*	4	48	46.5	49.5	364.7	3976654_1al_3742	8.39	1.67	1.46	0.21	-0.01	0, 0.01	N
DIAM	*Qdiam.tamu.1A.4*	4	53	52.5	54.5	390.1	IWB31924	8.27	1.64	1.46	0.17	-0.01	0, 0.01	N
DIAM	*Qdiam.tamu.1A.5*	5	59	58.5	60.5	458.4	IWB74868	8.09	1.69	1.45	0.23	-0.01	0, 0.01	N
DIAM	*Qdiam.tamu.1A.5*	5	64	62.5	64.5	485.2	3894604_1al_116	7.36	1.51	1.38	0.13	-0.01	0, -0.01	N
DIAM	*Qdiam.tamu.1D.11*	11	26	21.5	28.5	12.3	IWB14343	8.22	1.74	1.52	0.22	0.01	0, -0.01	N
DIAM	*Qdiam.tamu.2D.24*	24	113	111.5	115	531.4	9852937_2dl_2983	17.97	3.91	3.30	0.61	0.02	0, -0.01	Y
DIAM	*Qdiam.tamu.4B.38*	38	117	114.5	117	671.7	IWB9483	6.84	1.72	1.38	0.34	-0.01	0, -0.01	N
DIAM	*Qdiam.tamu.4D.39*	39	6	3.5	7.5	29.0	IWB30733	7.83	1.49	0.48	1.01	0.01	0, -0.02	N
DIAM	*Qdiam.tamu.5D.52*	52	21	18.5	21	385.6	4522185_5dl_458	7.16	1.07	0.63	0.44	-0.01	0, 0.01	Y
DIAM	*Qdiam.tamu.6A.54*	54	87	85.5	91.5	104.4	IWB23452	7.67	1.25	0.77	0.47	-0.01	0, 0.01	Y
DIAM	*Qdiam.tamu.7D.71*	71	65	57.5	69.5	38.5	IWB60795	7.09	1.51	1.38	0.13	0.01	0, 0.01	N
DIAM	*Qdiam.tamu.7D.73*	73	126	124.5	129.5	123.3	10396674_3b_3606	9.84	1.93	1.86	0.07	-0.01	0, 0	N
SKW	*Qskw.tamu.2D.24*	24	114	112.5	115	531.4	9852937_2dl_2983	15.92	13.19	8.10	5.10	0.33	0.02, 0.5	Y
SKW	*Qskw.tamu.4D.42*	42	22	21.5	22.5	366.3	IWB10053	10.79	13.69	4.75	8.94	-0.25	0.15, -0.66	Y

Table 3.4 Continued

Traits[†]	QTL Name	QTL ID	Peak (cM)	LeftCI[‡]	RightCI[§]	Mbp[¶]	Peak SNP	LOD[#]	R^2[††]	R^2 (A)[‡‡]	R^2 (A×E)[§§]	A[¶¶]	AE[##]	I-E[†††]
SKW	*Qskw.tamu.5B.51*	51	153	150.5	156	704.8	IWB53784	8.37	8.30	5.05	3.25	0.26	0.01, 0.43	Y
SKW	*Qskw.tamu.7D.71*	71	59	58.5	64.5	38.5	IWB60795	8.90	7.37	6.04	1.34	0.28	-0.01, -0.23	N
SKW	*Qskw.tamu.7D.72*	72	91	86.5	92.5	78.5	IWB44453	8.61	8.58	5.21	3.37	0.26	-0.01, 0.42	Y
FYLD	*Qfyld.tamu.1A.6*	6	88	87.5	88.5	533.4	IWA4536	6.99	10.72	4.66	6.06	-0.30	0.05, -0.79	N
FYLD	*Qfyld.tamu.1B.9*	9	74	73.5	74.5	430.3	3884244_1al_6978	7.10	6.88	4.27	2.61	-0.29	-0.03, 0.31	N
FYLD	*Qfyld.tamu.2B.21*	21	135	134.5	136.5	734.4	7939581_2bl_9591	6.82	6.97	5.79	1.17	-0.34	-0.01, -0.3	N
FYLD	*Qfyld.tamu.4D.40*	40	13	11.5	13.5	109.8	2279925_4ds_1008	15.03	30.13	8.08	22.05	0.39	-0.11, 1.47	Y
FMOIST	*Qfmoist.tamu.2D.23*	23	103	97.5	105.5	82.0	5329935_2ds_3804	7.28	22.54	4.78	17.76	0.00	-0.01, 0.06	Y
PROT14	*Qprot14.tamu.4B.34*	34	32	26.5	32.5	47.4	4962193_4bs_3020	6.73	5.43	5.04	0.39	-0.09	0, -0.05	N
PROT14	*Qprot14.tamu.4B.35*	35	36	33.5	36.5	181.4	4909258_4bs_448	6.96	5.76	5.30	0.46	-0.09	0, -0.05	N
PROT14	*Qprot14.tamu.4B.37*	37	51	45.5	57.5	404.0	7040005_4bl_5774	8.41	5.35	5.06	0.28	-0.09	0, -0.05	N
PROT14	*Qprot14.tamu.4D.39*	39	5	4.5	7.5	29.0	IWB30733	10.44	11.04	1.30	9.74	0.05	-0.02, 0.29	Y
PROT14	*Qprot14.tamu.4D.40*	40	13	12.5	13.5	109.8	2279925_4ds_1008	36.11	49.96	6.74	43.22	0.10	-0.04, 0.64	Y
PROT14	*Qprot14.tamu.4D.41*	41	18	17.5	18.5	182.6	2273804_4ds_1113	18.18	17.50	3.36	14.14	-0.07	-0.02, -0.36	Y
PROT14	*Qprot14.tamu.4D.43*	43	28	25.5	28.5	445.5	IWB3336	11.08	8.11	1.69	6.42	-0.05	-0.05, -0.18	Y
PROT14	*Qprot14.tamu.5B.50*	50	74	68.5	74.5	588.2	IWB36196	7.56	7.50	4.19	3.31	-0.08	-0.01, -0.14	Y
ASH14	*Qash14.tamu.2A.16*	16	93	92.5	93.5	684.1	6337088_2al_8303	9.02	6.07	4.13	1.94	0.00	0, -0.01	Y
ASH14	*Qash14.tamu.3D.32*	32	69	68.5	69.5	573.6	6936842_3dl_1518	7.51	7.18	6.24	0.94	0.00	0, 0	N
ASH14	*Qash14.tamu.6B.58*	58	20	18.5	20.5	662.3	3252764_6dl_2803	10.38	8.54	4.76	3.78	0.00	0, 0.01	Y
WABS	*Qwabs.tamu.4B.37*	37	53	46.5	58.5	404.0	7040005_4bl_5774	7.83	6.83	5.90	0.93	-0.12	0, -0.1	N
WABS	*Qwabs.tamu.4D.39*	39	6	4.5	7.5	29.0	IWB30733	8.88	16.41	1.44	14.97	0.06	-0.01, 0.42	Y
WABS	*Qwabs.tamu.4D.40*	40	13	12.5	13.5	109.8	2279925_4ds_1008	36.14	77.16	10.25	66.91	0.16	-0.08, 0.96	Y
WABS	*Qwabs.tamu.4D.41*	41	18	17.5	18.5	182.6	2273804_4ds_1113	18.36	27.12	4.59	22.53	-0.10	0.03, -0.55	Y
WABS	*Qwabs.tamu.4D.43*	43	28	25.5	28.5	445.5	IWB3336	9.73	11.27	1.50	9.77	-0.06	0.07, -0.23	Y
MLPT	*Qmlpt.tamu.1A.1*	1	12	10.5	13.5	14.4	IWB10932	7.18	0.00	0.00	0.00	-0.12	-0.01, 0.11	N
MLPT	*Qmlpt.tamu.1A.2*	2	22	21.5	22.5	232.6	3877153_1al_1567	7.24	0.00	0.00	0.00	-0.12	-0.01, 0.13	N
MLPT	*Qmlpt.tamu.1A.2*	2	24	23.5	24.5	251.3	3923134_1al_161	7.64	0.00	0.00	0.00	-0.12	-0.01, 0.13	N
MLPT	*Qmlpt.tamu.1A.2*	2	27	25.5	28.5	283.1	3922416_1al_1034	7.56	0.00	0.00	0.00	-0.12	-0.01, 0.14	N
MLPT	*Qmlpt.tamu.1A.3*	3	34	33.5	35.5	304.1	3916820_1al_4455	6.86	0.00	0.00	0.00	-0.11	-0.01, 0.13	Y
MLPT	*Qmlpt.tamu.1A.3*	3	38	36.5	39.5	333.5	3939178_1al_9799	7.03	0.00	0.00	0.00	-0.11	-0.01, 0.13	Y
MLPT	*Qmlpt.tamu.1A.3*	3	43	42.5	43.5	357.6	3966094_1al_942	14.13	0.00	0.00	0.00	-0.18	0, -0.19	Y
MLPT	*Qmlpt.tamu.1A.4*	4	50	47.5	52.5	367.1	3900873_1al_350	9.14	0.00	0.00	0.00	-0.13	-0.01, 0.14	N
MLPT	*Qmlpt.tamu.1A.4*	4	56	55.5	57.5	399.2	3920586_1al_9412	8.54	0.00	0.00	0.00	-0.12	-0.02, 0.13	N
MLPT	*Qmlpt.tamu.1A.5*	5	60	58.5	63.5	465.5	IWB65944	8.56	0.00	0.00	0.00	-0.12	-0.02, 0.13	N
MLPT	*Qmlpt.tamu.1B.7*	7	0	0	1.5	0.6	3473141_1bs_756	8.07	0.00	0.00	0.00	0.11	0.02, 0.16	Y
MLPT	*Qmlpt.tamu.1B.7*	7	4	3.5	4.5	1.4	3482114_1bs_10487	11.59	0.00	0.00	0.00	0.15	0.02, -0.16	Y
MLPT	*Qmlpt.tamu.1B.7*	7	6	5.5	9.5	7.2	3285535_1bs_1678	13.30	0.00	0.00	0.00	0.14	-0.02, -0.17	Y
MLPT	*Qmlpt.tamu.1B.10*	10	90	87.5	90.5	570.3	IWA5160	7.09	0.00	0.00	0.00	0.12	0.02, -0.11	N
MLPT	*Qmlpt.tamu.1D.13*	13	58	57.5	58.5	412.0	IWB58572	24.65	0.00	0.00	0.00	0.16	-0.13, 0.46	Y
MLPT	*Qmlpt.tamu.1D.13*	13	60	59.5	60.5	413.2	2236927_1dl_656	32.93	0.00	0.00	0.00	0.18	-0.13, 0.5	N
MLPT	*Qmlpt.tamu.5A.44*	44	25	24.5	25.5	17.2	1514513_5as_10557	11.27	0.00	0.00	0.00	0.15	0, -0.17	N

Table 3.4 Continued

Traits[†]	QTL Name	QTL ID	Peak (cM)	LeftCI[‡]	RightCI[§]	Mbp[¶]	Peak SNP	LOD[#]	R^2[††]	R^2 (A)[‡‡]	R^2 (A×E)[§§]	A[¶¶]	AE[##]	I-E[†††]
MLPT	*Qmlpt.tamu.7A.65*	65	131	127.5	134	657.7	4557355_7al_14033	7.18	0.00	0.00	0.00	-0.09	-0.01, 0.13	N
MLPW	*Qmlpw.tamu.1A.1*	1	6	3.5	6.5	9.2	IWB33789	10.12	9.82	3.33	6.49	-0.55	0.17, -1.56	Y
MLPW	*Qmlpw.tamu.1A.5*	5	64	63.5	64.5	485.2	3894604_1al_116	7.75	9.67	3.83	5.84	-0.59	0.16, -1.59	Y
MLPW	*Qmlpw.tamu.4B.34*	34	32	30.5	32.5	47.4	4962193_4bs_3020	27.91	38.35	11.63	26.72	-1.03	0.46, -3.59	N
MLPI	*Qmlpi.tamu.1A.3*	3	43	42.5	43.5	357.6	3966094_1al_942	8.98	10.12	4.22	5.89	-4.45	-2.16, -9.81	Y
MLPI	*Qmlpi.tamu.1A.4*	4	51	50.5	51.5	380.7	3916130_1al_8063	8.89	7.33	3.36	3.96	-3.99	3, -6.13	N
MLPI	*Qmlpi.tamu.1A.5*	5	61	60.5	61.5	474.6	IWB44485	9.20	7.26	3.48	3.78	-4.05	3.06, -5.66	Y
MLPI	*Qmlpi.tamu.1B.7*	7	0	0	2.5	0.6	3473141_1bs_756	6.87	6.85	3.23	3.62	3.89	0.44, 5.32	Y
MLPI	*Qmlpi.tamu.1B.7*	7	4	3.5	4.5	1.4	3482114_1bs_10487	10.38	8.33	4.39	3.94	4.55	0.14, 6.94	Y
MLPI	*Qmlpi.tamu.1B.7*	7	6	5.5	10.5	7.2	3285535_1bs_1678	8.01	5.64	2.86	2.78	3.66	0.72, -4.98	Y
MLPI	*Qmlpi.tamu.1D.13*	13	58	57.5	58.5	412.0	IWB58572	29.54	32.53	8.88	23.65	6.45	5.06, 18.52	Y
MLPI	*Qmlpi.tamu.1D.13*	13	64	63.5	64.5	416.1	IWB35348	41.83	49.70	15.83	33.87	8.62	-6.8, 21.5	Y
MLPI	*Qmlpi.tamu.3A.26*	26	65	63.5	67.5	595.8	4308065_3al_1951	6.63	7.16	4.58	2.57	-4.64	0.01, -5.91	Y
MLPI	*Qmlpi.tamu.4B.38*	38	78	76.5	78.5	649.5	IWB53155	8.54	6.23	2.88	3.34	-3.68	0.19, 8.79	N
MLPI	*Qmlpi.tamu.4B.38*	38	88	87.5	88.5	654.3	2804533_5al_4865	12.55	10.05	1.30	8.76	2.47	-0.7, 14.74	N
MLPI	*Qmlpi.tamu.4D.39*	39	10	8.5	11.5	62.8	2305880_4ds_1018	7.09	4.55	2.54	2.00	3.46	1.16, -5.2	N
MLPI	*Qmlpi.tamu.5A.44*	44	25	23.5	25.5	17.2	1514513_5as_10557	13.73	10.32	7.52	2.80	5.98	-0.63, -6.99	Y
MLRS	*Qmlrs.tamu.1A.2*	2	20	19.5	20.5	227.9	3904015_1al_2374	7.07	7.11	4.24	2.87	0.18	0.1, -0.21	N
MLRS	*Qmlrs.tamu.1B.7*	7	6	5.5	10.5	7.2	3285535_1bs_1678	8.67	8.92	5.77	3.15	0.21	0.01, -0.33	Y
MLRS	*Qmlrs.tamu.1D.13*	13	60	59.5	60.5	413.2	2236927_1dl_656	13.61	17.22	8.95	8.26	0.27	0.02, 0.56	Y
MLRS	*Qmlrs.tamu.1D.13*	13	65	64.5	65.5	418.5	2252364_1dl_16749	9.49	10.41	5.71	4.70	0.21	-0.02, 0.41	Y
MLRW	*Qmlrw.tamu.1A.1*	1	12	11.5	12.5	14.4	IWB10932	8.20	2.37	0.96	1.41	-0.47	-0.03, 1.01	Y
MLRW	*Qmlrw.tamu.1D.13*	13	58	57.5	58.5	412.0	IWB58572	40.34	15.80	7.73	8.07	1.31	-0.09, 3.14	Y
MLRW	*Qmlrw.tamu.1D.13*	13	60	59.5	60.5	413.2	2236927_1dl_656	27.58	10.22	0.01	10.21	0.05	0, -3.5	Y
MLTW	*Qmltw.tamu.1B.7*	7	4	0	4.5	1.4	3482114_1bs_10487	6.85	11.63	5.38	6.25	0.50	-0.09, 1.02	Y
MLTW	*Qmltw.tamu.1B.7*	7	6	5.5	10.5	7.2	3285535_1bs_1678	11.49	19.18	10.81	8.36	0.70	-0.29, 1.08	Y
MLTW	*Qmltw.tamu.1D.13*	13	64	63.5	64.5	416.1	IWB35348	7.39	10.56	2.88	7.68	0.36	0.19, 1.38	Y
MLTW	*Qmltw.tamu.1D.13*	13	75	74.5	75.5	433.3	IWB49445	7.15	20.53	1.21	19.32	0.23	-0.06, 2.22	Y
MLTW	*Qmltw.tamu.7D.74*	74	181	180.5	182.5	591.204218	IWB10006	10.17	19.25	7.78	11.47	0.60	-0.12, 1.74	Y

[†] HARD, hardness index; GMOIST, grain moisture; DIAM, kernel diameter; SKW, single kernel weight; FYLD, flour yield %; FMOIST, flour moisture; PROT14, flour protein at 14% moisture basis; ASH14, flour ash content at 14% moisture; WABS, water absorption; MLPT, midline peak time; MLPW, midline peak width; MLPV, midline peak value; MLPI, midline peak integral; MLRS, midline right slope; MLRW, midline right width

[‡] Left Confidence interval for QTL position

[§] Right confidence interval for QTL position

[¶] IWGSC RefSeq v1.0 pseudomolecule position in Mega base pair

[#] Logarithm of odds for total genetic effects

[††] total Phenotypic variance explained by each QTL

[‡‡] phenotypic variance explained by additive effect

Table 3.4 Continued

[§§] phenotypic variance explained by additive by environmental effect

[¶¶] Additive effect of each QTL, negative additive effects indicate high value allele (HAV) from TAM 111, positive values correspond to HVA from TAM 112; MLTW, midline tail width

[##] AE, additive-by-environment interaction effect, Negative value indicates the additive-by-environment reduced the trait, positive value increased the trait

[†††] I-E, Individual environment analysis; Y, corresponding QTL was also detected in individual-environment analysis; N, corresponding QTL was detected only in multi-environment analysis

From the individual environment and multiple-environment analysis, QTLs for grain moisture (GMOIST) were found on chromosome 1B (*Qgmoist.tamu.1B* at 0.6 Mb), 4D (*Qgmoist.tamu.4D* at 29.0-62.8 Mb), and 7D (*Qgmoist.tamu.7D* at 60.6 Mb) (Table 3.3 and 3.4). Additional QTLs were detected on chromosome 4B (*Qgmoist.tamu.4B* at 404.0 Mb), 4D (*Qgmoist.tamu.4D* at 312.7, 408.8 Mb) from individual environment analysis, and on 7B (*Qgmoist.tamu.7B* at 709.6 Mb) from multi-environment trial (Table 3.3 and 3.4). High value allele for QTL on chromosome 1B, 7B and 7D came from TAM 111 while it came from TAM 112 for rest. QTLs for grain moisture explained 8.16%-32.18% of the variation in grain moisture (Table 3.3), and 1.66%-12.45% of the variation in QTL-by-environment interaction (Table 3.4) and AE ranged from 0.007-0.09% (Table 3.4), A ranged from 0.05-0.1 (Table 3.3).

QTLs for kernel diameter (DIAM) were detected on chromosome 2D (*Qdiam.tamu.2D* at 531.4 Mb), 5D (*Qdiam.tamu.5D* at 385.6 Mb), and 6A (*Qdiam.tamu.6A* at 104.4 Mb) from both individual environment analysis and multi-trait environment analysis. From multi-environment analysis, additional QTLs were detected on chromosome 1A (*Qdiam.tamu.1A* at 3.4-13.8, 23), 1D (*Qdiam.tamu.1D* at 12.3 Mb), 4B (*Qdiam.tamu.4B* at 671.7 Mb), 4D (*Qdiam.tamu.4D* at 29.0 Mb), and 7D (*Qdiam.tamu.7D* at 38.5 and 123.3 Mb) (Table 3.4). High value alleles for QTLs on chromosome 2D and, 7D came from TAM 112 parent, and for QTL on 5D and 6A it was from TAM 111. Additive effect ranged from 0.02-0.03 mm in diameter from these QTLs accounting up to 17.5 % of the variation. Significant AE interaction was observed for diameter, accounting for 0.07%-1.01% of the variation.

QTLs linked to single kernel weight (SKW) were mapping on chromosome 2D (*Qskw.tamu.2D* at 531.4 Mb), 4D (*Qskw.tamu.4D* at 366.3 Mb), 5B (*Qskw.tamu.5B* at 704.8 Mb), and 7D (*Qskw.tamu.7D* at 78.5 Mb) from both individual and multi-environment analysis. Additional QTLs were detected on chromosome 1D (*Qskw.tamu.1D* at 8.6 Mb) from the individual environment, and on 7D (*Qskw.tamu.7D* at 38.5 Mb) from the multi-environment analysis. QTLs for single kernel weight explained 10.8%-21.4% of the variation present in SKW. The beneficial effect came from TAM 112 for QTLs on chromosome 1D, 2D, 5B, and 7D, whereas for QTLs on chromosome 4D, it came from TAM 111. QTL-by-environment (AE) explained up to 8.9% of the variation in SKW, with its effect ranging from 0.005-0.6 mg (Table A5).

QTL for Flour yield and characteristics

Flour yield (FYLD) related QTLs were mapped on chromosome 1A (*Qfyld.tamu.1A* at 485.2 Mb), 4D (*Qfyld.tamu.4D* at 109.8 Mb), and on 7D (*Qfyld.tamu.7D* at 596.9 Mb) from individual environment analysis (Table 3.3). QTLs on 4D (*Qfyld.tamu.4D* at 109.8 Mb) were also detected in multi-environment analysis. QTLs on chromosome 1A (*Qfyld.tamu.1A* at 533.4 Mb), 1B (*Qfyld.tamu.1B* at 430.3 Mb), 2B (*Qfyld.tamu.2B* at 734.4 Mb) were also linked to flour yield from multi-environment analysis (Table 3.4). The main additive effect for FYLD QTLs from single environment analysis ranged 0.68-1.11, which explained up to 12.9% of the variation present in this trait. Significant AE effect was present for this trait, explaining 1.1%-22% of the variation. When combined, main effect and AE effect explained up to 30.1% of the variation in flour yield (Table 3.4).

For flour moisture (FMOIST), QTLs were present on chromosome 2A (*Qfmoist.tamu.2A* at 36.8 and 742.1 Mb), 2D (*Qfmoist.tamu.2D* at 82.0 Mb), and 4D (*Qfmoist.tamu.4D* at 82.0 Mb) from single environment analysis. QTL *Qfmoist.tamu.2D* at 82.0 Mb was also detected in the multi-environment analysis. The R^2 for flour moisture QTLs explained 9.4%- 15.5% of the variation. High value allele came from TAM 112 for QTLS on chromosome 2D, while it came from TAM 111 for rest of the QTLs for FMOIST (Table 3.3).

The QTLs linked to flour protein at 14% moisture basis (PROT14) were detected on chromosome 4D (*Qprot14.tamu.4D* at 29.0, 109.8, 182.6 and 445.5 Mb), 5B (*Qprot14.tamu.5B* at 588.2 Mb) both in individual and multi-environment analysis (Table 3.3 and 3.4). Additional QTL were detected on chromosome 7B (*Qprot14.tmau.7B* at 126.1 Mb) from individual environment analysis, and on chromosome 4B (*Qprot14.tamu.4B* at 47.7, 181.4, 404.0 Mb) from multi-environment analysis. QTLs related to PROT14 on chromosome 4D at 182.6 and 445.5 Mb, and 5B received favorable allele from TAM 111 but those on chromosome 4D at 29.0 and 109.8 Mb, and on 7B at 126.1 Mb were from TAM 112 (Table 3.3). The R^2 ranged from 9.3%- 27.2% for these QTLs, with effect increased from 0.2-0.8. AE interaction for QTL on 4D (*Qprot14.tamu.4D* at 109.8 Mb) explained 43.2% of the variation alone (Table 3.4). Rest of the QTL by environment interaction ranged almost zero (0) to 0.7 (Table A5).

For flour ash content at 14% moisture basis (ASH14), QTLs were detected on chromosome 2A (*Qash14.tamu.2A* at 684.1 Mb) and 6B (*Qash14.tamu.6B* at 662.3 Mb) from both individual and multi-environment analysis. QTLs on chromosome 2A

(*Qash14.tamu.2A* at 728.8 Mb), 2B (*Qash14.tamui.2B* at 730.6 Mb) were detected additionally for ASH14 on individual environment analysis. In multi-environment analysis, QTL *Qash14.tamu.3D* at 573.6 Mb on chromosome 3D was additionally detected.

QTLs linked to flour water absorption (WABS) were detected on chromosome 4D (*Qwabs.tamu.4D* at 29.0, 109.8, 182.6 and 445.5 Mb) from the individual as well as multi-environment analysis. Additional QTLs on chromosome 7B (*Qwabs.tamu.7B* at 126.1 Mb) from individual environment analysis, and on 4B (*Qwabs.tamu.4B* at 404.0) from the multi-environment analysis. Like PROT14, high value allele came from TAM 112 for QTLs on chromosome 4D at 29.0 and 109.8 Mb and those came from TAM 111 for QTLs on chromosome 4D at 182.6 and 445.5 Mb. Combined R^2 for A and AE ranged from 6.8%-77.1% of the total variation on WABS.

QTL for Mixograph Traits

QTLs linked to midline peak time (MLPT) were detected on group 1 homeologs chromosome from both analyses. QTLs *Qmlpt.tamu.1A* at 357.6 Mb, *Qmlpt.tamu.1B* at 1.4-7.2 Mb, *Qmlpt.tamu.1D* at 412.5 Mb explained 6.4%-54.6% of the variation present in the MLPT. Except for the QTL on chromosome 1A, high value alleles were contributed by TAM 112 (Table 3.3). However, additional QTLs detected on chromosome 1A (*Qmlpt.tamu.1A* at 14.4, 232.6-251.3, 367.1-399.2, 465.5 Mb) and 5A at 17.2 Mb from multi-environment analysis, receiving high value allele from TAM 111 (Table 3.4). These QTLs had additive effect ranging from 0.25 min – 0.74 min. Even though significant AE interaction was present, the proportion of variation explained by these QTLs was almost equal to zero (Table 3.4).

Midline peak width (MLPW) QTLs were detected on chromosome 1A (*Qmlpw.tamu.1A* at 9.2, 485.2 Mb) in both individual and multi-environment analysis. Additional QTLs were detected on chromosome 1A (*Qmlpw.tamu.1A* at 230.0 Mb), 1D (*Qmlpw.tamu.1D* at 10.4 Mb) from individual environment analysis (Table 3.3), and on 4B (*Qmlpw.tamu.4B* at 47.4 Mb) from multi-environment analysis (Table 3.4). Except for the QTL on chromosome 1D, HVA for other QTLs originated from TAM 111 explaining up to 24.1% of the variation in MLPW. Significant AE interaction explained up to 26.7% of the variation with effect ranging from 0.16 in 13EP3 to 3.6 in 14EP4 (Table A5).

Only one QTL for midline peak value (MLPV) was detected on chromosome 1A (*Qmlpv.tamu.1A* at 14.4 Mb) receiving high value allele from TAM 111 using individual environment analysis. This QTL explained 13.7% of the variation present in MLPV with the additive effect of 2.5 (Table 3.3).

Like MLPT and MLPW, QTLs linked to midline peak integral (MLPI) were detected on group 1 homoeologous chromosome (at 357.6, 474.6, 1.4-7.2 and 412.0-416.1 Mb) from both individual and multi-environment analysis. Common QTLs was detected on chromosome 3A (*Qmlpi.tamu.3A* at 608.4 Mb), and on 5A (*Qmpli.tamu.5A* at 17.2 Mb) from both analyses. Additional QTLs were detected on chromosome 1A (*Qmlpi.tamu.1A* at 13.8 and 227.9 Mb) in individual environment analysis, and on chromosome 4B (*Qmlpi.tamu.4B* at 649.5-654.3 Mb) and 4D (*Qmlpi.tamu.4D* at 62.8

Mb) from multi-environment analysis. High value alleles originated from TAM 112 for QTLs on 1A at 227.9, 1B, 1D, and 5A. QTL *Qmlpi.tamu.4B* at 649.5-654.3 Mb showed significant AE interaction by switching HVA from TAM 112 in 13EP2 and 13EP3 to TAM 111 in the rest of the environments (Table A5). QTLs for MLPI explained from 4.8%- 42.4% of the variation in MLPI with the additive effects ranging from 9.2 in 14EP5 to 30.8 in 13EP5. AE interaction for these QTLs ranged from 0.01 to 21.5, covering 33.8 % of the phenotypic variation in MLPI (Table A5).

QTLs associated with tolerance, midline right slope (MLRS), were detected on group 1 homologous chromosomes. QTLs on chromosome 1A (*Qmlrs.tamu.1B* at 7.2 Mb), 1D (*Qmlrs.tamu.1B* at 413.2-418.5 Mb) were confirmed in both individual and multi-environment analysis. Additionally, one QTL on chromosome 1A (*Qmlrs.tamu.1A* at 227.9 Mb) was identified by multi-environment QTL analysis. For MLRS, all the favorable allele came from TAM 112 explaining 13.8%-17.9% of the variation in it. The additive effect for QTLs identified ranged from 0.6-0.8 (Table 3.3). In combination with the additive effect, AE of these QTLs explained up to 17.2 % of the variation present in MLRS (Table 3.4).

For midline right width (MLRW), two QTLs were detected by both analyses. First QTL was on chromosome 1A (*Qmlrw.tamu.1A* at 14.4 Mb), and second on 1D (*Qmlrs.tamu.1D* at 412.0 Mb). One additional QTL was detected on chromosome 5A for MLRW (*Qmlrw.tamu.5A* at 17.2 Mb). Effects combined these QTLs explained up to 23% of the variation present in MLRW (Table 3.3). High value alleles for QTL on 1A originated from TAM 111 and for rest, it came from TAM 1112.

Like other mixograph traits, QTLs for midline tail width (MLTW) were clustered on group 1 homoeologous chromosome. QTLs on chromosome 1B (*Qmltw.tamu.1B* at 0.6-7.2 Mb), 1D (*Qmltw.tamu.1D* at 412.0-416.1 Mb), and 7D (*Qmltw.tamu.7D* at 591.2 Mb) were detected in both individual environment and multi-environment analysis. High value alleles for all the detected QTLs came from TAM 112 except QTLs on chromosome 6B (*Qmltw.tamu.6B* at 3.2 Mb) and 7D (*Qmltw.tamu.7D* at 58.9 Mb). These QTLs explained 8.5%- 15.9% of the variation present on MLTW, across seven different environments (Table 3.3). The additive effect for these QTLs were in the range of 0.8 – 2.03, and AE interaction effect was in 0.05- 2.2 (Table A5).

QTL clusters and stable QTL

From individual environment or multi-environment analysis, ten genomic regions were associated with more than a single trait. These traits were identified as multi-trait QTL or QTL clusters (abbreviated as *Qmt.tamu.chr*). From individual environment analysis, 17 QTLs were detected in more than one environment for hardness index, grain moisture, kernel diameter, single kernel weight, flour ash content at 14% moisture basis, midline pea time, midline peak integral, midline right slope, and midline tail width. These QTLs were identified as stable QTLs or consistent QTLs (abbreviated as *Qcon.tamu.chr*). First cluster (*Qmt.tamu.1A*, #1) was on the short arm of chromosome 1A (3.4-14.4 Mb). At this region, QTLs were co-located for hardness index, kernel diameter, midline peak time, midline peak width, midline peak value, midline peak integral, and midline right width, explaining R^2 of 1.67 for diameter to 31.3% for hardness index (Table 3.5).

Table 3.5. Multi-trait QTL (QTL clusters) for end-use quality detected from individual and multi-environment QTL analysis

QTL Name	QTL ID	Mbp[†]	Peak SNP	LOD range	R^{2}[‡]	A[§]	HAV[¶]	Traits[#]
Qmt.tamu.1A	1	3.4-14.4	IWB55537	4.13-30.43	31.33, 1.62, 0.0, 24.1, 13.6, 30.65, 14.8	4.0, 0.01, 0.12, 2.13, 26.9, 1.45	P1, P2, P2, P2, P2, P2, P2	HARD, DIAM, MLPT, MLPW, MLPV, MLPI, MLRW
Qmt.tamu.1A	4	364.7-399.2	3916130_1al_8063	4.46-13.31	14.9, 1.67, 7.3	1.75, 0.01, 3.99	P1, P2, P2	HARD, DIAM, MLPT
Qmt.tamu.1A	5	458.4- 475.6	3974856_1al_3401	3.38-19.02	26.1, 1.7, 12.9, 0.0, 17.1, 8.29	4.56, 0.01, 1.11, 0.12, 2.38, 9.9	P1, P2, P2, P2, P2, P2	HARD, DIAM, FYLD, MLPT, MLPW, MLPI
Qmt.tamu.1B	7	0.6-7.2	3285535_1bs_1678	3.56-57.4	33.9, 8.1, 13.7, 8.3, 16.3, 19.2	2.8, 0.05, 0.3, 11.2, 0.7, 1.7	P1, P2, P1, P1, P1, P1	HARD, GMOIST, MLPT, MLPI, MLRS, MLTW
Qmt.tamu.1D	13	412- 433.3	2252364_1dl_16749	3.64-41.83	48.2, 49.7, 17.9, 15.8, 1.8	0.7, 30.81, 0.8, 1.3, 1.76	P1, P1, P1, P1, P1	MLPT, MLPI, MLRS, MLRW, MLTW
Qmt.tamu.2D	24	531.4	9852937_2dl_2983	3.5-17.97	17.5, 15.0	0.03, 0.8	P1, P1	DIAM, SKW
Qmt.tamu.4D	39	20.6-62.8	2305190_4ds_510	3.61-19.59	19.3, 32.2, 1.5, 13.1, 23.2, 21.5, 4.5	2, 0.1, 0.01, 0.07, 0.3, 0.5, 3.46	P1, P1, P1, P2, P1, P1, P1	HARD, GMOIST, DIAM, FMOIST, PROT14, WABS, MLPI
Qmt.tamu.4D	42	312.7-366.3	2867136_4dl_v2_357	3.86-10.79	3.9, 19.7, 19	0.7, 0.07, 0.9	P1, P1, P2	HARD, GMOIST, SKW
Qmt.tamu.7D	72	58.9-91.1	IWA1247	4.16-25.13	14.7, 11.8, 14.4, 21.4, 9.7	3.2, 0.07, 0.03, 0.8, 1.5	P2, P2, P1, P1, P2	HARD, GMOIST, DIAM, SKW, MLTW

[†] Position, IWGSC RefSeq v1.0 pseudomolecule position

[‡] R^{2}, maximum phenotypic variance explained by additive effect to each trait

[§] A, maximum additive effect corresponding to each trait

[¶] HVA, high value allele corresponding to each trait; P1=TAM 112, P2=TAM 111

[#] Traits, HARD, hardness index; GMOIST, grain moisture; DIAM, kernel diameter; SKW, single kernel weight; FYLD, flour yield %; FMOIST, flour moisture; PROT14, flour protein at 14% moisture basis; ASH14, flour ash content at 14% moisture; WABS, water absorption; MLPT, midline peak time; MLPW, midline peak width; MLPV, midline peak value; MLPI, midline peak integral; MLRS, midline right slope; MLRW, midline right width

At this region, hardness QTL (*Qcon.tamu.1A* at 3.4-14.4 Mb) was detected consistently in 14EP4, 14EP5, and irrigated environment (Table 3.6). The genomic region at 364.7 – 399.2 Mb on chromosome 1A co-expressed QTL for hardness index, diameter and midline peak time (Table 3.5). Hardness index QTL (*Qcon.tamu.1A* at 364.7-399.2 Mb) was consistently detected in 13EP3, and 13EP4 environment (Table 3.6). On chromosome 1A, another multi-trait QTL (*Qmt.tamu.1A* at 458.4-475.6 Mb) were detected for hardness index, kernel diameter, flour yield, midline peak time, midline peak width, and midline peak integral (Table 3.5). Like previous two consistent QTLs on chromosome 1A, QTL for hardness (*Qcon.tamu.1A* at 458.4-475.6 Mb) were detected 13EP2, 14CH, DRY, and COMB. QTL at short arm of chromosome 1B was a hotspot for many mixograph traits and their consistent expression over the ranges of environment. QTLs were co-located for hardness index, grain moisture, midline peak time, midline peak integral, midline right slope, and midline tail width (Table 3.5). Midline peak integral QTL (*Qcon.tamu.1B* at 0.6-7.2 Mb) were detected in 13EP3, 13EP4, DRY, and COMB environment (Table 3.6). Midline tail width QTL (*Qcon.tamu.1B* at 0.6-7.2 Mb) were also consistent across 13EP2, 13EP5, 14CH, DRY, and COMB environment. Hardness QTL (*Qcon.tamu.1B* at 0.6-7.2 Mb) were stably expressed in all the environment except 14CH (Table 3.6). The physical region at 412-433.3 Mb on chromosome 1D is another hotspot for co-localization and stable detection of many mixograph traits. QTL associated with MLPT, MLPI, MLRS, MLRW, and MLTW were co-segregated at this region. MLP, MLPI, MLRS, and MLTW were detected in multiple environments.

Table 3.6. Stable and consistent QTL for end-use quality detected from individual environment QTL analysis

Traits[†]	QTL Name	QTL ID	Mbp[‡]	Peak SNP	LOD range	$R^{2§}$	A[¶]	HAV[#]	Environments[††]
HARD	*Qcon.tamu.1A*	1	3.4-14.4	IWB55537	14.72-16.98	27.97-31.3	2.8-3.7	P1	14EP4, 14EP5, IRR
HARD	*Qcon.tamu.1A*	4	364.7-399.2	3916130_1al_8063	4.46-9.22	11.2- 14.9	1.6-1.7	P1	13EP3, 13EP4
HARD	*Qcon.tamu.1A*	5	458.4- 475.6	3974856_1al_3401	3.62-19.02	7.76-30.9	1.29-4.5	P1	13EP2, 14CH, DRY, COMB
HARD	*Qcon.tamu.1B*	7	0.6-7.2	3285535_1bs_1678	6.86-17.03	14.3-33.9	1.8-2.8	P1	13EP2, 13EP3, 13EP4, 13EP5, 14EP4, 14EP5, DRY, IRRI, COMB
HARD	*Qcon.tamu.7D*	72	58.9-91.1	IWA1247	4.06-8.19	5.3-12.9	1.4-3.2	P2	13EP4, 14CH, 14EP4, 14EP5, DRY, IRR, COMB
GMOIST	*Qcon.tamu.4D*	39	20.6-62.8	2305190_4ds_510	6.05-17.92	17.6-31.8	0.08-0.1	P1	13EP5, 14CH, 14EP5, 14EP5, DRY, IRR, COMB
GMOIST	*Qcon.tamu.7D*	72	58.9-91.1	IWA1247	8.76-11.81	8.76-11.8	0.04-0.07	P2	14EP4, 14EP5, DRY, IRR
DIAM	*Qcon.tamu.2D*	24	531.4	9852937_2dl_2983	4.28-6.77	14.6-17.8	0.02-0.03	P1	13EP2, 13EP4, 13EP5, DRY, IRR, COMB
SKW	*Qcon.tamu.2D*	24	531.4	9852937_2dl_2983	3.5-4.95	10.9-15.3	0.33-0.8	P1	13EP2, 13EP4, 13EP5, DRY, IRR, COMB
SKW	*Qcon.tamu.4D*	42	312.7-366.3	2867136_4dl_v2_357	3.39-6.28	11.2-18.9	0.58-0.91	P2	14EP4, 14EP5
ASH14	*Qcon.tamu.6B*	58	662.3	3252764_6dl_2803	3.35-6.21	12.3-17.9	0.01	P2	13EP5, 14EP4, IRR
MLPT	*Qcon.tamu.1D*	13	412- 433.3	2252364_1dl_16749	11.25-30.22	34.6-56.4	0.5-0.8	P1	13EP2, 12EP3, 13EP5, DRY, IRR, COMB
MLPI	*Qcon.tamu.1B*	7	0.6-7.2	3285535_1bs_1678	3.78-6.98	3.4-5.6	6.2-11.2	P1	13EP3, 14EP4, DRY, COMB
MLPI	*Qcon.tamu.1D*	13	412- 433.3	2252364_1dl_16749	11.19-30.37	17.1-49.2	20.1-30.8	P1	13EP2, 13EP3, 13EP5, DRY, IRRI, COMB
MLRS	*Qcon.tamu.1D*	13	412- 433.3	2252364_1dl_16749	4.57-8.52	1.25-17.9	0.2-0.8	P1	13EP2, 13EP3, DRY, IRR, COMB
MLTW	*Qcon.tamu.1B*	7	0.6-7.2	3285535_1bs_1678	3.68-6.25	12.4-16.6	0.97-1.65	P1	13EP2, 13EP5, 14CH, DRY, COMB
MLTW	*Qcon.tamu.1D*	13	412- 433.3	2252364_1dl_16749	4.04-9.45	8.9-25.9	0.9-1.8	P1	13EP5, 14CH, 14EP4, 14EP5, DRY, IRR, COMB

[†] Traits, HARD, hardness index; GMOIST, grain moisture; DIAM, kernel diameter; SKW, single kernel weight; FYLD, flour yield %; FMOIST, flour moisture; PROT14, flour protein at 14% moisture basis; ASH14, flour ash content at 14% moisture; WABS, water absorption; MLPT, midline peak time; MLPW, midline peak width; MLPV, midline peak value; MLPI, midline peak integral; MLRS, midline right slope; MLRW, midline right width

[‡] Position, IWGSC RefSeq v1.0 pseudomolecule position

[§] R^2, maximum Phenotypic variance explained by additive effect to each trait

[¶] A, maximum Additive effect corresponding to each trait

[#] HVA, high value allele corresponding to each trait; P1=TAM 112, P2=TAM 111

[††] Environments; 13EP2, 2013 Etter pivot 2; 13EP3, 2013 Etter pivot 3; 13EP4, 2013 Etter pivot 5; 13EP5, 2013 Etter pivot 5, 14CH, 2014 Chillicothe; 14EP4, 2014 Etter pivot 4; 14EP5, 2014 Etter pivot 5; DRY, dry environments; IRR, irrigated environments; COMB, combined environments

These QTLs explained up to 49.2% of the variation in mixograph traits and HVA originated from TAM 112 only (Table 3.6). Other regions that exhibited co-location of multiple trait QTLs were on long arm of chromosome 2D (*Qmt.tamu.2D* at 531.4 Mb), short arm of chromosome 4D (*Qmt.tamu.4D* at 20.6-62.8 Mb), long arm of 4D (*Qmt.tamu.4D* at 312.7-366.3 Mb) and on short arm of 7D (*Qmt.tamu.7D* at 58.9-91.1 Mb) (Table 3.5). For each of these, QTL for diameter (*Qcons.tamu.2D* at 531.4 Mb), grain moisture (*Qcon.tamu.4D* at 20.6-62.8 Mb), single kernel weight (*Qcon.tamu.4D* at 312.7-366.3), and hardness index and grain moisture (*Qcon.tamu.7D* at 58.9-91.1 Mb) were detected in multiple environments (Table 3.6).

Epistasis

Significant epistasis (A×A or A×A×E) were found for hardness index, grain moisture, midline peak integral and midline peak time (Table 3.7). QTL-by-QTL (AA, additive-by-additive) interaction for hardness index across genome accounted 2-3% of the phenotypic variation. Recombination of parental alleles at two loci on a given chromosome increase the mean trait value, as indicated by negative AA effect. Significant Epistasis-by-environment (A×A×E) were observed for the hardness index, increasing the mean phenotypic value of the hardness index. A×A and A×A×E interaction for grain moisture explained up to 5-6 % of the phenotypic variation, both leading to increased grain moisture. QTLs for mixograph traits on group 1 homolog were interacting with QTLs on another chromosome. These interactions explained up to 3% of the total variation present in mixograph traits.

Table 3.7. Additive-by-additive epistatic interaction, and epistatic-by-environment interaction among significant loci

Traits	QTL 1 Name	Mbp 1[†]	QTL ID 1	Peak SNP 1	QTL 2 Name	Mbp 2	QTL ID 2	Peak SNP 2	R^2 (A * A)[‡]	R^2 (AA*E)[§]	A*A[¶]	A*A*E[#]
HARD	*Qhard.tamu.1A*	548.41	6	IWB26168	*Qhard.tamu.6A*	5.12	53	4427795_6as_12820	2.44	0.6	-0.94	-1.46
HARD	*Qhard.tamu.1B*	0.57	7	3473141_1bs_756	*Qhard.tamu.2A*	623.95	16	6341271_2al_905	2.38	1.08	0.93	-1.43
HARD	*Qhard.tamu.2D*	1.67	22	IWB34642	*Qhard.tamu.3A*	639.15	26	IWB8470	2.49	0.16	0.95	-0.81
HARD	*Qhard.tamu.2D*	14.42	22	IWA4746	*Qhard.tamu.3B*	28.36	28	IWB56882	2.53	0.5	-0.95	-1.39
HARD	*Qhard.tamu.3A*	1.32	25	3335448_3as_4124	*Qhard.tamu.6D*	350.42	60	3254329_6dl_5253	2.36	0.37	-0.94	-1.26
HARD	*Qhard.tamu.5A*	548.82	46	1134341_5al_336	*Qhard.tamu.7B*	19.11	67	3096912_7bs_110	2.4	0.26	-0.94	-0.89
MOIST	*Qmoist.tamu.2B*	39.2	18	IWB22828	*Qmoist.tamu.6D*	438.34	61	3325327_6dl_5670	4.93	0.17	-0.04	-0.02
MOIST	*Qmoist.tamu.3A*	21.01	25	3442664_3as_2715	*Qmoist.tamu.3B*	557.99	29	10446102_3b_9187	5.46	0.42	-0.05	-0.03
MLPT	*Qmlpt.tamu.1B*	570.28	10	IWA5160	*Qmlpt.tamu.7A*	623.96	64	4433586_7al_347	2.28	0.21	-0.16	-0.15
MLPT	*Qmlpt.tamu.1D*	0.39	11	1881608_1ds_7447	*Qmlpt.tamu.7D*	15.32	71	IWB12582	2.19	0.37	0.16	-0.21
MLPT	*Qmlpt.tamu.4B*	649.68	38	6975707_4bl_1851	*Qmlpt.tamu.4B*	652.78	38	IWA4490	0.69	0	-0.27	-0.3
MLPT	*Qmlpt.tamu.4D*	408.79	43	IWA5751	*Qmlpt.tamu.5B*	682.84	51	IWB64985	1.92	0.43	0.15	-0.18
MLPI	*Qmlpi.tamu.1A*	227.88	2	3904015_1al_2374	*Qmlpi.tamu.1A*	393.79	4	3928641_1al_1202	0.33	0	-14.37	-20.52
MLPI	*Qmlpi.tamu.2B*	596.21	20	8042513_2bl_9079	*Qmlpi.tamu.7D*	549.36	74	3395678_7dl_6495	2.35	0.63	-6.44	-10.86

[†] Position, IWGSC RefSeq v1.0 pseudomolecule position

[‡] R^2(A*A), phenotypic variance explained by epistasis (additive-by-additive) effect

[§] R^2 (AA*E), phenotypic variance explained by epistasis-by-environment effect

[¶] A*A, additive-by-additive effect. Negative sign indicates the recombination of the parental alleles increased the traits, positive sign indicates parental allelic combination reduced the traits

[#] A*A*E, range of additive-by-additive-by-environment effect. Negative value indicates the epistasis-by-environment reduced the trait, positive value increased the trait

DISCUSSION

Traits that are highly heritable and repeatable are important to breeders. All the end-use quality traits analyzed in this study were moderate to highly heritable except midline right width (MLRW). From variance partitioning, the genotypic variance is apparently higher than the residual variance, which is confounding effect of residual and genotype-by-environment interaction. Higher heritability and higher genotypic variance indicated that these traits are genetically controlled, which makes it suitable for genetic gain from selection in a breeding program. Higher heritability of end-use traits is also reported by El-Feki et al (2013) and Simons et al (2012). The significant genotypic variance was present in all the traits except for midline peak integral (MLPI). Due to the resource, time and financial constraints, single sample for each line was tested. Since we fitted the individual environments as pseudo-replication, we couldn’t test environmental significance. Significant differences existed between parents for hardness index, flour protein content, midline peak time, midline peak integral and midline tail width, with TAM 112 better than TAM 111 for most of the end-use quality traits. This result is further strengthened by finding from a subset of the same population from a single environment (Jondiko et al., 2016).

The winter wheat bread-making quality is a complex trait that is described by many parameters and determined by many factors. The bread-making quality of hard wheat is strongly influenced by the allelic variation of HMW-GS and LMW-GS genes (Payne, 1987). Given there are multiple alleles at each of the glutenin loci, the significance of these genes on dough rheology in any given cross will be largely determined by which alleles are carried by the parents. From the screening of *Glu-D1* markers, our mapping population was segregating at *Glu-D1* locus on the long arm of chromosome 1D. TAM 112 possesses *Glu-D1d* alleles (5x + 10y subunits), whereas TAM 111 possessed *Glu-D1a* alleles (2x + 12y subunits). Also, TAM 112 possess wheat-rye translocation 1AL.1RS on short arm of chromosome 1A (Dhakal et al., 2017). According to Gupta et al. (1991) and Liang et al. (2010), subunits 5x +10x gives significantly better effects for dough mixing strength and bread-making performance than subunits 2x+12y. Mixograph is a powerful tool to discriminate inter-genotypic variation in dough properties of lines carrying alleles 5x+10y and 2x+12y at *Glu-D1* locus (Primard et al., 1991). In accordance with Cooper et al. (2016), lines carrying *Glu-D1a* alleles showed greater midline peak height than alternative alleles. TAM 111 carried *Glu-D1a* alleles and its MLPH value is greater than that of TAM 112 carrying *Glu-D1d* allele. The detrimental effect of rye translocation 1RS in end-use quality trait of lines is reported (Graybosch, 2001; Graybosch et al., 1993). The 1BL.1RS translocation results in reduced tolerance to overmixing, production of ‘sticky’ doughs. Even though lines carrying 1AL.1RS translocation have better end-use quality trait than lines carrying 1BL.1RS, still lines carrying 1AL.1RS is not better than non-1RS lines (Graybosch, 2001; Graybosch et al., 1993) which is partly explained by the loss of LMW-GS *Glu-A3* and *Gli-A1*, and *Glu-B1* and *Gli-B1* from the short of chromosome 1A and 1B in the translocated lines, respectively.

Mixograph parameters are located on group 1 homolog, with QTL for midline peak time (*Qmlpt.tamu.1D*) and midline peak integral (*Qmlpi.tamu.1D*) at 412.433.3 Mb explaining up to 48.2% and 49.7% of the trait variation (Table 3.5). Both the QTLs received favorable allele from TAM 112. The physical location of the peak marker 2252364_1dl_16749 linked to both QTLs was at 412-433.3 Mb region across different environments tested, which is the exact physical location of *Glu-D1* gene (Rasheed et al., 2016). QTL for midline tail width (*Qmltw.tamu.1A* at 458.4-475.6 Mb) on the long arm of chromosome 1A explained 17.1% of the variation. However physical location of this QTL was 25 Mb upstream of *Glu-A1* loci that is at 508.72 Mb (Rasheed et al., 2016). A major determinant of hardness is located on 5DS at 3.6 Mb. Presence of hardness QTLs in the same cluster with mixograph traits on group 1 homolog was contradictory to its real physical position. Aussenac et al. (2012) found that *Glu-D1* has a significant effect on hardness with the d alleles (5x+10y) significantly higher than that with an allele (2x+12y). Research has shown the physical structure and strength of the protein matrix influence wheat hardness (Stenvert and Kingswood, 1977). Nevertheless, different studies showed that the number and chromosomal locations of QTL varied greatly, depending on the genetic crosses, complex nature of traits (Groos et al., 2004; Huang et al., 2006; Tsilo et al., 2010)

Clustering of QTLs in certain genomic regions was observed. Highly correlated traits were consistent with clustering of QTLs associated with them, with allele effects originating from the same parents in those traits. Mixograph traits are highly correlated and repeatable (Martinant et al., 1998). Mixograph traits including midline peak time, midline peak width, midline right slope is highly correlated and shared QTL location on chromosome 1A, 1B and 1D. This also agrees with the result from Tsilo et al. (2011a;

2011b). Single kernel weight (SKW) and kernel diameter (DIAM) were also highly correlated (r = 0.71, P < 0.01) and were clustered on chromosome 2D and 7D. Flour protein and WABS are highly correlated, which is true given the predicted water absorption is derived from the flour protein. These two traits also clustered chromosome 4D at 20.6-62.8 Mb region. For such traits, it is not possible to tease apart individual genetic effect separately if selection is practiced in opposite direction. But it helps to improve these traits concurrently. It is also common to see QTLs for traits with weaker or no correlation were also in the same cluster in some cases, such as QTLs for hardness (HARD) and kernel diameter (DIAM) on short arm and long arm of chromosome 1A, QTLs for hardness and mixograph traits on group 1 homologs, and QTLs for hardness and grain moisture on chromosome 1B, 4D, and 7D. A weaker correlation was present between diameter and flour yield in this study, with QTLs (*Qmt.tamu.1A* at 458.4-475.6 Mb) for these two clustered on the long arm of chromosome 1A (Table 3.5). In general, higher flour yield is expected from larger seed size (Wiersma et al., 2001). For traits with weak or no correlation, it is possible to select traits with combination at opposite direction. It also avoids the undesirable effect of one QTL by selecting against it while improving another QTL. Desirable bread making quality is associated with strong gluten, which is revealed by high values for MLPT and MLPH, combined with mixing tolerance, indicated by less negative values for MLRS (Campbell et al., 2001). Higher values for MLPW and MLRW are also considered favorable (Zheng et al., 2009). Midline peak value (MLPV) is correlated with hardness (HARD). During the mixing process, when grain hardness increases, the dough viscosity, as measured by MLPV, increases due to extensive starch damage (Martinant et al., 1998). However, in this study relationship between MLPV and HARD were correlated but in opposite direction. MLPV is also a key determinant of optimal water absorption as differences in MLPV is partly explained by differences in water absorption among the samples (Bettge and Morris, 2000). A positive correlation between MLPV and WABS in this study supports the above finding. Harder grain produces coarse flour with more fractured starch granules, which absorbs more water during the baking process. A plausible explanation of clustering of QTLs with positively and negatively related traits is the linkage between them in coupling and repulsion phase, respectively.

Stable expression of the same QTL in multiple environments is a way of confirming the worthiness of pursuing. However, it is common to detect a QTL in one environment and not in other. In this study, we categorized seven environments into either dry and irrigated environment to confirm stable expression of QTLs in different management conditions as well. Our results indicate that 10 QTLs corresponding to hardness index, grain moisture, diameter, single kernel weight, ash content, midline peak time, midline peak integral, midline right slope, and midline tail width on chromosome 1A, 1B, 1D, 2D, 4D, 6B, and 7D were detected in more than one environment with high value alleles contributed by same parent (Table 3.6). QTLs detected in individual environment analysis were not detected in either of DRY, IRR, and COMB analysis for hardness on chromosome 1A at 3.4-14.4 and 364.7-399.2 Mb, grain moisture on 7D at 58.9-91.1 Mb, single kernel weight on 4D at 312.7-366.3 Mb, and flour ash content on 6B at 662.3 Mb (Table 3.6). Similarly, QTLs for flour yield, flour moisture content, midline peak width, midline peak value, and midline right width were expressed in only one environment. Also, QTL analysis was carried out on phenotypic data collected from diverse environmental conditions, making QTL unable to express in multiple environments. These finding strongly imply the presence of G × E effects on quality traits although we couldn’t partition G × E from residual error term in this study. High error variance in certain environment inhibits the expression of QTLs (Bernardo, 2008). Except for midline peak value and midline right width, rest of the traits had less error variance as revealed by heritability. For midline peak value, one QTL was detected in 13EP3 with minor additive effects. In addition, QTLs detection for midline right width is also reduced compared to other traits with low residual variance. We observed the shift in QTL peak for hardness (*Qhard.tamu.7D* at 78.5-91.1 Mb), grain moisture (*Qgmoist.tamu.4D* at 29.0-62.8 Mb), midline tail width (*Qmltw.tamu.1B* at 0.6-7.2 Mb), and midline peak integral (*Qmlpi.tamu.1D* at 412.5-413.2 Mb) indicating that these traits are likely controlled by multiple genes expressed in different environments.

CONCLUSION

In conclusion, we had 124 recombinant inbred lines from hard red winter wheat crosses. This population was characterized for 14 end-use quality traits collected from 14 environments during two cropping seasons. All the traits had moderate to high heritability with most of the phenotypic variation due to genotypic value. A total of 163 QTLs were detected from individual environment analysis, and 109 QTLs from multi-environment trails. As expected, most of mixograph traits were detected on chromosome 1A, 1B and 1D, with peak marker for QTL on 1D positioned on *Glu-D1* locus. Due to a major gene effect, kernel hardness is found to influence mixograph traits. We found nine genomic regions on chromosome 1A, 1B, 1D, 2D, 4D and 7D that are related with more than a single trait analyzed. QTLs for hardness, grain moisture, midline peak time, and midline peak integral on these clusters were consistently expressed in multiple environments. Because of the complex inheritance of these traits, it will be necessary to validate these QTL in different wheat background evaluated in similar growth conditions before developing markers for marker-assisted selection.

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CHAPTER IV

GENETIC DISSECTION OF YIELD AND AGRONOMIC TRAITS IN TAM WHEAT

INTRODUCTION

Grain yield in wheat (*Triticum aestivum* L) is one of the major goals to most of the wheat breeding program, particularly in moisture stressed condition. In the Southern High Plains, bread wheat is grown under wide range of mega environments that differ for soil moisture and rainfall pattern. Given the unpredictable nature of environmental factors, cultivars that can maintain grain yield (GY) in stressed environments would be of prime importance to all the stakeholders involved in the wheat production. Grain yield is affected by agronomic traits like heading date and plant height and all of them interact with each other to dictate final grain yield of wheat. Each trait is the controlled by complex genetic interactions of multiple loci and their interactions with environmental conditions and cultural practices (Dhungana et al., 2007; Xing and Zhang, 2010). The genetics of GY and other important traits are frequently complicated by the occurrence of epistatic interactions among the multiple QTL/genes controlling the target trait (Kusterer et al., 2007; Li et al., 2003).

There are many *Rht* genes responsible for plant height reduction. Semi-dwarfing, Norin-10 genes (*Rht-B1b* and *Rht-D1b*) introduced into global wheat during the green revolution are very important since they increased straw strength and harvest index (HI) and grain yield (Addisu et al., 2010; Borlaug, 1968; Worland, 1996). *Rht-D1b* was associated with increased grain yield through improved harvest index, rather than increased aboveground biomass (Addisu et al., 2010). The height-reducing genes and their alleles influence grain yield in wheat by reducing the internal competition for assimilate supply between the developing ears and the stems. Semi-dwarfing *Rht* genes possess a positive effect on grain yield under favorable growing condition (Trethowan et al., 2007). However, several dwarfing genes can reduce early season growth in low input environment (Addisu et al., 2010).

Heading date is another key adaptive trait influenced by many traits, namely vernalization, photoperiod, and earliness. These traits are under the control of three group of genes, *Ppd* gene for photoperiod on homeologus group 2, *Vrn* gene for vernalization on homeologus group 5, and *Efl* gene for earliness in flowering on 2D, 3A, 4D, 6B, 6D, 7B (Scarth and Law, 1984; Sourdille et al., 2000; Worland et al., 1998). *Ppd-D1a* was associated with earlier flowering, reduced height and grain yield (Addisu et al., 2010). Heading time is controlled by several main and epistatic effect QTLs through their control of vernalization, photoperiod response, and earliness (Distelfeld et al., 2009; Reif et al., 2011). Like GY, epistatic interactions contributed to a low extent to the genotypic variance for flowering time (Griffiths et al., 2009).

Grain yield and associated morphological traits show significant genotype, environment and genotype-by-environment interactions, which reduces the genetic gain achieved by phenotypic selection. Change in the relative performance of lines across environments further complicate the selection. Plant breeders often utilize multi-environment trials on as many heterogeneous environments as possible to predict the performance of genotypes across years and locations. However, the genetic and environmental basis of yield, agronomic traits and their interaction with environments is not well understood. With the advent of cost-effective genotyping and dense marker coverage of chromosomes, QTL mapping has enabled the dissection of complicated trait like yield into component loci and their relative effects (Doerge, 2002). It is now possible to quantify gene-gene and genes-environment interaction. With the help of molecular marker and QTL analysis selecting genes for grain yield would be rapid and efficient. QTL analysis identifies the targets for marker-assisted selection of genotype, which can later be used to selection genotype.

In the present study, we used molecular markers from 90K Illumina Infinium array single nucleotide polymorphism (SNP) and double digest restriction-site associated DNA sequencing (ddRADSeq) to genotype 124 RIL lines derived from TAM 112/TAM 111. The objective of this study was to understand and identify the genetic components controlling grain yield and agronomic traits of wheat. In the multi-environment trials of hard red winter wheat from 2011-2017, grain yield (GY), plant height (HT), heading date (HD) and test weight (TW) were investigated. The complex genetic basis of yield and agronomic trait was analyzed using QTL IciMapping software with inclusive composite interval mapping (ICIM) mapping function.

MATERIALS AND METHODS

Population, trials and phenotyping

A recombinant inbred line (RIL) population of 124 F5:7 lines from the cross of TAM 112 (PI 643143) and TAM 111 (PI 631352) was generated to map grain yield and agronomic traits. TAM 111 and TAM 112 are both well-adapted HRWW in the Southern Great Plains of the United States, developed by Texas A&M AgriLife Research (Lazar et al., 2004; Rudd et al., 2014). TAM 112 is adapted to drought stress conditions, while TAM 111 is high yielding cultivars in moderate-high input environments. The RIL plus parents were planted in Bushland, TX (35° 06' N, 102° 27' W), Chillicothe, TX (34° 15' N, 99° 30' W), Clovis, NM (34° 24' N, 103° 12' W), Etter, TX (35° 51' N, 101° 58' W), and Uvalde, TX (29° 21' N, 99° 75' W) from year 2011-2014, and 2017. A total of 28-year-site combinations (environments) were harvested: Bushland dryland in 2011, 2012 and 2017 (11BD, 12BD, 17BD), Bushland irrigated in 2017 (17BI), Chillicothe in 2011, 2012, and 2014 (11CH, 12CH, 14CH), Clovis irrigated in 2017 (17CVI), Etter with five irrigation levels (0% evapotranspiration demand (EP1), 40% ET demand (EP2), 60% ET demand (EP3), 75% of ET demand (EP4), 100% ET demand (EP5)) in 2011, 2012, 1013, 2014, and 2017 (11EP1, 11EP2, 11EP3, 11EP4, 11EP5, 12EP1, 12EP2, 12EP3, 13EP2, 13EP3, 13EP4, 13EP5, 14EP5, 14EP5, 17EP5), Uvalde with four irrigation levels (0% irrigation level (UVLD), 50% irrigation (UV5), 70% irrigation (UV7), and 100% irrigation (UVL)) in 2012 and 2013 (12UVLD, 12UV5, 12UV7, 12UVL, 13UVL, and 13UVLD). Dry environment consisted of 11BD, 12BD, 17BD, 11CH, 12CH, 14CH, 11EP1, 11EP2, 11EP3, 12EP1, 12EP3, 12EP3, 13EP2, 13EP3, 12UVLD, 12UV5, 13UVLD), while irrigated environment consisted of 17BI, 17CVI, 11EP4, 11EP5, 13EP4, 13EP5, 14EP4, 14EP7, 17EP5, 12UV7, 12UVL, 13UVL). All trails were replicated twice in alpha-lattice design with an incomplete block size of five plots, and three occurrences of each parent in a replication. Plot dimension was 6.09 m by 1.52 m on the dry environments and 4.57 m by 1.52 m on the irrigated environments with 0.3 meter between plots. Standard agronomic practices were carried out for each environment.

Grain yield (GY) was measured on all environments, whereas and test weight (TW), days to heading (HD), and plant height (HT) were measured in a subset of environments. Test weight data were collected from 19 environments (11EP5, 11BD, 12CH, 12EP1, 12EP2, 12EP3, 12UV5, 12UV7, 12UVL, 13EP2, 13EP3, 13EP4, 13EP5, 14CH, 14EP4, 14EP5, 17BD, 17BI, 17EP5), heading date from 11 environments (11BD, 11EP1, 11EP2, 11EP3, 11EP4, 11EP5, 12BD, 12EP1, 12EP2, 12EP3, 17BD), and plant height from 11 environments (11BD, 11EP1, 11EP2, 11EP3, 11EP4, 11EP5, 12BD, 12CH, 17BD, 17CVI, 17EP5). Heading date were recorded at visible head stage (Feekes growth stage 10.1) when half of the plants were fully visible. At ripening stage (Feekes growth stage 11), plant height was measured in centimeters (cm) from representative plants in each plot as the distance from the base of the stem to the tip of the spike excluding awns. All trials were harvested using a combine harvester and the total plot weight was used to calculate yield in metric kg ha-1. Test weight, in lb bu-1, was measured using Seedburo equipment (www.seedburo.com, Des Plaines, IL, USA).

Phenotypic data analysis

Descriptive statistics including means, minimum, maximum, standard deviation, and coefficient of variation were calculated to evaluate the variability of the examined traits. Each location-by-year combination was considered as a single environment. Phenotypic traits within each environment were analyzed as an individual environment analysis. The phenotypic mean of a trait across environments was analyzed as single trait analysis. Best linear unbiased predictor (BLUP) mean for all the traits combined across environments were analyzed as combined analysis. BLUP was calculated using a restricted maximum likelihood (REML) approach implemented in ‘lme4’ package on META-R (Alvarado et al., 2018). The individual environment analysis of variance (ANOVA) followed a statistical linear model as follows:

$$Y_{ilp} = \mu + R_p + B_{l(p)} + G_i + \varepsilon_{ilp}$$

Where Y_{ilp} is the observed phenotypic value of the i^{th} genotype in p^{th} repetition in l^{th} block, μ is the overall mean, R_p is the rep effect, $B_{l(p)}$ is the block effect, G_i is the genetic effect of i^{th} genotype and ε_{ilp} is the residual term. Replication and incomplete block were fitted as random term. The combined environment analysis of variance (ANOVA) followed a statistical linear model as follows:

$$Y_{ijlp} = \mu + R_{p(j)} + B_{l(pj)} + G_i + E_j + (GE)_{ij} + \varepsilon_{ijpl}$$

Where Y_{ilp} is the observed phenotypic value of the i^{th} genotype in j^{th} environment in p^{th} repletion in l^{th} block, μ is the overall mean, $R_{p(j)}$ is the effect of p^{th} rep effect in j^{th} environment, $B_{l(pj)}$ is the effect of i^{th} block within the p^{th} replication in the j^{th} environment, G_i is the genetic effect of i^{th} genotype, E_j is the effect of the j^{th} environment, $(GE)_{ij}$ is the effect of the interaction of the i^{th} genotype in the j^{th} environment, and ε_{ijpl} is the residual term. Replication, incomplete block was fitted as random effect. Combined analysis of variance (ANOVA) for all the traits was determined for the significance of genetic variance, phenotypic variance and genotype-by-environment interaction (GEI) components in each environment. The ANOVA and significance were calculated using PROC MIXED with replication and incomplete block as random effect in SAS 9.4 (SAS Institute Inc., 2015) The variance components were calculated to estimate the share of the factors and their interactions in the total variability of the examined traits. The variance components were computed using PROC VARCOMP in SAS 9.4 assuming a random model (SAS Institute Inc., 2015). The entry-mean heritability estimate for combined environment was calculated according to Fehr et al. (1987) using the formula:

$$h^2 = \frac{\sigma_g^2}{\sigma_e^2/_{rt} + \sigma_{ge}^2/_{t} + \sigma_g^2}$$

Where r is the number of replication (rep), t is the number of environments, σ2g is the genotype variance, σ2ge is the G×E interaction variance, and σ2e is the residual variance. PROC CORR in SAS was used to compute Pearson correlations (r_P) based on the following formula:

$$r_P = \frac{Cov_{x,y}}{(\sigma_x^2\ \sigma_y^2)^{1/2}}$$

Genotyping and linkage map construction

Total genomic DNA was isolated from young leaf tissue of each RIL using the cetyl trimethylammonium bromide (CTAB) method with minor modifications (Doyle and Doyle, 1990; Liu et al., 2013). DNA extraction, purification and quantification were conducted in the wheat genetics lab at Texas A&M AgriLife Research, Amarillo, TX. DNA from RIL lines along with four set of parental was genotyped with Illumina Infinium iSelect 90K array-SNP based on the manufacturer’s protocol (www.illumina.com) in USDA-ARS, Fargo, ND. The fluorescence signal captured by Illumina scanner were color coded with red color representing homozygous AA genotype, blue color for homozygous BB genotype and grey color for the heterozygotes (AB). Automatic clustering followed by manual curation of clusters for every marker was done in Genotyping module of GenomeStudio software. Linkage map construction followed the procedures in these research (Assanga et al., 2017a; Assanga et al., 2017b; Liu et al., 2016). This population along with the three sets of parents was also genotyped with double digest restriction-site associated DNA sequencing (ddRADSeq) method developed by Peterson et al (2012) with slight modification in Texas A&M AgriLife Research's Genomics and bioinformatics center, College Station, TX (Wang et al., 2014). GBS libraries were sequenced with Illumina HiSeq 2500 platform (2*125 bp paired-end) at the Genomics and Bioinformatics Center, Texas A&M AgriLife Research at College Station. Custom Perl pipeline utilized to analyses the raw genotypic data. The analysis procedure and parameter settings were conducted according to the description in Wang et al. (2014) with slight modification. SNPs with less than 5 % minor allele frequency (MAF) are filtered. GBS with more than 20 % missing values and heterozygotes more than 10 % were also excluded from the dataset along with all monomorphic GBSs.

SNPs with significant chi-square segregation distortion ($P < 0.01$) or similarity of 100% were eliminated to improve computational efficiency. A total of 5948 polymorphic SNPs, and GBS markers were mapped into 25 linkage groups covering 21 chromosomes using maximum likelihood (ML) algorithm using JoinMap v4.0 software

(Van Ooijen, 2006). Minimum independence LOD score of 3 was set for linkage grouping with an incremental walking speed of 1cM. Linkage groups were assigned to chromosomes and physical locations of corresponding SNPs were extracted from the International Wheat Genome Sequencing Consortium (IWGSC) reference sequence version 1.0 (IWGSC RefSeq v1.0) (Consortium, 2014).

QTL analysis

One-dimensional scanning for mapping additive QTL and two-dimensional scanning for mapping epistasis were undertaken using both the adjusted and unadjusted data in the QTL IciMapping software (Wang et al., 2016). Unadjusted data from individual environment were ran as individual environment QTL analysis. Raw data for a trait across multiple environments were analyzed as multi-environment QTL analysis. The genetic position and effects of QTL were determined by integrated composite interval mapping (ICIM) mapping function in QTL IciMapping for additive effect (ICIM-ADD) and epistasis effect (ICIM-EPI). Stepwise regression with a walking speed of 1cM for additive mapping (ICIM-ADD) and 5cM for epistasis mapping (ICIM-EPI) was set. Two flanking markers for ICIM-ADD and two pairs of flanking markers for ICIM-EPI were selected automatically to control for genetic background in additive and epistasis mapping. The probability for entering variables in stepwise regression of residual phenotype on marker variables was set at 0.001 for ICIM-ADD, and 0.0001 for ICIM-EPI. Threshold for declaring the presence of a QTL was determined through permutation analysis (n=1000) for each trait in each environment to obtain a 0.05 genome-wide probability level of Type I error. The QTL position was estimated as the point on the LOD curve with a peak score greater than the threshold. The QTL were designated according to guidelines in (McIntosh et al., 2003) with a slight change as *QX.tamu.Y*(.#N), where x is a trait, tamu is Texas A&M University, Y is chromosome on which the QTL is located, and N is the unique QTL identifier (optional) given to genomic regions within 50 Mb of the QTL.

RESULTS

ANOVA and heritability

Combined ANOVA showed significant genotypic differences ($P < 0.01$) for grain yield, test weight, heading date and plant height (Table 4.1). Significant differences were also observed for the environments (year-location combination). Grain yield, heading date and plant height exhibited significant difference for incomplete block nested within replication and environment. As expected, significant genotype-by-environment (GE) interactions were present for the four traits analyzed. Except for grain yield, genotype differences explained more variation than genotype-by-environment variation. Traits with entry-mean heritability ≤ 0.3 were categorized as lowly heritable, 0.4 – 0.6 as moderately heritable and > 0.6 as highly heritable traits. All the traits were highly heritable (0.77-0.96). Grain yield showed high heritability (0.77) with an average yield of 2877.4 kg ha-1. An average test weight was 59.1 lb bu-1 with entry-mean heritability of 0.94.

Table 4.1. Analysis of variance, heritability and mean performance of grain yield and agronomic traits

Traits	Units	σ^2_{Geno}[†]	σ^2_{Env}[‡]	$\sigma^2_{\text{Rep (Env)}}$[‡]	$\sigma^2_{\text{Iblk (Rep*Env)}}$[§]	σ^2_{GE}[‡]	σ^2_{Res}[¶]	h^2[#]	LSD	$\bar{X}$±SD	TAM 112	TAM 111
Grain yield (GY)	Kg/ha	26561**	1797204.4**	28148.4**	57564.5**	85329.9**	79569.2**	0.77	552.9	2877.4 ± 1394.4	3043.9	2986.4
Test weight (TW)	lb/bu	0.87**	3.25**	0.08	0.13	0.82**	0.16**	0.94	0.78	59.1 ± 2.1	59.60	59.84
Heading Date (HD)	Days from Jan 1	3.05**	15.46**	0.01	0.21**	1.30**	1.28**	0.96	2.22	115.5 ± 4.01	113.68	117.36
Plant Height (HT)	cm	4.31**	404.71**	0.83	2.41**	3.48**	13.16**	0.87	7.11	73.8 ± 19.01	72.74	73.95

[†] σ^2_{Geno}, genotypic variance

[‡] σ^2_{Rep}, variance due to replication (environment) in percentage

[§] $\sigma^2_{\text{Iblk (Rep)}}$, variance due to incomplete block nested within replication (environment) in percentage

[¶] σ^2_{Res}, residual variance in percentage

[#] h^2, entry-mean heritability

*, **, significant at 0.05, and 0.01 probability levels, respectively

Heading date, recorded in Julian days, were highly heritable with mean heading date of 114 days. An average plant height was 72.74 cm with high heritability (0.87). Transgressive segregates were present for all the traits analyzed (Table 4.1). No significant differences were found between parents for all the traits analyzed except heading date.

Pearson correlation

The phenotypic relationship between traits on combined data was determined using Pearson correlation coefficients (Table 4.2). Correlation coefficients ≤ 0.3 between two traits were categorized as low correlation, 0.4 - 0.6 as moderate correlation, and > 0.6 as high correlation. GY showed significant negative correlation with heading date, but this correlation was weaker (0.26). Correlation between GY and HT on adjusted data from dry environment showed positive correlation in 12BD and 17BD, and significant positive (0.31) in 11BD (Table A6). In irrigated environment, negative correlation (0.23) was observed between GY and HT. Similar correlation and direction was observed between GY and HT in 17EI. Even though no significant correlation was found between GY and HD on combined data, significant negative correlation was found in dry environment, which is further supported by the similar finding from 11BD and 17BD. In irrigated environment, this relationship was positive but not significant as seen in 11EP5 and 11EP4 (Table A6). Positive significant correlation (0.3) was found between GY and TW in both dry and irrigated environment. Negative correlation was found between heading date and plant height in dry environment. This relationship was positive in irrigated environments as seen in 11EP4 and 11EP5.

Table 4.2. Correlation matrix for grain yield and agronomic traits for predicted means (BLUP) across environments

Traits[†]	GY	TW	HD
TW	0.05461		
HD	0.14238	-0.14448	
HT	-0.26039**	0.12404	-0.1489

[†] GY, grain yield; TW, test weight; HD, heading date; HT, plant height
*, **, significant at 0.05, and 0.01 probability levels, respectively

QTL for grain yield

From the individual environment and multi-environment analysis, 17 unique QTLs were detected for grain yield (Table 4.3 and 4.4). Among them, five QTLs were detected in both the analysis. QTLs for grain yield on chromosome 1D (*Qyld.tamu.1D*.11 at 421.8 Mb), 4B (*Qyld.tamu.4B*.33 at 266.8 Mb), 4D (*Qyld.tamu.4D.36* at 109.8 Mb, and *Qyld.tamu.4D*.38 at 445.5 Mb) and 7D (*Qyld.tamu.7D*.63 at 60.6-84.3 Mb) were detected in individual and multi-environment QTL analysis (Table 4.3 and 4.4). These QTLs on chromosome 1D, 4B and 7D received high value allele (HAV) from TAM 112, while remaining QTLs received it from TAM 111. These five QTLs explained R^2 from 6.8-28% of the variation present in the yield, with the additive effects (A) up to 374.1 kg ha-1(Table 4.3). Additive-by-environment (AE) interaction explained up to 96.7% of the variation, which is 378.2 kg ha^{-1}(Table 4.4).

Table 4.3. Significant grain yield and agronomic trait QTLs, additive effects detected in individual environment analysis

Traits†	Env ‡	QTL name	QTL ID	Peak (cM)	Mbp§	Peak SNP	LOD¶	R^2#	A††	M-E‡‡
HD	11BD	*Qhd.tamu.1D.11*	11	68	420.9	2236906_1dl_5649	3.9	8.4	-0.8	N
HD	12EP1	*Qhd.tamu.1D.12*	12	114	486.8	IWB41436	3.6	8.8	0.7	Y
HD	12EP3	*Qhd.tamu.1D.12*	12	114	486.8	IWB41436	3.7	7.3	0.5	Y
HD	17BD	*Qhd.tamu.1D.12*	12	114	486.8	IWB41436	29.7	29.9	1.1	Y
HD	11EP5	*Qhd.tamu.2B.18*	18	61	39.2	IWB22828	4.0	11.3	0.9	N
HD	11EP1	*Qhd.tamu.2B.19*	19	64	65.1	IWB72841	5.0	11.3	1.0	N
HD	11EP1	*Qhd.tamu.2D.21*	21	29	16.0	IWB8481	5.8	13.1	1.1	Y
HD	11EP2	*Qhd.tamu.3A.25*	25	59	507.5	4285803_3al_628	3.7	9.4	-1.1	N
HD	11EP2	*Qhd.tamu.4B.34*	34	94	659.2	IWA27	6.7	18.3	1.5	Y
HD	12EP3	*Qhd.tamu.7B.59*	59	21	8.5	IWB6455	3.8	8.0	0.5	Y
HD	11BD	*Qhd.tamu.7D.63*	63	82	64.3	3950120_7ds_5316	8.8	22.4	-1.3	Y
HD	11EP4	*Qhd.tamu.7D.63*	63	81	64.3	3950120_7ds_5316	5.8	15.2	-1.1	Y
HD	11EP5	*Qhd.tamu.7D.63*	63	82	64.3	3950120_7ds_5316	5.6	16.1	-1.1	Y
HD	12BD	*Qhd.tamu.7D.63*	63	82	64.3	3950120_7ds_5316	13.2	31.9	-0.9	Y
HD	12EP1	*Qhd.tamu.7D.63*	63	81	64.3	3950120_7ds_5316	6.0	16.8	-1.0	Y
HD	12EP2	*Qhd.tamu.7D.63*	63	81	64.3	3950120_7ds_5316	5.4	18.3	-0.7	Y
HD	12EP3	*Qhd.tamu.7D.63*	63	81	64.3	3950120_7ds_5316	8.4	18.5	-0.8	Y
HD	17BD	*Qhd.tamu.7D.63*	63	80	64.3	3950120_7ds_5316	11.4	7.6	-0.6	Y
HD	11EP1	*Qhd.tamu.7D.63*	63	89	78.5	IWB44453	7.9	20.4	-1.4	Y
HT	12BD	*Qht.tamu.1A.3*	3	33	296.2	3888483_1al_4013	10.4	16.5	-0.5	Y
HT	12BD	*Qht.tamu.1A.5*	5	77	520.4	3904706_1al_3369	4.0	5.7	0.3	N
HT	12BD	*Qht.tamu.1D.12*	12	80	444.0	2285810_1dl_1627	3.9	5.7	0.3	Y
HT	11EP4	*Qht.tamu.1D.12*	12	118	492.2	IWA3764	4.4	11.0	2.3	Y
HT	12BD	*Qht.tamu.4D.35*	35	0	20.6	IWB15038	4.2	5.9	0.3	Y
HT	12BD	*Qht.tamu.6A.48*	48	16	7.6	IWB11242	5.0	7.1	0.4	Y
HT	12BD	*Qht.tamu.7A.57*	57	90	85.8	4219271_7as_2211	4.0	5.6	0.3	N
HT	12CH	*Qht.tamu.7D.62*	62	50	21.7	IWB21023	5.6	16.8	1.1	Y
HT	17EI	*Qht.tamu.7D.63*	63	79	60.6	IWB35446	3.3	8.1	-1.0	Y
HT	11EP5	*Qht.tamu.7D.63*	63	80	64.3	3950120_7ds_5316	3.8	13.5	-1.6	Y
HT	12BD	*Qht.tamu.7D.64*	64	126	123.3	10396674_3b_3606	4.0	5.6	0.3	N
TW	13EP5	*Qtw.tamu.1A.5*	5	64	485.2	3894604_1al_116	4.1	5.4	-0.4	Y
TW	12EP3	*Qtw.tamu.1D.11*	11	46	375.4	2263785_1dl_1257	4.9	11.8	0.5	Y
TW	12CH	*Qtw.tamu.1D.11*	11	69	421.8	2237051_1dl_3543	3.8	11.3	0.4	Y
TW	13EP5	*Qtw.tamu.2B.20*	20	124	708.7	8055466_2bl_812	7.3	10.5	0.5	Y
TW	12EP3	*Qtw.tamu.2B.20*	20	141	745.9	8091350_2bl_6123	3.6	8.6	0.4	Y
TW	13EP5	*Qtw.tamu.2D.22*	22	103	82.0	5329935_2ds_3804	5.3	7.2	0.4	Y
TW	13EP4	*Qtw.tamu.4B.32*	32	27	17.0	IWB49194	3.6	10.0	-0.6	N
TW	12UV7	*Qtw.tamu.4D.35*	35	5	29.0	IWB30733	5.6	2.5	0.6	Y
TW	17BD	*Qtw.tamu.4D.35*	35	9	35.4	2305190_4ds_510	4.8	13.6	0.5	Y
TW	12BD	*Qtw.tamu.4D.35*	35	10	62.8	2305880_4ds_1018	3.9	8.5	0.3	Y

Table 4.3 Continued

Traits[†]	Env [‡]	QTL name	QTL ID	Peak (cM)	Mbp[§]	Peak SNP	LOD[¶]	R^2[#]	A[††]	M-E[‡‡]
TW	12EP1	*Qtw.tamu.4D.35*	35	10	62.8	2305880_4ds_1018	4.2	13.3	0.5	Y
TW	12EP3	*Qtw.tamu.4D.35*	35	10	62.8	2305880_4ds_1018	6.2	15.2	0.5	Y
TW	13EP2	*Qtw.tamu.4D.35*	35	11	62.8	2305880_4ds_1018	7.8	16.3	0.8	Y
TW	14CH	*Qtw.tamu.4D.35*	35	11	62.8	2305880_4ds_1018	4.8	12.0	0.6	Y
TW	12UV5	*Qtw.tamu.4D.36*	36	13	109.8	2279925_4ds_1008	3.5	9.9	0.5	N
TW	12UVL	*Qtw.tamu.4D.37*	37	22	366.3	IWB10053	4.2	10.8	0.5	N
TW	12BD	*Qtw.tamu.6A.48*	48	20	12.4	4344525_6as_6773	4.1	9.1	0.3	Y
TW	12UV7	*Qtw.tamu.6A.49*	49	134	603.3	IWB11675	20.0	11.6	1.3	Y
TW	13EP5	*Qtw.tamu.6A.49*	49	139	608.5	IWB45148	4.6	6.0	-0.4	Y
TW	12CH	*Qtw.tamu.6A.49*	49	144	613.5	IWB42057	3.4	9.7	-0.4	Y
TW	12UVL	*Qtw.tamu.6B.50*	50	1	130.3	IWB38972	6.5	17.6	0.6	Y
TW	14EP4	*Qtw.tamu.6B.50*	50	0	130.3	IWB38972	5.0	13.7	0.3	Y
TW	11EP5	*Qtw.tamu.6B.51*	51	6	466.0	4352366_6bl_1112	5.5	11.8	0.5	Y
TW	12BD	*Qtw.tamu.6B.51*	51	7	466.0	4352366_6bl_1112	5.0	11.1	0.3	Y
TW	13EP2	*Qtw.tamu.6B.51*	51	7	466.0	4352366_6bl_1112	4.5	9.0	0.6	Y
TW	14CH	*Qtw.tamu.6B.51*	51	7	466.0	4352366_6bl_1112	3.8	9.3	0.6	Y
TW	17BD	*Qtw.tamu.6B.51*	51	6	466.0	4352366_6bl_1112	3.8	10.0	0.5	Y
TW	13EP5	*Qtw.tamu.6B.52*	52	8	559.4	IWB14861	10.4	16.0	0.7	N
TW	12BD	*Qtw.tamu.6D.56*	56	96	458.5	3290494_6dl_50	4.3	9.5	-0.3	Y
TW	12UV5	*Qtw.tamu.6D.56*	56	97	459.2	IWB24926	4.0	11.3	-0.6	Y
TW	11EP5	*Qtw.tamu.7D.63*	63	79	60.6	IWB35446	9.2	21.6	0.7	Y
TW	12CH	*Qtw.tamu.7D.63*	63	79	60.6	IWB35446	4.0	11.9	0.4	Y
TW	13EP2	*Qtw.tamu.7D.65*	65	188	745.9	Gb3P4y	3.8	7.5	-0.5	N
YLD	17EI	*Qyld.tamu.1A.4*	4	58	411.7	3975933_1al_3664	5.2	12.9	-102.2	N
YLD	12CH	*Qyld.tamu.1D.11*	11	69	421.8	2237051_1dl_3543	5.6	9.9	68.7	Y
YLD	13EP3	*Qyld.tamu.2A.17*	17	125	734.5	6415190_2al_16820	5.0	10.8	96.6	N
YLD	12UVL	*Qyld.tamu.3B.27*	27	5	48.6	10435017_3b_750	4.8	9.9	-174.0	N
YLD	17CVI	*Qyld.tamu.4B.33*	33	39	266.8	4883984_4bs_7910	20.4	22.3	-374.1	Y
YLD	14EP4	*Qyld.tamu.4B.34*	34	94	659.2	IWA27	3.6	9.8	98.8	N
YLD	12UVLD	*Qyld.tamu.4B.34*	34	99	660.9	IWB32997	4.3	11.9	96.5	N
YLD	17CVI	*Qyld.tamu.4D.35*	35	2	20.6	IWB15038	5.6	4.9	-173.2	N
YLD	17BI	*Qyld.tamu.4D.36*	36	13	109.8	2279925_4ds_1008	8.3	18.4	-280.6	Y
YLD	14CH	*Qyld.tamu.4D.38*	38	28	445.5	IWB3336	13.4	28.2	85.9	Y
YLD	17BI	*Qyld.tamu.6A.48*	48	20	12.4	4344525_6as_6773	4.4	8.9	-195.8	N
YLD	14CH	*Qyld.tamu.6D.54*	54	1	19.6	2080712_6ds_6490	4.3	7.7	45.2	N
YLD	12CH	*Qyld.tamu.7B.59*	59	24	15.6	IWA1089	6.0	10.9	-72.3	N
YLD	12CH	*Qyld.tamu.7B.60*	60	100	617.0	6722360_7bl_819	5.1	9.3	67.0	N
YLD	12UVLD	*Qyld.tamu.7D.63*	63	79	60.6	IWB35446	3.5	9.7	87.3	Y
YLD	12CH	*Qyld.tamu.7D.63*	63	80	64.3	3950120_7ds_5316	5.0	8.8	64.5	Y
YLD	17BD	*Qyld.tamu.7D.63*	63	80	64.3	3950120_7ds_5316	3.9	12.5	60.1	Y
YLD	14CH	*Qyld.tamu.7D.63*	63	86	72.9	IWA1247	3.7	6.8	42.4	Y

Table 4.3 Continued

Traits[†]	Env [‡]	QTL name	QTL ID	Peak (cM)	Mbp[§]	Peak SNP	LOD[¶]	$R^{2\#}$	A[††]	M-E[‡‡]
YLD	17BI	*Qyld.tamu.7D.63*	63	97	84.3	3938880_7ds_2029	5.0	11.1	-218.0	Y
YLD	12BD	*Qyld.tamu.7D.65*	65	181	591.2	IWB10006	4.7	13.5	24.7	N
YLD	13EP4	*Qyld.tamu.7D.65*	65	198	598.6	IWB45562	3.4	9.0	45.2	N

[†] HD, heading date; HT, plant height; TW, test weight; YLD, grain yield

[‡] Env, environments; 11BD, 2011 Bushland dryland; 12BD, 2012 Bushland dryland; 17BD, 2017 Bushland dryland; 17BI, 2017 Bushland irrigated; 11CH, 2011 Chillicothe, 12CH, 2012 Chillicothe; 14CH, 2014 Chillicothe; 17CVI, 2017 Clovis irrigated; 11EP1, 2011 Etter 0% ET; 11EP2, 2011 Etter 40% ET; 11EP3, 2011 Etter 60% ET; 11EP4, 2011 Etter 75% ET; 11EP5, 2011 Etter 100% ET; 12EP1, 2012 Etter 0% ET; 12EP2, 2012 Etter 40% ET; 12EP3, 2012 Etter 60% ET; 13EP2, 2013 Etter 40% ET; 13EP3, 2013 Etter 60% ET; 13EP4, 2013 Etter 75% ET; 13EP5, 2013 Etter 100% ET; 14EP4, 2014 Etter 75% ET; 14EP5, 2014 Etter 100% ET; 17EI, 2017 Etter 100% ET; 12UVLD, 2012 Uvalde dryland; 12UV5, 2012 Uvalde 50% ET; 12UV7, 2012 Uvalde 70% ET; 12UVL, 2012 Uvalde irrigated; 13UVL, 2013 Uvalde irrigated; 13UVLD, 2013 Uvalde dryland

[§] IWGSC RefSeq v1.0 pseudomolecule position in mega base pair (Mbp)

[¶] Logarithm of odds

[#] Phenotypic variance explained by each QTL

[††] Additive effect of each QTL, negative additive effects indicate high value allele (HAV) from TAM 111, positive values correspond to HVA from TAM 112

[‡‡] M-E, multi-environment QTL analysis; Y, QTL was also detected in multi-environment analysis; N, QTL was detected only in individual environment analysis

Table 4.4. Significant QTLs, additive effects and additive-by-environment interaction effects from single trait-multi environment analysis

Traits[†]	QTL Name	QTL ID	Peak (cM)	Mbp[‡]	Peak SNP	LOD[§]	R^2[¶]	R^2 (A)[#]	R^2 (A×E)[††]	A[‡‡]	AE[§§]	I-E[¶¶]
HD	*Qhd.tamu.1A.1*	1	0	1.2	IWA974	9.2	3.2	2.3112	0.8818	0.3	0.01 – (-0.3)	N
HD	*Qhd.tamu.1A.1*	1	9	11.8	IWB46642	8.6	3.1	2.0789	0.9987	0.3	-0.01 – 0.3	N
HD	*Qhd.tamu.1A.2*	2	19	224.2	3932290_1al_708	9.8	3.4	2.4612	0.9683	0.3	-0.02 – (-0.3)	N
HD	*Qhd.tamu.1A.2*	2	23	238.3	3975622_1al_1296	9.4	3.3	2.3501	0.9597	0.3	0 – 0.3	N
HD	*Qhd.tamu.1A.3*	3	30	294.7	3915571_1al_4855	9.6	3.7	2.4099	1.291	0.3	0.01 – 0.35	N
HD	*Qhd.tamu.1D.12*	12	114	486.8	IWB41436	41.3	6.9	3.2428	3.6474	0.4	0.07 – 0.73	Y
HD	*Qhd.tamu.2A.15*	15	71	533.5	IWB24910	9.9	3.5	2.9102	0.6053	-0.3	-0.01 – (-0.38)	N
HD	*Qhd.tamu.2A.16*	16	82	635.6	IWB68780	9.0	3.3	2.2262	1.0935	-0.3	0 – (-0.41)	N
HD	*Qhd.tamu.2D.21*	21	29	16.0	IWB8481	11.6	4.7	2.2471	2.4654	0.3	0 - 0.81	Y
HD	*Qhd.tamu.4B.34*	34	92	657.2	IWB4448	8.8	2.4	1.7016	0.6852	0.3	0.04 - 0.28	Y
HD	*Qhd.tamu.4B.34*	34	94	659.2	IWA27	12.4	7.2	2.9689	4.2658	0.3	0.06 - 1.2	Y
HD	*Qhd.tamu.7B.59*	59	24	15.6	IWA1089	8.7	2.2	1.6068	0.6017	0.2	0.01 - 0.25	Y
HD	*Qhd.tamu.7D.63*	63	81	64.3	3950120_7ds_5316	64.9	16.5	14.091	2.4389	-0.7	0.01 - 0.47	Y
HT	*Qht.tamu.1A.3*	3	33	296.2	3888483_1al_4013	14.5	4.6	1.4407	3.1119	-0.2	-0.01 - 0.76	Y
HT	*Qht.tamu.1B.9*	9	118	642.8	3915619_1bl_1936	11.7	7.6	4.3392	3.2858	-0.4	0.12 – (-0.71)	N
HT	*Qht.tamu.1D.12*	12	118	492.2	IWA3764	9.4	17.1	6.6893	10.4564	0.5	-0.03 - 1.78	Y
HT	*Qht.tamu.4D.35*	35	0	20.6	IWB15038	8.8	4.9	1.1922	3.6798	0.2	0.04 - 0.9	Y
HT	*Qht.tamu.6A.48*	48	16	7.6	IWB11242	8.6	3.9	2.1859	1.7627	0.3	0.04 - 0.53	Y
HT	*Qht.tamu.7D.62*	62	47	21.1	3916420_7ds_3323	8.5	4.5	1.0147	3.5229	0.2	-0.08 - 0.82	Y
HT	*Qht.tamu.7D.63*	63	80	64.3	3950120_7ds_5316	13.2	19.6	4.6483	14.9664	-0.4	-0.15 – (-1.51)	Y
TW	*Qtw.tamu.1A.1*	1	9	11.8	IWB46642	11.3	0.0	0	0	-0.2	0 – (-0.26)	N
TW	*Qtw.tamu.1A.1*	1	13	21.0	IWB21788	12.5	0.0	0	0	-0.2	-0.01 – (-0.31)	N
TW	*Qtw.tamu.1A.1*	1	15	25.5	3310348_1as_2438	11.9	0.0	0	0	-0.2	-0.01 – (-0.3)	N
TW	*Qtw.tamu.1A.2*	2	22	232.6	3877153_1al_1567	12.2	0.0	0	0	-0.2	-0.01 – (-0.29)	N
TW	*Qtw.tamu.1A.3*	3	29	290.7	3909230_1al_1823	12.8	0.0	0	0	-0.2	0 – (-0.31)	N
TW	*Qtw.tamu.1A.3*	3	34	304.1	3916820_1al_4455	12.5	0.0	0	0	-0.2	-0.01 – (-0.31)	N
TW	*Qtw.tamu.1A.3*	3	39	339.4	3895363_1al_1924	12.6	0.0	0	0	-0.2	0 – (-0.29)	N
TW	*Qtw.tamu.1A.4*	4	44	358.8	3944816_1al_8842	11.9	0.0	0	0	-0.2	0.02 – (-0.23)	N
TW	*Qtw.tamu.1A.4*	4	51	380.7	3916130_1al_8063	13.4	0.0	0	0	-0.2	0 - 0.24	N
TW	*Qtw.tamu.1A.4*	4	53	390.1	IWB31924	12.9	0.0	0	0	-0.2	0 – (-0.27)	N
TW	*Qtw.tamu.1A.5*	5	64	485.2	3894604_1al_116	16.4	0.0	0	0	-0.2	0 – (-0.21)	Y
TW	*Qtw.tamu.1D.11*	11	46	375.4	2263785_1dl_1257	13.1	0.0	0	0	0.1	0 – (-0.37)	Y
TW	*Qtw.tamu.1D.11*	11	69	421.8	2237051_1dl_3543	20.0	0.0	0	0	0.2	0.01 - 0.34	Y
TW	*Qtw.tamu.1D.12*	12	117	489.7	IWB17626	11.8	0.0	0	0	0.2	-0.01 - 0.92	N
TW	*Qtw.tamu.2B.20*	20	124	708.7	8055466_2bl_812	20.5	0.0	0	0	0.1	0 – (-1.25)	Y
TW	*Qtw.tamu.2D.22*	22	103	82.0	5329935_2ds_3804	18.9	0.0	0	0	0.2	0 - 0.98	Y
TW	*Qtw.tamu.2D.23*	23	115	533.0	9842271_2dl_198	13.0	0.0	0	0	0.2	-0.03 - 0.93	N
TW	*Qtw.tamu.3B.28*	28	27	507.0	10680128_3b_818	13.0	0.0	0	0	-0.1	-0.03 – (-0.25)	N
TW	*Qtw.tamu.3D.30*	30	53	548.6	6926803_3dl_1308	15.6	0.0	0	0	-0.2	-0.02 – (-0.87)	N

Table 4.4 Continued

Traits[†]	QTL Name	QTL ID	Peak (cM)	Mbp[‡]	Peak SNP	LOD[§]	R^2[¶]	R^2 (A)[#]	R^2 (A×E)[††]	A[‡‡]	AE[§§]	I-E[¶¶]
TW	*Qtw.tamu.3D.30*	30	58	554.7	6956616_3dl_71	16.0	0.0	0	0	-0.2	0 – (-0.89)	N
TW	*Qtw.tamu.3D.30*	30	63	562.7	IWB8129	13.9	0.0	0	0	-0.2	0 – (-0.82)	N
TW	*Qtw.tamu.4D.35*	35	11	62.8	2305880_4ds_1018	35.7	0.0	0	0	0.3	0 - 0.54	Y
TW	*Qtw.tamu.5A.39*	39	40	73.8	IWB2928	13.9	0.0	0	0	0.2	0 – (-0.26)	N
TW	*Qtw.tamu.5A.40*	40	43	157.3	1500192_5as_1232	13.1	0.0	0	0	0.2	0 – (-0.25)	N
TW	*Qtw.tamu.5A.44*	44	194	702.0	IWB28861	13.5	0.0	0	0	0.1	0 – (-0.76)	N
TW	*Qtw.tamu.5B.45*	45	75	589.4	IWB26282	14.6	0.0	0	0	-0.2	0 – (-0.27)	N
TW	*Qtw.tamu.5B.45*	45	94	646.0	10851545_5bl_762	14.0	0.0	0	0	-0.2	0 – (-0.82)	N
TW	*Qtw.tamu.6A.48*	48	12	7.2	4348240_6as_16935	14.6	0.0	0	0	0.2	0 - 0.29	Y
TW	*Qtw.tamu.6A.48*	48	17	9.9	4426950_6as_3288	13.1	0.0	0	0	0.1	0 – (-0.74)	Y
TW	*Qtw.tamu.6A.48*	48	20	12.4	4344525_6as_6773	17.0	0.0	0	0	0.1	0 – (-0.75)	Y
TW	*Qtw.tamu.6A.49*	49	134	603.3	IWB11675	24.7	0.0	0	0	-0.1	0 - 1.34	Y
TW	*Qtw.tamu.6A.49*	49	139	608.5	IWB45148	13.9	0.0	0	0	-0.2	-0.02 – (-0.24)	Y
TW	*Qtw.tamu.6A.49*	49	143	611.6	IWB67460	14.4	0.0	0	0	-0.2	0 – (-0.34)	Y
TW	*Qtw.tamu.6B.50*	50	1	130.3	IWB38972	14.3	0.0	0	0	0.2	0.06 - 0.75	Y
TW	*Qtw.tamu.6B.51*	51	7	466.0	4352366_6bl_1112	22.8	0.0	0	0	0.2	0.07 - 0.74	Y
TW	*Qtw.tamu.6D.56*	56	97	459.2	IWB24926	18.6	0.0	0	0	-0.2	-0.01 – (-0.35)	Y
TW	*Qtw.tamu.6D.56*	56	99	459.2	IWB24926	17.1	0.0	0	0	-0.2	0.01 - 0.23	Y
TW	*Qtw.tamu.7B.59*	59	19	8.5	IWB6455	17.2	0.0	0	0	-0.1	0 - 0.45	N
TW	*Qtw.tamu.7B.59*	59	48	64.5	3136917_7bs_1218	12.3	0.0	0	0	-0.1	0 - 0.37	N
TW	*Qtw.tamu.7B.61*	61	1	707.4	6728417_7bl_5629	13.3	0.0	0	0	0.2	-0.02 - 0.79	N
TW	*Qtw.tamu.7D.63*	63	79	60.6	IWB35446	26.6	0.0	0	0	0.2	0 - 0.47	Y
YLD	*Qyld.tamu.1B.8*	8	85	556.3	3859439_1bl_2195	14.7	22.5	10.6996	11.8119	25.9	2.6 – (-66.81)	N
YLD	*Qyld.tamu.1D.11*	11	69	421.8	2237051_1dl_3543	17.0	19.4	5.5049	13.8567	18.6	-1.97 - 70.82	Y
YLD	*Qyld.tamu.3A.24*	24	8	9.6	IWB7693	16.2	24.8	0.2719	24.4824	-4.2	-2.54 – (-80.56)	N
YLD	*Qyld.tamu.4B.33*	33	39	266.8	4883984_4bs_7910	28.1	97.0	0.2736	96.7129	4.2	-0.31 – (-378.28)	Y
YLD	*Qyld.tamu.4D.36*	36	13	109.8	2279925_4ds_1008	18.0	63.1	4.2978	58.8142	-16.4	1.66 – (-262.41)	Y
YLD	*Qyld.tamu.4D.38*	38	28	445.5	IWB3336	21.2	19.8	0.3519	19.4101	-4.7	0.62 – (-110.06)	Y
YLD	*Qyld.tamu.7D.63*	63	79	60.6	IWB35446	22.1	30.7	2.4349	28.2264	12.4	-0.47 - 97.84	Y
YLD	*Qyld.tamu.7D.63*	63	97	84.3	3938880_7ds_2029	17.0	44.1	0	44.0885	0.0	0.73 – (-202.97)	Y

[†] HD, heading date; HT, plant height; TW, test weight; YLD, grain yield

[‡] IWGSC RefSeq v1.0 pseudomolecule position in Mega base pair (Mbp)

[§] Logarithm of odds

[¶] total Phenotypic variance explained by each QTL

[#] phenotypic variance explained by additive effect

[††] phenotypic variance explained by additive by environmental effect

[‡‡] Additive effect of each QTL, negative additive effects indicate high value allele (HAV) from TAM 111, positive values correspond to HVA from TAM 112

[§§] AE, additive-by-environment interaction effect, Negative value indicates the additive-by-environment reduced the trait, positive value increased the trait

Table 4.4 Continued

[¶¶] I-E, Individual environment analysis; Y, corresponding QTL was also detected in individual-environment analysis; N, corresponding QTL was detected only in multi-environment analysis

Additional QTLs were detected on chromosome 1A (*Qyld.tamu.1A.4* at 411.7 Mb), 2A (*Qyld.tamu.2A.17* at 734.5 Mb), 3B (*Qyld.tamu.3B.27* at 48.6 Mb), 4B (*Qyld.tamu.4B.34* at 659.2-660.9 Mb), 4D (*Qyld.tamu.4D.35* at 20.6 Mb), 6A (*Qyld.tamu.6A.48* at 12.4 Mb), 6D (*Qyld.tamu.6D.54* at 19.6 Mb), 7B (*Qyld.tamu.7B.59* at 15.6 Mb and *Qyld.tamu.7B.60* at 617 Mb) and 7D (*Qyld.tamu.7D.65* at 591.2-598.6 Mb) by individual environment QTL analysis (Table 4.3). Similarly, multi-environment QTL analysis detected two additional QTLs on chromosome 1B (*Qyld.tamu.1B.8* at 556 Mb) and on 3A (*Qyld.tamu.3A.24* at 9.6 Mb) (Table 4.4).

QTL for plant height

For plant height, QTLs on chromosome 1A (*Qht.tamu.1A.3* at 296.2 Mb), 1D (*Qht.tamu.1D.12* at 492.2 Mb), 4D (*Qht.tamu.4D.35* at 20.6 Mb), 6A (*Qht.tamu.6A.48* at 7.6 Mb) and 7D (*Qht.tamu.7D.62* at 21.7 Mb and *Qht.tamu.7D.63* at 64.3 Mb) were identified both in individual environment and multi-environment QTL analysis (Table 4.3 and 4.4). Additional QTLs were detected on chromosome 1A (*Qht.tamu.1A.5* at 520.4 Mb), 7A (*Qht.tamu.7A.57* at 85.8 Mb) and 7D (*Qht.tamu.7D.64* at 123.3 Mb) from individual environment QTL analysis, and on chromosome 1B (*Qht.tamu.1B.9* at 643 Mb) from multi-environment QTL analysis (Table 4.4). QTLs on chromosome 1A (296.2 Mb), 1B, and 7D (60.6-64.3 Mb) received high value allele from TAM 111 with these alleles explaining up to 17.0 % of the variation present in plant height in 12BD. AE for QTL on 7D (64.3 Mb) explained up to 14.9% of the phenotypic variance with the corresponding reduction of 1.36 cm in plant height (Table 4.4).

QTL for heading date

Individual environment QTL analysis detected QTL for plant heading date on chromosome 1D (*Qhd.tamu.1D.12* at 486.8 Mb), 2D (*Qhd.tamu.2D.21* at 16 Mb), 4B (*Qhd.tamu.4B.34* at 659.2 Mb) and 7D (*Qhd.tamu.7D.63* at 64.3 Mb) (Table 4.3). Presence of these QTLs was also confirmed by multi-environment QTL analysis (Table 4.4). Additional QTLs on chromosome 1D (*Qhd.tamu.1D.11* at 420.9 Mb), 2B (*Qhd.tamu.2B.18* at 39.2 Mb and *Qhd.tamu.2B.19* at 65.1 Mb), 3A (*Qhd.tamu.3A.25* at 507.5 Mb) were also detected by individual environment analysis. Multi-environment QTL analysis detected additional QTLs on chromosome 1A (*Qhd.tamu.1A.1* at 8.6-9.2 Mb, *Qhd.tamu.1A.2* at 224-238 Mb and *Qhd.tamu.1A.3* at 295 Mb) and 2A (*Qhd.tamu.2A.15* at 534 Mb, *Qhd.tamu.2A.16* at 636 Mb). High value alleles for heading date QTLs on chromosome 1A, 1D (at 486.8 Mb), 2B, 2D, 4B, 7B originated from TAM 112 with these alleles explaining up to 18.3% of the variation in heading date, as seen in 11EP2 (Table 4.3). HVA alleles coming from TAM 112 increasing heading date by 2 days in this environment. Compared to the main additive effect (A), AE contributed proportionally less variation, up to 4.3% of the variation in heading date (Table 4.4). HVA allele originating from TAM 111 explained up to 32 % of the variation in heading date as seen in 12BD with increase of a day in heading date (Table 4.3).

QTL for test weight

Test weight QTLs were detected by both individual environment and multi-environment QTL analysis on chromosome 1A (*Qtw.tamu.1A.5* at 485.2 Mb), 1D (*Qtw.tamu.1D.11* at 375.4-421.8 Mb), 2B (*Qtw.tamu.2B.20* at 745.9 Mb), 2D

(*Qtw.tamu.2D.22* at 82 Mb), 4D (*Qtw.tamu.4D.35* at 29-62.8 Mb), 6A (*Qtw.tamu.6A.48* at 12.4 Mb, *Qtw.tamu.6A.49* at 603.3-613.5 Mb), 6B (*Qtw.tamu.6B.51* at 466 Mb), 6D (*Qtw.tamu.6D.56* at 458.5-459.2 Mb) and 7D (*Qtw.tamu.7D.63* at 60.6 Mb) (Table 4.3 and 5.4). Additional QTLs were detected on chromosome 4B (*Qtw.tamu.4B.32* at 17 Mb), 4D (*Qtw.tamu.4D.36* at 109.8 Mb, *Qtw.tamu.4D.37* at 366.6 Mb), 6B (*Qtw.tamu.6B.52* at 559.2 Mb) and 7D (*Qtw.tamu.7D.65* at 745.8 Mb) from individual environment QTL analysis (Table 4.3). Multi-environment QTL analysis detected extra QTLs on chromosome 1A (*Qtw.tamu.1A.1* at 11.8-25.5 Mb, *Qtw.tamu.1A.2* at 232.6 Mb, *Qtw.tamu.1A.3* at 304.1-339.4 Mb and *Qtw.tamu.1A.4* at 358.8-390.1 Mb), 1D (*Qtw.tamu.1D.12* at 489.1 Mb), 2D (*Qtw.tamu.2D.23* at 533 Mb), 3B (*Qtw.tamu.3B.28* at 507 Mb), 3D (*Qtw.tamu.3D.30* at 548.6-562.7 Mb), 5A (*Qtw.tamu.5A.39* at 73.8 Mb, *Qtw.tamu.5A.40* at 157.3 Mb and *Qtw.tamu.5A.44* at 702 Mb), 5B (*Qtw.tamu.5B.45* at 589.4-646 Mb) and 7B (*Qtw.tamu.7B.59* at 8.5-64.5 Mb and *Qtw.tamu.7B.61* at 707.4 Mb) (Table 4.4). QTL on chromosome 6B (*Qtw.tamu.6B.50* at 130.3 Mb) in 12UVL explained up to 17.6% of the variation in test weight. For QTL on chromosome 6A (*Qtw.tamu.6A.49* at 603.3 Mb), alleles contributed by TAM 112 increased test weight by 1.3 lb bu-1 (Table 4.3). For QTLs on chromosome 2B, 2D, 4D, 6B, 7D (60.6 Mb), high value allele was contributed by TAM 112. QTL on chromosome 6A (*Qtw.tamu.6A.49* at 603.3-613.5 Mb) showed significant AE interaction as HAV switched from TAM 1112 in 12BD and 17UVL to TAM 111 in 13EP5 and 12CH.

QTL cluster and stable QTL

From individual or multi-environment analysis, five genomic regions were associated with more than a single trait (Table 4.5). These QTLs were identified as multi-trait QTL or QTL cluster (abbreviated as *Qmt.tamu.chromosome.QTL ID*). From individual environment analysis, five QTLs were detected in more than one environment for heading data, plant height, test weight and grain yield (Table 4.6). These QTLs were identified as stable QTLs or consistent QTL (abbreviated as *Qcon.tamu.chromosme.QTL ID*). QTL on chromosome 1D (395.4-421.8 Mb and 439.5-492.2 Mb), 4B (638.1-666.3 Mb), 4D (20.6-62.8 Mb), and on 7D (60.6-108.2 Mb) appeared to be consistent and harbored QTLs for multiple traits (Tables 4.3, 4.4 and 4.5). QTL on chromosome 1D (*Qmt.tamu.1D* at 375.4-421.8 Mb) controlled heading date, test weight and grain yield. This QTL explained R^2 up to 8.4% for heading date and up to 19.4% in grain yield. For this QTL, TAM 112 contributed 68.7 kg ha-1 increment, while TAM 112 imparted increase in heading date by a day (Table 4.5). QTL *Qmt.tamu.1D* on chromosome 1D at 439.5-492.2 Mb controlled heading date, plant height and test weight, for which TAM 112 contributed favorable allele to increase test weight. For QTL on chromosome 4B (*Qmt.tamu.4B* at 638.1-666.3 Mb), TAM 112 was contributing alleles for longer heading date and higher grain yield. Both parents contributed favorable allele for QTL cluster on chromosome 4D (*Qmt.tamu.4D* at 20.6-62.8 Mb) but for different traits.

Table 4.5. Multi-trait QTL (QTL clusters) for grain yield and agronomic traits detected from individual and multi-environment QTL analysis

QTL Name	QTL ID	Mbp[†]	Peak SNP	LOD range	$R^{2‡}$	A[§]	HAV[¶]	Traits[#]
Qmt.tamu.1D	11	375.4-421.8	2237051_1dl_3543	3.8-17.0	8.4, 11.8, 19.4	-0.8, 0.5, 68.7	P2, P1, P1	HD, TW, YLD
Qmt.tamu.1D	12	439.5-492.2	IWB41436	3.6-41.3	29.9, 17.1, 0.0	0.7, 0.5, 0.2	P1, P1, P1	HD, HT, TW
Qmt.tamu.4B	34	638.1-666.3	IWA27	4.3-12.4	18.3, 11.9	1.5, 98.8	P1, P1	HD, YLD
Qmt.tamu.4D	35	20.6-62.8	2305880_4ds_1018	4.2-35.7	5.9, 15.2, 4.9	0.3, 0.8, -173.2	P1, P1, P2	HT, TW, YLD
Qmt.tamu.7D	63	60.6-108.2	3950120_7ds_5316	3.5-64.9	31.9, 19.6, 21.6, 12.5	-1.3, -1.6, 0.7, -218.0	P2, P2, P1, P1/P2	HD, HT, TW, YLD

[†] Position, IWGSC RefSeq v1.0 pseudomolecule position

[‡] R^2, maximum phenotypic variance explained by additive effect to each trait

[§] A, maximum additive effect corresponding to each trait

[¶] HVA, high value allele corresponding to each trait; P1=TAM 112, P2=TAM 111

[#] Traits, HD, heading date; HT, plant height; TW, test weight; YLD, grain yield

QTL *Qmt.tamu.7D* at 60.6-108.2 Mb explained up to 31.9% variation in heading date, with TAM 111 allele increasing heading date by 1.3 days and plant height by 1.6 cm and could increase grain yield by 173.2 kg ha-1. The same QTL, however, received beneficial alleles from both parents depending on the environment, explaining up to 12.5% of the total variation for yield with the highest increase of 218.0 kg ha-1 from TAM 111 alleles (Table 4.5).

Consistent QTL for test weight on chromosome 1D (*Qcon.tamu.1D* at 375.4-421.8 Mb) were detected in 12EP3, 12CH and dry environment (Table 4.6). High value allele for this QTL originated form TAM 112, explaining up to 11.8% of the variation in test weight. For heading date and plant height, QTL *Qcon.tamu.1D* at 439.5-492.2 Mb was expressed in multiple environments. This QTL explained up to 29.9% of the phenotypic variation, and additive effect of a day increased by TAM 112 alleles in three environments (Table 4.6). The same QTL explained up to 11.1% of the variation in plant height and detected in 12BD and 11EP4. At this QTL TAM 112 allele contributed up to 2.3 cm increase in plant height. QTL on chromosome 4B (*Qcon.tamu.4B* at 638.1-666.3 Mb) explained up to 11.9% variation present in grain yield. This QTL was detected in 14EP4 and 12UVLD, with additive effect up to 98.5 kg ha-1 increase by TAM 1112. QTL for test weight on chromosome 4D (*Qcon.tamu.4D* at 20.6-62.8 Mb) was detected in seven environments as well as dry environment. High value allele for this QTL was originated from TAM 112 explaining up to 16.3% of the variation. QTL on chromosome 7D (*Qcon.tamu.7D* at 60.6-108.2 Mb) were also expressed in multiple environment for multiple traits.

Table 4.6. Stable and consistent QTL for grain yield and agronomic traits detected from individual environment QTL analysis

Traits[†]	QTL Name	QTL ID	Mbp[‡]	Peak SNP	LOD range	R^2[§]	A[¶]	HAV[#]	Environments[††]
HD	*Qcon.tamu.1D*	12	439.5-492.2	IWB41436	3.6-29.7	5.5-29.9	-0.4-1.1	P2, P1	12EP1, 12EP3, 17BD, DRY
HD	*Qcon.tamu.7D*	63	60.6-108.2	3950120_7ds_5316	5.4-15.8	7.6-31.9	-0.6- (-1.9)	P2	11BD, 11EP4, 11EP5, 12BD, 12EP1, 12EP2, 12EP3, 17BD, 11EP1, DRY
HT	*Qcon.tamu.1D*	12	439.5-492.2	IWA3764	3.9-4.4	5.7-11.0	0.3-2.3	P1	12BD, 11EP4
HT	*Qcon.tamu.7D*	63	60.6-108.2	3950120_7ds_5316	3.3-3.8	8.1-13.5	-1.0- (-1.6)	P2	17EI, 11EP5
TW	*Qcon.tamu.1D*	11	375.4-421.8	2237051_1dl_3543	3.8-4.9	10.8-11.8	0.3-0.5	P1	12EP3, 12CH, DRY
TW	*Qcon.tamu.4D*	35	20.6-62.8	2305880_4ds_1018	3.9-7.8	2.5-16.3	0.3-0.8	P1	12UV7, 17BD, 12BD, 12EP1, 12EP3, 13EP2,14CH, DRY
TW	*Qcon.tamu.7D*	63	60.6-108.2	IWB35446	4.0-9.2	11.9-21.6	0.4-0.7	P1	11EP5, 12CH
YLD	*Qcon.tamu.4B*	34	638.1-666.3	IWA27	3.6-4.3	9.8-11.9	96.5-98.5	P1	14EP4, 12UVLD
YLD	*Qcon.tamu.7D*	63	60.6-108.2	3950120_7ds_5316	3.5-6.9	2.7-12.5	42.4- (-218.0)	P1-P2	12UVLD, 12CH, 17BD, 14CH, 17BI, DRY

[†] Traits, HARD, hardness index; GMOIST, grain moisture; DIAM, kernel diameter; SKW, single kernel weight; FYLD, flour yield %; FMOIST, flour moisture; PROT14, flour protein at 14% moisture basis; ASH14, flour ash content at 14% moisture; WABS, water absorption; MLPT, midline peak time; MLPW, midline peak width; MLPV, midline peak value; MLPI, midline peak integral; MLRS, midline right slope; MLRW, midline right width

[‡] Position, IWGSC RefSeq v1.0 pseudomolecule position

[§] R^2, maximum Phenotypic variance explained by additive effect to each trait

[¶] A, maximum Additive effect corresponding to each trait

[#] HVA, high value allele corresponding to each trait; P1=TAM 112, P2=TAM 111; range of A is corresponding to range of HVA

[††] Environments; 11BD, 2011 Bushland dryland; 12BD, 2012 Bushland dryland; 17BD, 2017 Bushland dryland; 17BI, 2017 Bushland irrigated; 11CH, 2011 Chillicothe, 12CH, 2012 Chillicothe; 14CH, 2014 Chillicothe; 17CVI, 2017 Clovis irrigated; 11EP1, 2011 Etter 0% ET; 11EP2, 2011 Etter 40% ET; 11EP3, 2011 Etter 60% ET; 11EP4, 2011 Etter 75% ET; 11EP5, 2011 Etter 100% ET; 12EP1, 2012 Etter 0% ET; 12EP2, 2012 Etter 40% ET; 12EP3, 2012 Etter 60% ET; 13EP2, 2013 Etter 40% ET; 13EP3, 2013 Etter 60% ET; 13EP4, 2013 Etter 75% ET; 13EP5, 2013 Etter 100% ET; 14EP4, 2014 Etter 75% ET; 14EP5, 2014 Etter 100% ET; 17EI, 2017 Etter 100% ET; 12UVLD, 2012 Uvalde dryland; 12UV5, 2012 Uvalde 50% ET; 12UV7, 2012 Uvalde 70% ET; 12UVL, 2012 Uvalde irrigated; 13UVL, 2013 Uvalde irrigated; 13UVLD, 2013 Uvalde dryland; DRY, dry environments; IRR, irrigated environments; COMB, combined environment

This QTL controlled heading date, plant height, test weight and grain yield on at least more than two environments. This QTL explained up to 31.9 %, 13.5%, 21.6%, and 12.5% of the variation in heading date, plant height, test weight and grain yield, respectively.

Epistasis

Significant epistasis AA and epistasis-by-environment AAE interactions were found for heading date, plant height, test weight and grain yield (Table 4.7). For heading date, AA epistatic explained up to 2.3% of the variation, and AAE interaction explaining up to 1.3% of the variation. However, the effect of AA and AAE interactions was very small. AA and AAE interaction explained up to 1.9% and 3.2% of the variation in plant height. These two interactions accounted for 0.63 cm and 2.7 cm in plan height, both of which received alleles from TAM 112. For test weight, up to 4.7% of the variation was explained by AA and AAE interaction. These interactions increased test weight by a maximum of 6.81 lb bu-1. Very small variation was explained by either of the interaction for grain yield. Maximum of 2.0% variation in grain yield were contributed by the AA and AAE interaction. Up to 150.03 kg ha-1 yield increment was due to epistatic and epistasis by environment interaction.

Table 4.7. Additive-by-additive epistatic interaction, and epistatic-by-environment interaction among significant loci

Traits	QTL 1 Name	Mbp 1[†]	QTL ID 1	Peak SNP 1	QTL 2 Name	Mbp 2	QTL ID 2	Peak SNP 2	R^2 (A * A)[‡]	R^2 (AA*E)[§]	A*A[¶]	A*A*E[#]
HD	*Qhd.tamu.6A.49*	609.0	49	IWA6537	*Qhd.tamu.7B.60*	611.6	60	6680752_7bl_3474	2.2171	0.6275	-0.3836	0 - 0.4
HD	*Qhd.tamu.1B.9*	686.8	9	IWB4789	*Qhd.tamu.2B.20*	729.5	20	IWB59461	2.2987	0.4034	-0.3929	-0.01 – (-0.24)
HD	*Qhd.tamu.2B.18*	39.2	18	IWB22828	*Qhd.tamu.3B.28*	558.0	28	10446102_3b_9187	1.842	0.6425	0.344	-0.01 - 0.37
HD	*Qhd.tamu.1A.6*	587.8	6	3971039_1al_2867	*Qhd.tamu.6A.48*	7.6	48	IWB11242	1.8196	0.3586	0.3469	-0.01 - 0.38
HD	*Qhd.tamu.6D.54*	24.0	54	IWB6829	*Qhd.tamu.7A.58*	586.4	58	4445500_7al_1082	1.7579	1.3298	0.3394	0.01 - 0.89
HD	*Qhd.tamu.2A.13*	22.2	13	5237958_2as_10729	*Qhd.tamu.5A.43*	683.0	43	2805270_5al_2730	1.796	0.523	0.3472	0.05 – (-0.34)
HD	*Qhd.tamu.2A.17*	755.4	17	6337310_2al_1925	*Qhd.tamu.6A.49*	613.8	49	5800366_6al_6132	1.7552	0.6275	0.345	0 - 0.51
HD	*Qhd.tamu.2B.19*	69.0	19	IWB61862	*Qhd.tamu.7D.65*	593.5	65	3356799_7dl_7319	1.5859	0.6126	-0.3254	0 – (-0.49)
HT	*Qht.tamu.3D.30*	560.2	30	IWB32805	*Qht.tamu.7B.59*	1.3	59	6380245_2al_4723	1.8881	0.7332	0.5244	0.03 - 0.65
HT	*Qht.tamu.1B.7*	68.4	7	3432579_1bs_4957	*Qht.tamu.5A.43*	633.5	43	4541388_5dl_2248	1.5595	0.8486	0.4677	-0.03 - 0.93
HT	*Qht.tamu.1A.5*	465.5	5	IWB65944	*Qht.tamu.6A.48*	5.1	48	4427795_6as_12820	1.8685	0.6317	-0.5141	-0.01 – (-0.49)
HT	*Qht.tamu.2A.17*	759.1	17	6382018_2al_8250	*Qht.tamu.7B.59*	19.1	59	3096912_7bs_110	1.7778	1.0446	0.5142	-0.21 - 0.58
HT	*Qht.tamu.4B.34*	666.3	34	IWB55790	*Qht.tamu.5A.41*	430.2	41	IWB34498	1.6575	1.0586	-0.4876	0.02 – (-0.7)
HT	*Qht.tamu.1B.8*	570.3	8	IWA5160	*Qht.tamu.3D.30*	560.2	30	IWB32805	1.8095	1.2966	-0.507	0.23 – (-0.84)
HT	*Qht.tamu.2A.16*	674.2	16	IWB20877	*Qht.tamu.5B.46*	705.9	46	10827029_5bl_1233	1.7163	0.9116	0.4974	-0.13 - 0.72
HT	*Qht.tamu.2A.17*	734.5	17	6415190_2al_16820	*Qht.tamu.7D.62*	13.7	62	3933813_7ds_676	1.6246	1.1933	-0.4923	-0.14 – (-0.82)
HT	*Qht.tamu.1D.10*	12.3	10	IWB14343	*Qht.tamu.2B.19*	65.9	19	5174164_2bs_1900	1.5738	2.4532	0.4728	-0.02 - 1.38
HT	*Qht.tamu.3B.29*	771.4	29	10505374_3b_18831	*Qht.tamu.7D.63*	64.3	63	3950120_7ds_5316	1.6206	3.2476	0.4739	0.03 - 1.7
HT	*Qht.tamu.4A.31*	632.6	31	7156920_4al_5391	*Qht.tamu.5D.47*	349.9	47	IWA3429	1.5671	0.4252	0.4688	0.01 – (-0.43)
HT	*Qht.tamu.2A.17*	734.5	17	6415190_2al_16820	*Qht.tamu.6A.48*	6.7	48	4354844_6as_593	1.5063	1.6413	-0.4692	0.07 - 1.2
HT	*Qht.tamu.3D.30*	560.2	30	IWB32805	*Qht.tamu.5B.46*	693.4	46	10848805_5bl_3948	1.4057	1.5345	0.454	-0.04 - 0.88
HT	*Qht.tamu.7B.59*	47.3	59	3138767_7bs_7628	*Qht.tamu.7D.63*	108.2	63	3946880_7ds_1493	1.4331	1.0936	-0.4529	0.01 – (-0.95)
HT	*Qht.tamu.5A.41*	440.8	41	2774965_5al_1437	*Qht.tamu.7D.65*	-	65	Sec61	1.3149	1.3561	-0.4344	0.03 – (-0.8)
HT	*Qht.tamu.2A.17*	751.7	17	1023555_2al_3138	*Qht.tamu.4B.34*	638.1	34	IWA3040	1.2761	0.7174	0.4278	-0.06 - 0.69
HT	*Qht.tamu.7B.61*	707.4	61	6550874_7bl_349	*Qht.tamu.7B.61*	722.2	61	6666775_7bl_1452	0.3089	0	0.6317	-0.17 - 2.67
TW	*Qtw.tamu.3A.26*	711.7	26	4448357_3al_6941	*Qtw.tamu.7D.62*	13.7	62	3933813_7ds_676	2.0874	2.7422	0.367	0.02 - 1.95
TW	*Qtw.tamu.2B.18*	29.6	18	IWB47594	*Qtw.tamu.4D.35*	20.6	35	IWB15038	1.9997	1.6405	-0.3526	0 – (-1.27)
TW	*Qtw.tamu.7D.62*	13.7	62	3933813_7ds_676	*Qtw.tamu.7D.62*	15.3	62	IWB12582	0.0901	0	0.3241	0.01 - 4.69
TW	*Qtw.tamu.2A.16*	684.9	16	6437445_2al_5185	*Qtw.tamu.2A.17*	701.0	17	IWB11977	0.3581	0	0.4473	-0.09 - 6.81
YLD	*Qyld.tamu.6D.55*	350.4	55	3254329_6dl_5253	*Qyld.tamu.7D.65*	568.7	65	3388911_7dl_2689	0.0008	1.9167	-0.9427	0.67 – (-150.03)
YLD	*Qyld.tamu.2D.21*	0.2	21	5387977_2ds_265	*Qyld.tamu.3B.29*	777.0	29	10764714_3b_3097	0.0321	1.6496	5.8459	0.92 - 123.04
YLD	*Qyld.tamu.5B.46*	680.1	46	10875123_5bl_6505	*Qyld.tamu.7D.63*	72.9	63	IWA1247	0.5048	1.7305	23.3454	-5.47 - 118.25
YLD	*Qyld.tamu.3A.26*	702.6	26	4365353_3al_191	*Qyld.tamu.6A.48*	23.2	48	IWB28195	0.4024	1.1232	-20.8121	0.27 - 57.93
YLD	*Qyld.tamu.4B.32*	17.0	32	IWB49194	*Qyld.tamu.4D.36*	121.6	36	2298011_4ds_5609	0.1288	1.2149	11.6338	1.62 – (-69.21)
YLD	*Qyld.tamu.1B.9*	675.6	9	IWB73713	*Qyld.tamu.6D.56*	461.4	56	IWA1924	0.0633	2.0197	8.5023	-0.9 - 106.52
YLD	*Qyld.tamu.1D.10*	8.6	10	IWA1788	*Qyld.tamu.7D.62*	21.1	62	3916420_7ds_3323	0.1397	1.571	12.2372	-3.02 – (-95.65)
YLD	*Qyld.tamu.1A.6*	557.0	6	3882773_1al_4725	*Qyld.tamu.2B.18*	8.3	18	IWB9673	0.0157	1.4487	3.9326	1.09 - 109.64
YLD	*Qyld.tamu.1B.9*	686.8	9	IWB4789	*Qyld.tamu.2B.20*	734.4	20	7939581_2bl_9591	0.2144	1.4642	-15.2365	-0.47 – (-94.87)
YLD	*Qyld.tamu.6B.53*	688.3	53	IWB6854	*Qyld.tamu.6D.54*	33.7	54	4251907_7as_438	0.0291	1.2201	-5.4783	0.05 - 109.74

Table 4.7. Continued

[†] Position, IWGSC RefSeq v1.0 pseudomolecule position

[‡] R^2(A*A), phenotypic variance explained by epistasis (additive-by-additive) effect

[§] R^2 (AA*E), phenotypic variance explained by epistasis-by-environment effect

[¶] A*A, additive-by-additive effect. Negative sign indicates the recombination of the parental alleles increased the traits, positive sign indicates parental allelic combination reduced the traits

[#] A*A*E, range of additive-by-additive-by-environment effect. Negative value indicates the epistasis-by-environment reduced the trait, positive value increased the trait

DISCUSSION

Traits that are highly heritable and repeatable are important to breeders. All the grain yield and agronomic traits analyzed in this study were highly heritable. From variance partitioning, the genotypic variance is apparently higher than the genotype-by-environment interaction and residual variance. We have planted in all the range of stresses possible in this study, including diverse soil, precipitation and temperature. Our testing environment included location with day temperature >30 0C in southern Texas to location with day temperature <10 0C in the High Plains of Texas. These two environmental covariables significantly alters genotype expression across environments in wheat grain yield (Kuchel et al., 2007; Saini and Aspinall, 1982). Give all the possible environmental conditions of this study, observing significant environmental and genotype-by-environment interaction is expected. Higher heritability and higher genotypic variance indicated that these traits are genetically controlled, which makes it suitable for genetic gain from selection in a breeding program. Higher heritability of grain yield and agronomic traits is also reported by Zhang et al. (2018). Since yield is controlled by many genes with small effect and influenced by environment, it was unusual to see high heritability for grain yield (0.7) (Li et al., 2007). A plausible explanation of that could be a better experimental design that partitioned total error into environment, replication and incomplete block as employed in this study.

Global wheat benefitted from reduced height as it increased harvest index (HI), straw strength and grain yield (Slafer et al., 1996). Similar results were observed in this study. GY showed negative correlation with plant height, suggesting reduced plant weight was linked to increased GY. It is also known that reduced height when accompanied with higher input level, imparted significant increase in yield (Borlaug, 1968). Our study indicated that GY showed positive correlation with plant height in dry environment, suggesting that tall plants performed better in dry environment. For irrigated environments, reduced height was associated with increased yield except for 11EP4 (Table A6). A severe drought, when accompanied by high temperatures, lowers yields in nearly all crops in water-limited production agriculture (Hossain et al., 2012). Our testing environments included location like Bushland (BD) and Chillicothe (CH) where moderate to severe drought is common and Uvalde (UV) with heat stress. However, plants utilize different drought tolerance mechanism to sustain yield under drought and heat stress. In dry environment early maturing cultivars (HD), were able to avoid drought and terminal heat stress, and maintained higher grain yield as seen by negative association between GY and heading date from this study. Also, late flowering genotypes were disadvantageous since there is less chance of setting florets and higher chance of sterile spikelet.

In this study, we identified 65 unique QTL region, as denoted by QTL ID, that expands within 50 Mb regions. Even though significant genotypic variance was present, parents were not differing significantly for grain yield, test weight and plant height. Despite no significant differences between parents, the number of QTLs detected in this study was surprisingly high. Smaller population size, 124 lines in this study, can lead to a severe bias in QTL detection (Beavis, 1998). We used predicted means (BLUP) of the genotypes to analyzed QTL even though predicted means underestimate the gene effects due to shrinkage of means towards zero. As seen with best linear unbiassed estimate (BLUE), where environments with lower heritability show large QTL effects, use of BLUP would be accurate information to present. To validate the QTL finding of this study, we looked for some phenological development genes with known effects on the traits measured in this study. Additionally, we have found phenological development gene independent QTL. For GY, we identified QTL *Qyld.tamu.1A.6* at 587.0 Mb regions with peak marker IWB34513 explaining 25.4% variation in grain yield. At this locus, allele from TAM 112 increased grain yield up to 137.5 kg ha-1 in dry environments (Table 4.3). Position of peak marker for this QTL is very close to peak marker IWA1644 linked to early flowering gene Elf3 at 590 Mb (Alvarez et al., 2016; Zhang et al., 2018) (Table A7, A8). Early flowering is an escape mechanism adopted by some genotypes to avoid water stress. In the US Southern High Plains, it is common to moderate-to severe water stress and early flowering would be a helpful to cope with water stress. Another QTL *Qyld.tamu.3B.27* for grain yield at 48.6 Mb was identified, explaining 9.9% variation. Assanga et al. (2017b) mapped grain yield QTL at 42.56 Mb region on this chromosome with peak marker IWA3983. However, location of this QTL is very close to *Rht5* gene for reduced plant height (Ellis et al., 2005) (Table A9). We also identified morphological independent QTLs on chromosome 6D (*Qyld.tamu.6D.54* at 19.6 Mb) and on 7D (*Qyld.tamu.7D.63* at 60.6-84.3 Mb region). Presence of morphological independent QTL on 6D in study was also detected by Assanga et al. (2017b) (Table A7, A8). QTL *Qyld.tamu.7D.63* at 60.4-84.3 Mb region was expressed in multiple environments irrespective of irrigation. However, this QTL received high value allele from TAM 111 in irrigated environments, accounting for up to 218 kg ha-1, and from TAM 112 in dry environment, accounting for up to 64.5 kg ha-1 increase in dry env. Similar findings were observed by Thapa et al. (2018) in their glasshouse study using TAM 111 and TAM 112. TAM 112 was able to yield more grains that TAM 111 in dry environments, due to their gas exchange efficiency and other genetic differences.

Three of the QTLs identified for test weight in this study were very close to the phenological development genes *Rht* and *Vrn-1*. QTL *Qtw.tamu.2B.20* on the long arm of chromosome 2B (708.7-745.9 Mb region) were very close to GY QTL identified by Assanga et al. (2017b). This QTL is also very close to *Rht4* gene, which is also located on the long arm of the chromosome 2B (Ellis et al., 2005) (Table A8). QTL *Qtw.tamu.4B.32* at 17.0 Mb for test weight is also very close to *Rht1* gene (*Rht-B1b*), which are the major loci that has been most widely used in breeding program after the green revolution (Borlaug, 1968; Rasheed et al., 2016). QTL *Qtw.tamu.5B.45* at 589.4 Mb regions was very close to *Vrn-B1* located on 573.8 Mb on the long arm of chromosome 5B (Rasheed et al., 2016; Worland et al., 1998). Zheng et al. (2018) detected QTL for spikelet number per spike (SPS) at this locus with flanking marker IWB6746 (Table A7, A8). Phenological development gene independent test weight QTLs were also identified on chromosome 4D (*Qtw.tamu.4D.35* at 62.8 Mb) and on 6B (*Qtw.tamu.6B.50* at 130.3 Mb). Both the QTLs explained higher phenotypic variance (16.3-17.6%) and high value alleles were contributed by TAM 112. The QTL *Qtw.tamu.6B.50* was also collocated with grain yield QTL identified by Zhang et al. (2018) (Table A7, A8). For plant height, one of the QTL identified on chromosome 4D

(*Qht.tamu.4D.35* at 20.6 Mb) was 2.1 Mb away from another green revolution gene *Rht2* (*Rht-D1b*) (Rasheed et al., 2016; Worland et al., 1998). Other phenological gene independent genes were also identified on chromosome 1A (*Qht.tamu.1A.3* at 296.2 Mb) and on 1D (*Qht.tamu.1D.12* at 492.2 Mb), with latter QTL reducing plant height by up to 2.3 cM. QTL identified for heading date on chromosome 2B at 39.2 Mb, explaining 11.3% of the variation and additive effect of 1 day from TAM 112. This QTL is within 10 Mb regions from *Ppd-B1* gene (Rasheed et al., 2016). Other QTLs, independent of major phenology related genes, were identified on chromosome 1D (*Qhd.tamu.1D.12* at 486.8 Mb) explaining 29.9% of the variation with 1-day effect from TAM112, and on chromosome 7D (*Qhd.tamu.7D.63* at 64.3 Mb) explaining 31.9% of the variation with 1-day effect from TAM111.

Clustering of QTLs in certain genomic regions was observed. QTLs for traits with weaker or no correlation was also in the same cluster in some cases, such as QTLs for heading date, test weight and grain yield on long arm of chromosome 1D (*Qmt.tamu.1D* at 375.4-421.8 Mb and *Qmt.tamu.1D* at 439.5-492.2 Mb), QTLs for heading date and grain yield on long arm of chromosome 4B (*Qmt.tamu.4B*), and QTLs for plant height, test weight and grain yield on chromosome 4B (*Qmt.tamu.4D*) and 7D (*Qmt.tamu.7D*). For traits with weak or no correlation, it is possible to select traits with the combinations at opposite direction. It also avoids the undesirable effect of one QTL by selecting against it while improving another QTL. Stable expression of the same QTL in multiple environments is a way of confirming the worthiness of pursuing. However, it is common to detect a QTL in one environment and not in another environment. In this study, we categorized 28 environments into either dry and irrigated environment to confirm stable expression of QTLs in different management conditions as well. Our results indicate that five QTLs corresponding to heading date, plant height, test weight and grain weight on chromosome 1D, 4B, 4D and 7D were detected in more than one environment with high value alleles contributed by same parent (Table 4.6). QTLs detected in individual environment analysis were not detected in either of DRY, IRR, and COMB analysis for plant height on chromosome 1D at 439.5-492.2 Mb, and 7D at 60.6-108.2 Mb, test weight on chromosome 7D at 60.6-108.2 Mb, grain yield on 4B at 638.1-666.3 Mb (Table 4.6). Similarly, QTLs for heading date, plant height, test weight and grain yield were expressed in only one environment (Table 4.3). Also, QTL analysis was carried out on phenotypic data collected from diverse environmental conditions, making QTL unable to express in multiple environments. These finding strongly imply the presence of G × E effects on grain yield and agronomic traits. We observed the shift in QTL peak for yield (*Qyld.tamu.7D.63* at 60.6-84.3 Mb), test weight (*Qtw.tamu.6A.49* at 603.3-613.5 Mb indicating that these traits are likely controlled by multiple genes expressed in different environments.

CONCLUSION

In conclusion, we had 124 recombinant inbred lines from hard red winter wheat crosses. This population was characterized for grain yield (GY), plant height (HT), heading date (HD) and test weight (TW) collected from 28 environments during five cropping seasons. All the traits had high heritability with most of the phenotypic variation due to genotypic value and environmental value. A total of 65 unique QTLs were detected from three different QTL analysis. Individual environment QTL analysis detected 84 QTLs and multi-environment QTL analysis detected 69 QTLs for the four traits analyzed with 60 QTLs in common. Phenological development gene dependent QTLs were identified on chromosome 1A, 3B for grain yield, and 2B, 4B and 5B for test weight. Phonological development gene independent QTLs were also identified on chromosome 6D, 7D for grain yield, and on 4D, 6B for test weight. We found five genomic regions on chromosome 1D, 4B, 4D and 7D that are related with more than a single trait analyzed. QTLs for grain yield, heading date, plant height and test weight on these clusters were consistently expressed in multiple environments. Because of the complex inheritance of these traits, it will be necessary to validate these QTL in different wheat background evaluated in similar growth conditions before developing markers for marker-assisted selection.

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CHAPTER V

SUMMARY AND CONCLUSION

This dissertation studied and dissected number traits using different QTL mapping approach. We utilized classical linkage mapping as well as association analysis to connect 90K and GBS SNPs with grain yield, agronomic traits and end-use quality traits. Grain yield is the major traits that determines the profitability and sustained production of wheat. However, grain yield affected by multiple developmental genes. End-use quality is also important target trait for wheat.

Chapter II of this dissertation studied end-use quality of synthetic derived wheat. With 76K GBS SNPs included in the study, association analysis found 727, 603 and 44 significant marker-trait association. Majority of the markers associated with hardness index were detected on the short arm of chromosome 5D. Hardness index decreased by 8.5% or increased up to 7.7% for a locus. These markers explained 10.2% - 32.5 % of the total variation present in the hardness index. Flour yield related markers were also clustered on the short arm of the chromosome 5D, most of them collocated with hardness index marker loci. Phenotypic variation in flour yield explained by these markers ranged from 9.8% - 27%. Depending upon the marker and alleles, mean flour yield reduced by 2.7% or increased by 1.94% for some locus. Markers for midline right width and midline tail width were collocated on the short arm of chromosome 1B. Depending on locations, these markers explained up to 13% of the variation for each trait, and corresponding increase or decrease in trait value up to 2.9 % for some locus.

Chapter III of this dissertation studied end-use quality of bi-parental population from the cross of TAM1112/TAM 111 and genotyped with 90K and GBS SNPs. All the traits had moderate to high heritability with most of the phenotypic variation due to genotypic value. A total of 163 QTLs were detected from individual environment analysis, and 109 QTLs from multi-environment QTL analysis. As expected, most of mixograph traits were detected on chromosome 1A, 1B and 1D, with peak marker for QTL on 1D positioned on *Glu-D1* locus. For this locus, high value allele from TAM 112 increased mixograph parameters by up to 30.81 %, explaining 49.7% of the variation in midline peak integral. Due to a major gene effect, kernel hardness is found to influence mixograph traits. We found nine genomic regions on chromosome 1A, 1B, 1D, 2D, 4D and 7D that are related with more than a single trait analyzed. QTLs for hardness, grain moisture, midline peak time, and midline peak integral on these clusters were consistently expressed in multiple environments.

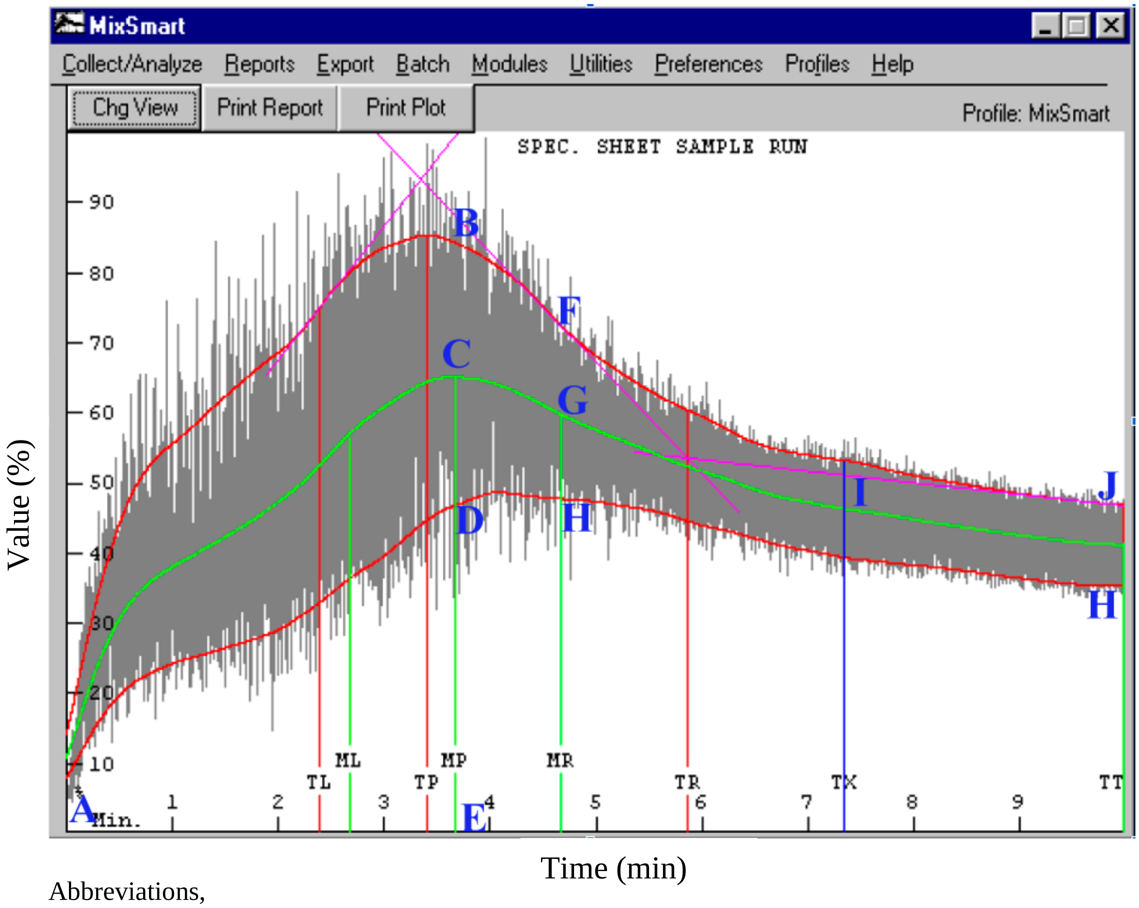
Chapter IV of this dissertation studied the same mapping population from chapter III and same SNPs set. This population was characterized for grain yield (GY), plant height (HT), heading date (HD) and test weight (TW) collected from 28 environments during five cropping seasons. All the traits had high heritability with most of the phenotypic variation due to genotypic value and environmental value. A total of 65 unique QTLs were detected from three different QTL analysis. Individual environment QTL analysis detected 84 QTLs and multi-environment QTL analysis detected 69 QTLs for the four traits analyzed with 60 QTLs in common. Phenological development gene dependent QTLs were identified on chromosome 1A, 3B for grain yield, and 2B, 4B and

5B for test weight. Phonological development gene independent QTLs were also identified on chromosome 6D, 7D for grain yield, and on 4D, 6B for test weight. We found five genomic regions on chromosome 1D, 4B, 4D and 7D that are related with more than a single trait analyzed. QTLs for grain yield, heading date, plant height and test weight on these clusters were consistently expressed in multiple environments.

The SNP associated with FYLD, HARD, MLRW, TAILW and PROT14 could be targeted in MAS for end-use quality traits and for future wheat breeding work. Due to the complex inheritance of these traits, it will be necessary to validate these QTL in different wheat background evaluated in similar growth conditions before developing markers for marker-assisted selection.

APPENDIX A

Figure A1: Description of mixograph traits analyzed in AMPSY population



Abbreviations,
TL, top left
TP, top peak
TR, top right
TX, Time X min
TT, Tail Time
ML, midline left
MP, midline peak
MR, midline right
AE: Midline peak time (MLPT)
CDE: Midline peak height (MLPT)
BCD: Midline peak width (MLPW)
FGH: Midline right width (MLRW)
GI: Midline right slope (MLRS)
JH: Midline tail width (MLTW)

Table A1
Significant marker trait association detected on individual environments, chromosome, position, effect for end-use quality traits in AMPSY population

Trait_loc_Yr[†]	Marker	Chr	Pos	CHR[‡]	Mb[§]	QTL ID	A[¶]	$R^{2\#}$	-log10(p)
FYLD_CLI_16	3305478_1as_3640	1A	272	1A	12818706	1	0.17	0.13	7.88
FYLD_CLI_16	3980528_1al_5184	1A	2017	1A	301131835	3	-0.78	0.13	8.18
FYLD_CLI_16	3927067_1al_12869	1A	2977	1A	389827066	4	-0.37	0.13	7.99
FYLD_CLI_16	3902709_1al_1308	UKN	125576	1A	428210584	4	0.55	0.15	8.18
FYLD_CLI_16	3902709_1al_1318	UKN	125599	1A	428210594	4	-0.88	0.13	7.32
FYLD_CLI_16	2278844_5bs_1907	UKN	127357	1B	60609112	6	-0.31	0.15	7.91
FYLD_CLI_16	3466711_1bs_2061	1B	7872	1B	101628236	7	0.45	0.13	8.06
FYLD_CLI_16	3466711_1bs_2020	1B	7870	1B	101628277	7	-0.45	0.13	8.06
FYLD_BD_16	3852692_1bl_3809	1B	7220	1B	280279027	9	1.92	0.12	7.35
FYLD_CLI_16	3892149_1bl_1985	1B	9895	1B	499635782	11	-0.29	0.13	7.92
FYLD_CLI_16	3858550_1bl_14890	1B	10735	1B	570836269	12	-0.46	0.13	8.00
FYLD_CLI_16	2282749_1dl_6803	1D	13916	1D	293607345	15	0.11	0.13	7.92
FYLD_CLI_16	2282749_1dl_6810	1D	13917	1D	293607352	15	-0.11	0.13	7.93
FYLD_CLI_16	2282749_1dl_6811	1D	13918	1D	293607353	15	-0.11	0.13	7.93
FYLD_CLI_16	2291838_1dl_7209	1D	15068	1D	317186574	15	-0.03	0.13	7.87
FYLD_CLI_16	2283167_1dl_17248	UKN	137672	1D	471086338	17	0.27	0.13	7.91
FYLD_CLI_16	2283167_1dl_17265	UKN	137673	1D	471086355	17	-0.27	0.13	7.92
FYLD_CLI_16	2283167_1dl_17277	UKN	137675	1D	471086367	17	-0.24	0.13	7.91
FYLD_CLI_16	5309070_2as_1364	2A	20709	2A	78755910	19	-0.20	0.13	7.89
FYLD_EP5_15	6435505_2al_8117	2A	19060	2A	347820702	21	0.02	0.16	9.29
FYLD_EP5_15	6324590_2al_2660	2A	18530	2A	566862511	22	-2.24	0.18	10.60
FYLD_CLI_16	6404696_2al_13964	UKN	137364	2A	628677518	23	0.15	0.14	7.82
FYLD_EP5_15	2461981_2al_3009	2A	22054	2A	695467552	24	0.21	0.16	9.32
FYLD_EP5_15	5184318_2bs_5233	2B	25524	2B	50715027	27	-0.30	0.16	9.27
FYLD_EP5_15	5184318_2bs_5090	2B	25520	2B	50715170	27	-0.48	0.16	9.42
FYLD_CLI_16	8028072_2bl_3018	2B	28049	2B	411000857	28	-0.45	0.13	7.96
FYLD_BI_16	5388307_2ds_14921	2D	35320	2D	56254194	34	-0.83	0.14	8.07
FYLD_EP5_15	2260462_2ds_419	UKN	121754	2D	73286123	34	-0.19	0.18	9.21
FYLD_CLI_16	9909878_2dl_8779	2D	38355	2D	590338112	38	-0.81	0.13	8.24
FYLD_EP5_15	9910341_2dl_2006	UKN	127683	2D	641955809	38	-0.05	0.19	9.32
FYLD_EP5_15	3387459_3as_6843	3A	40273	3A	41627157	39	-0.14	0.16	9.31
FYLD_CLI_16	3413956_3as_889	3A	40791	3A	86403737	40	0.03	0.13	7.85
FYLD_CLI_16	4450272_3al_830	3A	43324	3A	715420289	44	0.14	0.16	9.79
FYLD_CLI_16	4450272_3al_835	3A	43325	3A	715420289	44	-0.14	0.16	9.79
FYLD_CLI_16	4450272_3al_1054	3A	43327	3A	715420483	44	-0.01	0.13	7.87
FYLD_CLI_16	4297373_3al_307	3A	43714	3A	736099722	44	-0.21	0.13	7.89
FYLD_EP5_15	10605995_3b_1664	UKN	126545	3B	29498546	45	0.40	0.18	9.10
FYLD_EP5_15	10683916_3b_2192	UKN	128176	3B	117555037	47	-0.01	0.16	9.21
FYLD_EP5_15	10683916_3b_2167	UKN	128114	3B	117555062	47	-0.46	0.16	9.31
FYLD_CLI_16	10461448_3b_557	3B	46111	3B	534828537	51	-0.03	0.13	7.85
FYLD_CLI_16	10451971_3b_7480	UKN	135317	3B	602586559	52	-0.13	0.13	7.83
FYLD_CLI_16	10451971_3b_7321	UKN	135222	3B	602586718	52	-0.54	0.14	8.11
FYLD_CLI_16	6013263_4as_v2_7346	4A	50154	4A	30155367	58	1.31	0.14	8.89
FYLD_EP5_15	7079348_4al_382	UKN	121543	4A	637256685	62	0.22	0.19	9.39
FYLD_CLI_16	4057017_4al_591	4A	53762	4A	646117303	62	-0.62	0.13	8.09
FYLD_CLI_16	4057017_4al_596	4A	53763	4A	646117308	62	0.62	0.13	8.09
FYLD_CLI_16	4057017_4al_613	4A	53766	4A	646117325	62	-0.62	0.13	8.09
FYLD_EP5_15	7088979_4al_3699	UKN	131312	4A	658897102	62	0.89	0.18	9.43
FYLD_EP5_15	7120458_4al_2339	4A	55123	4A	720204970	63	-0.25	0.16	9.33
FYLD_EP5_15	7120458_4al_2378	4A	55126	4A	720205009	63	-0.36	0.16	9.39
FYLD_EP5_15	7120458_4al_2392	4A	55129	4A	720205023	63	0.42	0.16	9.44
FYLD_CLI_16	7083149_4al_7921	4A	55523	4A	725860581	63	0.29	0.13	7.93
FYLD_EP5_15	7039666_4bl_20663	4B	60061	4B	570150846	67	0.29	0.16	9.33
FYLD_CLI_16	6975707_4bl_1506	UKN	126144	4B	649679461	68	0.01	0.14	7.75
FYLD_CLI_16	1380443_4ds_2087	4D	62092	4D	94263283	70	0.54	0.14	8.87
FYLD_EP5_15	2309923_4ds_2070	4D	62838	4D	164595143	71	NA	0.13	8.74
FYLD_IRR_IRR	2309923_4ds_2070	4D	62838	4D	164595143	71	NA	0.12	8.19
FYLD_CLI_16	14304468_4dl_v2_1665	UKN	126557	4D	413041988	72	-0.06	0.16	9.24
FYLD_IRR_IRR	14304468_4dl_v2_1665	UKN	126557	4D	413041988	72	-0.19	0.14	8.20
FYLD_EP5_15	1506586_5as_5534	UKN	133818	5A	10213724	74	-1.43	0.18	10.23
FYLD_EP5_15	2476331_5al_1297	5A	63913	5A	279102105	75	-1.56	0.17	10.14
FYLD_EP5_15	10905888_5bl_8545	5B	70646	5B	399777517	80	0.40	0.16	9.50
FYLD_EP5_15	10905888_5bl_8543	5B	70645	5B	399777519	80	-0.40	0.16	9.50
FYLD_EP5_15	10905888_5bl_8533	5B	70642	5B	399777529	80	-0.39	0.16	9.49
FYLD_EP5_15	10905888_5bl_8523	5B	70641	5B	399777539	80	-0.39	0.16	9.48
FYLD_EP5_15	10905888_5bl_8511	5B	70640	5B	399777551	80	0.39	0.16	9.49
FYLD_CLI_16	10906178_5bl_4128	5B	70984	5B	445444817	81	-0.21	0.13	7.90
FYLD_CLI_16	10906178_5bl_4143	5B	70985	5B	445444832	81	-0.27	0.13	7.96

Table A1 Continued

Trait_loc_Yr[†]	Marker	Chr	Pos	CHR[‡]	Mb[§]	QTL ID	A[¶]	R^2[#]	-log10(p)
FYLD_CLI_16	10906178_5bl_4144	5B	70986	5B	445444833	81	-0.25	0.13	7.94
FYLD_CLI_16	10906178_5bl_4445	5B	70989	5B	445445134	81	0.26	0.13	7.95
FYLD_CLI_16	10807425_5bl_10093	5B	71312	5B	447844705	81	-0.56	0.13	8.07
FYLD_CLI_16	10847251_5bl_499	5B	71161	5B	463923822	81	0.15	0.12	7.09
FYLD_BD_16	10833329_5bl_3165	5B	73601	5B	595287398	83	-0.96	0.12	7.17
FYLD_BD_16	10833329_5bl_3193	5B	73603	5B	595287426	83	-1.03	0.12	7.33
FYLD_BD_16	10833329_5bl_3385	5B	73611	5B	595287618	83	-0.98	0.12	7.19
FYLD_BD_16	10833329_5bl_3390	5B	73613	5B	595287623	83	-1.03	0.12	7.33
FYLD_BD_16	10833329_5bl_3402	5B	73614	5B	595287635	83	-0.97	0.12	7.19
FYLD_EP5_15	10806569_5bl_2517	5B	74549	5B	636930195	83	-0.22	0.16	9.25
FYLD_EP5_15	10806569_5bl_2468	5B	74548	5B	636930244	83	-0.36	0.16	9.35
FYLD_EP5_15	10809422_5bl_3717	5B	75382	5B	684607248	84	-0.25	0.16	9.32
FYLD_CLI_16	10824756_5bl_1863	5B	75732	5B	703306588	84	-0.22	0.13	7.93
FYLD_BD_16	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.11	7.69
FYLD_BI_16	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.12	7.99
FYLD_DRY_DRY	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.19	11.97
FYLD_EP3_15	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.14	9.15
FYLD_EP4_14	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.18	11.92
FYLD_EP5_14	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.20	12.93
FYLD_EP5_15	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.13	8.55
FYLD_IRR_IRR	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.18	11.64
FYLD_BI_16	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.11	7.37
FYLD_CLI_16	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.12	8.36
FYLD_DRY_DRY	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.15	9.83
FYLD_EP3_15	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.14	9.66
FYLD_EP4_14	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.22	14.13
FYLD_EP5_14	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.19	12.34
FYLD_IRR_IRR	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.17	11.02
FYLD_BI_16	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.14	8.90
FYLD_CLI_16	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.20	12.50
FYLD_DRY_DRY	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.15	9.90
FYLD_EP3_15	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.18	11.45
FYLD_EP4_14	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.27	16.45
FYLD_EP5_14	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.25	15.32
FYLD_EP5_15	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.23	11.97
FYLD_IRR_IRR	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.27	15.96
FYLD_DRY_DRY	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.17	11.10
FYLD_EP3_15	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.14	9.32
FYLD_EP4_14	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.19	12.42
FYLD_EP5_14	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.24	15.05
FYLD_EP5_15	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.16	10.74
FYLD_IRR_IRR	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.17	10.94
FYLD_BD_16	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.11	7.78
FYLD_BI_16	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.11	7.64
FYLD_DRY_DRY	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.19	12.47
FYLD_EP3_15	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.15	10.24
FYLD_EP4_14	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.20	12.85
FYLD_EP5_14	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.26	15.78
FYLD_EP5_15	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.13	8.78
FYLD_IRR_IRR	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.17	11.01
FYLD_DRY_DRY	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.17	11.10
FYLD_EP3_15	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.14	9.32
FYLD_EP4_14	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.19	12.42
FYLD_EP5_14	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.24	15.05
FYLD_EP5_15	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.16	10.74
FYLD_IRR_IRR	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.17	10.94
FYLD_EP4_14	2770151_5ds_4035	5D	75899	5D	7257066	85	NA	0.11	7.98
FYLD_EP5_14	2739337_5ds_2304	5D	75953	5D	7485266	85	NA	0.11	7.12
FYLD_EP4_14	2781025_5ds_24425	5D	76006	5D	8018752	85	NA	0.10	7.15
FYLD_EP5_14	2781025_5ds_24425	5D	76006	5D	8018752	85	NA	0.13	8.91
FYLD_EP4_14	2781025_5ds_24421	5D	76005	5D	8018756	85	NA	0.10	7.15
FYLD_EP5_14	2781025_5ds_24421	5D	76005	5D	8018756	85	NA	0.13	8.91
FYLD_CLI_16	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.10	7.23
FYLD_DRY_DRY	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.14	9.56
FYLD_EP3_15	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.14	9.44
FYLD_EP4_14	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.11	7.67
FYLD_EP5_14	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.15	9.99
FYLD_EP5_15	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.11	7.47
FYLD_IRR_IRR	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.15	10.19
FYLD_IRR_IRR	2781671_5ds_9472	5D	75997	5D	9332000	85	NA	0.11	7.33

Table A1 Continued

Trait_loc_Yr†	Marker	Chr	Pos	CHR‡	Mb§	QTL ID	A¶	R^2#	-log10(p)
FYLD_EP4_14	2781671_5ds_9461	5D	75993	5D	9332011	85	NA	0.10	7.03
FYLD_IRR_IRR	2781671_5ds_9461	5D	75993	5D	9332011	85	NA	0.10	7.12
FYLD_EP4_14	2781671_5ds_9443	5D	75992	5D	9332029	85	NA	0.10	7.03
FYLD_IRR_IRR	2781671_5ds_9443	5D	75992	5D	9332029	85	NA	0.10	7.12
FYLD_EP4_14	2781671_5ds_9235	5D	75991	5D	9332237	85	NA	0.10	7.03
FYLD_IRR_IRR	2781671_5ds_9235	5D	75991	5D	9332237	85	NA	0.10	7.12
FYLD_EP4_14	2781671_5ds_9219	5D	75989	5D	9332253	85	NA	0.10	7.03
FYLD_IRR_IRR	2781671_5ds_9219	5D	75989	5D	9332253	85	NA	0.10	7.12
FYLD_EP4_14	2781671_5ds_9179	5D	75987	5D	9332293	85	NA	0.10	7.03
FYLD_IRR_IRR	2781671_5ds_9179	5D	75987	5D	9332293	85	NA	0.10	7.12
FYLD_EP5_15	2739401_5ds_20579	5D	76380	5D	11421190	85	-2.74	0.12	7.00
FYLD_CLI_16	2760386_5ds_1248	UKN	125360	5D	14719288	85	0.02	0.15	7.80
FYLD_CLI_16	2770949_5ds_845	5D	77116	5D	70819097	86	-0.35	0.13	7.94
FYLD_CLI_16	2783341_5ds_8399	5D	77064	5D	72551106	86	-0.16	0.13	7.88
FYLD_EP5_14	4599562_5dl_5399	5D	78574	5D	298137698	87	NA	0.10	7.22
FYLD_EP5_15	4590136_5dl_3635	5D	78026	5D	345935291	88	0.28	0.16	9.34
FYLD_CLI_16	4504942_5dl_1247	5D	78305	5D	346502034	88	-0.48	0.13	7.97
FYLD_EP5_15	4514657_5dl_1632	5D	79259	5D	385511140	88	-0.51	0.16	9.50
FYLD_CLI_16	4605319_5dl_3048	5D	79877	5D	434399580	89	0.11	0.13	7.87
FYLD_CLI_16	4544938_5dl_5497	5D	80179	5D	453882685	89	0.05	0.13	7.87
FYLD_CLI_16	4534695_5dl_15341	5D	81712	5D	526417202	90	0.13	0.13	7.89
FYLD_CLI_16	4412722_6as_11506	6A	82894	6A	1679610	92	0.01	0.13	7.87
FYLD_CLI_16	4429138_6as_4885	6A	84761	6A	81300931	93	0.33	0.13	7.95
FYLD_CLI_16	5779119_6al_30	6A	87072	6A	550280481	96	-0.28	0.13	7.95
FYLD_EP5_15	2104944_6ds_1907	6D	93021	6D	4373904	101	-0.41	0.16	9.43
FYLD_EP5_15	3241616_6dl_343	6D	95722	6D	225477162	102	-0.36	0.16	9.36
FYLD_CLI_16	4188922_7as_8493	UKN	136014	7A	32691576	104	-0.94	0.17	8.49
FYLD_EP5_15	4438480_7al_11172	7A	102537	7A	561615734	110	-0.02	0.16	9.29
FYLD_CLI_16	4556713_7al_3803	7A	102882	7A	581433764	110	0.36	0.13	7.94
FYLD_EP5_15	4466982_7al_4013	7A	105077	7A	733969740	111	0.00	0.16	9.28
FYLD_EP5_15	4466982_7al_4163	7A	105080	7A	733969890	111	-0.22	0.16	9.29
FYLD_CLI_16	3156753_7bs_820	7B	106579	7B	134714902	113	-0.09	0.13	7.87
FYLD_CLI_16	3856934_7ds_2095	7D	110002	7D	9376388	116	-0.54	0.13	8.00
FYLD_CLI_16	3856934_7ds_2056	7D	109998	7D	9376427	116	-0.20	0.12	7.68
FYLD_EP5_15	3898730_7ds_1216	7D	110209	7D	18207787	116	0.72	0.16	9.50
FYLD_EP5_15	5389722_2ds_5977	2D	34903	Un	24970654	33?	1.18	0.17	9.99
FYLD_CLI_16	3418003_3as_1194	3A	39385	Un	32236572	39?	-0.06	0.13	7.87
FYLD_CLI_16	5744793_6al_520	6A	88417	Un	75261141	92?	-0.23	0.13	7.91
FYLD_CLI_16	5744793_6al_542	6A	88418	Un	75261163	92?	0.11	0.13	7.87
HARD_BD_16	5176564_2bs_647	UKN	123039	2B	38620402	27	-0.70	0.12	7.11
HARD_BD_16	5176564_2bs_662	UKN	123097	2B	38620417	27	0.82	0.12	7.18
HARD_BD_16	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.18	11.70
HARD_BI_16	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.16	10.37
HARD_CH_14	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.17	11.09
HARD_CLI_16	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.22	13.47
HARD_DRY_DRY	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.21	13.33
HARD_EP3_15	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.23	13.87
HARD_EP4_14	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.21	12.68
HARD_EP4_15	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.25	15.19
HARD_EP5_14	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.21	13.32
HARD_EP5_15	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.24	14.63
HARD_IRR_IRR	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.23	13.97
HARD_CLI_16	1477005_5ds_2278	5D	75884	5D	344847	85	7.63	0.13	7.83
HARD_EP4_14	1477005_5ds_2278	5D	75884	5D	344847	85	NA	0.11	7.27
HARD_BD_16	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.21	13.14
HARD_BI_16	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.18	11.78
HARD_CH_14	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.20	12.79
HARD_CLI_16	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.25	15.23
HARD_DRY_DRY	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.27	16.44
HARD_EP3_15	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.29	17.28
HARD_EP4_14	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.23	13.72
HARD_EP4_15	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.33	18.93
HARD_EP5_14	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.23	14.13
HARD_EP5_15	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.28	16.77
HARD_IRR_IRR	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.27	16.28
HARD_BD_16	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.26	15.51
HARD_BI_16	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.23	13.82
HARD_CH_14	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.24	14.78
HARD_CLI_16	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.26	15.46
HARD_DRY_DRY	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.31	17.32

Table A1 Continued

Trait_loc_Yr†	Marker	Chr	Pos	CHR‡	Mb§	QTL ID	A¶	R^{2}#	-log10(p)
HARD_EP3_15	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.31	17.83
HARD_EP4_14	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.28	16.20
HARD_EP4_15	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.32	18.23
HARD_EP5_14	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.27	15.99
HARD_EP5_15	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.31	17.75
HARD_IRR_IRR	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.30	17.20
HARD_EP3_15	2765676_5ds_2839	5D	75901	5D	1344429	85	-8.56	0.13	7.86
HARD_BD_16	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.24	14.88
HARD_BI_16	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.19	12.43
HARD_CH_14	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.21	13.55
HARD_CLI_16	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.27	16.09
HARD_DRY_DRY	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.27	16.02
HARD_EP3_15	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.28	16.92
HARD_EP4_14	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.24	14.27
HARD_EP4_15	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.26	15.90
HARD_EP5_14	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.24	14.56
HARD_EP5_15	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.28	16.86
HARD_IRR_IRR	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.28	16.64
HARD_BD_16	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.26	15.68
HARD_BI_16	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.20	13.02
HARD_CH_14	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.23	14.48
HARD_CLI_16	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.29	17.40
HARD_DRY_DRY	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.29	17.10
HARD_EP3_15	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.30	17.84
HARD_EP4_14	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.24	14.57
HARD_EP4_15	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.29	16.97
HARD_EP5_14	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.26	15.60
HARD_EP5_15	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.29	17.20
HARD_IRR_IRR	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.29	17.22
HARD_BD_16	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.24	14.88
HARD_BI_16	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.19	12.43
HARD_CH_14	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.21	13.55
HARD_CLI_16	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.27	16.09
HARD_DRY_DRY	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.27	16.02
HARD_EP3_15	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.28	16.92
HARD_EP4_14	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.24	14.27
HARD_EP4_15	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.26	15.90
HARD_EP5_14	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.24	14.56
HARD_EP5_15	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.28	16.86
HARD_IRR_IRR	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.28	16.64
HARD_DRY_DRY	2770151_5ds_4035	5D	75899	5D	7257066	85	NA	0.12	8.00
HARD_EP3_15	2770151_5ds_4035	5D	75899	5D	7257066	85	NA	0.11	7.66
HARD_BD_16	2739337_5ds_2304	5D	75953	5D	7485266	85	NA	0.10	7.10
HARD_BI_16	2739337_5ds_2304	5D	75953	5D	7485266	85	NA	0.11	7.70
HARD_CLI_16	2739337_5ds_2304	5D	75953	5D	7485266	85	NA	0.14	8.80
HARD_DRY_DRY	2739337_5ds_2304	5D	75953	5D	7485266	85	NA	0.11	7.12
HARD_EP3_15	2739337_5ds_2304	5D	75953	5D	7485266	85	NA	0.11	7.27
HARD_EP4_14	2739337_5ds_2304	5D	75953	5D	7485266	85	NA	0.12	7.71
HARD_EP4_15	2739337_5ds_2304	5D	75953	5D	7485266	85	NA	0.11	7.33
HARD_EP5_15	2739337_5ds_2304	5D	75953	5D	7485266	85	NA	0.13	8.65
HARD_IRR_IRR	2739337_5ds_2304	5D	75953	5D	7485266	85	NA	0.15	9.60
HARD_BD_16	2781025_5ds_24425	5D	76006	5D	8018752	85	NA	0.15	9.86
HARD_BI_16	2781025_5ds_24425	5D	76006	5D	8018752	85	NA	0.15	10.03
HARD_CH_14	2781025_5ds_24425	5D	76006	5D	8018752	85	NA	0.14	9.18
HARD_CLI_16	2781025_5ds_24425	5D	76006	5D	8018752	85	NA	0.15	9.86
HARD_DRY_DRY	2781025_5ds_24425	5D	76006	5D	8018752	85	NA	0.16	10.13
HARD_EP3_15	2781025_5ds_24425	5D	76006	5D	8018752	85	NA	0.16	10.09
HARD_EP4_14	2781025_5ds_24425	5D	76006	5D	8018752	85	NA	0.14	8.91
HARD_EP4_15	2781025_5ds_24425	5D	76006	5D	8018752	85	NA	0.15	9.69
HARD_EP5_14	2781025_5ds_24425	5D	76006	5D	8018752	85	NA	0.12	8.19
HARD_EP5_15	2781025_5ds_24425	5D	76006	5D	8018752	85	NA	0.18	11.58
HARD_IRR_IRR	2781025_5ds_24425	5D	76006	5D	8018752	85	NA	0.18	11.50
HARD_BD_16	2781025_5ds_24421	5D	76005	5D	8018756	85	NA	0.15	9.86
HARD_BI_16	2781025_5ds_24421	5D	76005	5D	8018756	85	NA	0.15	10.03
HARD_CH_14	2781025_5ds_24421	5D	76005	5D	8018756	85	NA	0.14	9.18
HARD_CLI_16	2781025_5ds_24421	5D	76005	5D	8018756	85	NA	0.15	9.86
HARD_DRY_DRY	2781025_5ds_24421	5D	76005	5D	8018756	85	NA	0.16	10.13
HARD_EP3_15	2781025_5ds_24421	5D	76005	5D	8018756	85	NA	0.16	10.09
HARD_EP4_14	2781025_5ds_24421	5D	76005	5D	8018756	85	NA	0.14	8.91
HARD_EP4_15	2781025_5ds_24421	5D	76005	5D	8018756	85	NA	0.15	9.69

Table A1 Continued

Trait_loc_Yr†	Marker	Chr	Pos	CHR‡	Mb§	QTL ID	A¶	R^{2}#	-log10(p)
HARD_EP5_14	2781025_5ds_24421	5D	76005	5D	8018756	85	NA	0.12	8.19
HARD_EP5_15	2781025_5ds_24421	5D	76005	5D	8018756	85	NA	0.18	11.58
HARD_IRR_IRR	2781025_5ds_24421	5D	76005	5D	8018756	85	NA	0.18	11.50
HARD_BD_16	2745020_5ds_15344	5D	76053	5D	8419265	85	6.15	0.12	7.33
HARD_DRY_DRY	2745020_5ds_15344	5D	76053	5D	8419265	85	6.43	0.12	7.16
HARD_EP3_15	2745020_5ds_15344	5D	76053	5D	8419265	85	7.39	0.12	7.36
HARD_EP4_14	2745020_5ds_15344	5D	76053	5D	8419265	85	7.25	0.13	7.73
HARD_EP4_15	2745020_5ds_15344	5D	76053	5D	8419265	85	7.74	0.13	8.01
HARD_EP5_14	2745020_5ds_15344	5D	76053	5D	8419265	85	6.51	0.12	7.17
HARD_BD_16	2745020_5ds_15346	5D	76054	5D	8419267	85	6.15	0.12	7.33
HARD_DRY_DRY	2745020_5ds_15346	5D	76054	5D	8419267	85	6.43	0.12	7.16
HARD_EP3_15	2745020_5ds_15346	5D	76054	5D	8419267	85	7.39	0.12	7.36
HARD_EP4_14	2745020_5ds_15346	5D	76054	5D	8419267	85	7.25	0.13	7.73
HARD_EP4_15	2745020_5ds_15346	5D	76054	5D	8419267	85	7.74	0.13	8.01
HARD_EP5_14	2745020_5ds_15346	5D	76054	5D	8419267	85	6.51	0.12	7.17
HARD_BD_16	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.13	8.71
HARD_BI_16	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.12	8.05
HARD_CH_14	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.12	8.08
HARD_CLI_16	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.15	9.89
HARD_DRY_DRY	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.14	9.38
HARD_EP3_15	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.15	9.98
HARD_EP4_14	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.14	9.19
HARD_EP4_15	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.16	10.43
HARD_EP5_14	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.11	7.30
HARD_EP5_15	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.19	11.80
HARD_IRR_IRR	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.16	10.58
HARD_CLI_16	2781671_5ds_9472	5D	75997	5D	9332000	85	NA	0.11	7.47
HARD_EP3_15	2781671_5ds_9472	5D	75997	5D	9332000	85	NA	0.11	7.43
HARD_EP4_14	2781671_5ds_9472	5D	75997	5D	9332000	85	NA	0.11	7.33
HARD_EP4_15	2781671_5ds_9472	5D	75997	5D	9332000	85	NA	0.13	8.49
HARD_EP5_15	2781671_5ds_9472	5D	75997	5D	9332000	85	NA	0.13	8.94
HARD_IRR_IRR	2781671_5ds_9472	5D	75997	5D	9332000	85	NA	0.12	8.24
HARD_BD_16	2781671_5ds_9461	5D	75993	5D	9332011	85	NA	0.11	7.34
HARD_BI_16	2781671_5ds_9461	5D	75993	5D	9332011	85	NA	0.11	7.53
HARD_CH_14	2781671_5ds_9461	5D	75993	5D	9332011	85	NA	0.11	7.43
HARD_CLI_16	2781671_5ds_9461	5D	75993	5D	9332011	85	NA	0.12	8.04
HARD_DRY_DRY	2781671_5ds_9461	5D	75993	5D	9332011	85	NA	0.11	7.54
HARD_EP3_15	2781671_5ds_9461	5D	75993	5D	9332011	85	NA	0.12	8.01
HARD_EP4_14	2781671_5ds_9461	5D	75993	5D	9332011	85	NA	0.13	8.42
HARD_EP4_15	2781671_5ds_9461	5D	75993	5D	9332011	85	NA	0.14	9.20
HARD_EP5_14	2781671_5ds_9461	5D	75993	5D	9332011	85	NA	0.11	7.39
HARD_EP5_15	2781671_5ds_9461	5D	75993	5D	9332011	85	NA	0.14	9.30
HARD_IRR_IRR	2781671_5ds_9461	5D	75993	5D	9332011	85	NA	0.13	8.85
HARD_BD_16	2781671_5ds_9443	5D	75992	5D	9332029	85	NA	0.11	7.34
HARD_BI_16	2781671_5ds_9443	5D	75992	5D	9332029	85	NA	0.11	7.53
HARD_CH_14	2781671_5ds_9443	5D	75992	5D	9332029	85	NA	0.11	7.43
HARD_CLI_16	2781671_5ds_9443	5D	75992	5D	9332029	85	NA	0.12	8.04
HARD_DRY_DRY	2781671_5ds_9443	5D	75992	5D	9332029	85	NA	0.11	7.54
HARD_EP3_15	2781671_5ds_9443	5D	75992	5D	9332029	85	NA	0.12	8.01
HARD_EP4_14	2781671_5ds_9443	5D	75992	5D	9332029	85	NA	0.13	8.42
HARD_EP4_15	2781671_5ds_9443	5D	75992	5D	9332029	85	NA	0.14	9.20
HARD_EP5_14	2781671_5ds_9443	5D	75992	5D	9332029	85	NA	0.11	7.39
HARD_EP5_15	2781671_5ds_9443	5D	75992	5D	9332029	85	NA	0.14	9.30
HARD_IRR_IRR	2781671_5ds_9443	5D	75992	5D	9332029	85	NA	0.13	8.85
HARD_BD_16	2781671_5ds_9235	5D	75991	5D	9332237	85	NA	0.11	7.34
HARD_BI_16	2781671_5ds_9235	5D	75991	5D	9332237	85	NA	0.11	7.53
HARD_CH_14	2781671_5ds_9235	5D	75991	5D	9332237	85	NA	0.11	7.43
HARD_CLI_16	2781671_5ds_9235	5D	75991	5D	9332237	85	NA	0.12	8.04
HARD_DRY_DRY	2781671_5ds_9235	5D	75991	5D	9332237	85	NA	0.11	7.54
HARD_EP3_15	2781671_5ds_9235	5D	75991	5D	9332237	85	NA	0.12	8.01
HARD_EP4_14	2781671_5ds_9235	5D	75991	5D	9332237	85	NA	0.13	8.42
HARD_EP4_15	2781671_5ds_9235	5D	75991	5D	9332237	85	NA	0.14	9.20
HARD_EP5_14	2781671_5ds_9235	5D	75991	5D	9332237	85	NA	0.11	7.39
HARD_EP5_15	2781671_5ds_9235	5D	75991	5D	9332237	85	NA	0.14	9.30
HARD_IRR_IRR	2781671_5ds_9235	5D	75991	5D	9332237	85	NA	0.13	8.85
HARD_CLI_16	2781671_5ds_9223	5D	75990	5D	9332249	85	NA	0.11	7.22
HARD_EP3_15	2781671_5ds_9223	5D	75990	5D	9332249	85	NA	0.11	7.30
HARD_EP4_14	2781671_5ds_9223	5D	75990	5D	9332249	85	NA	0.11	7.38
HARD_EP4_15	2781671_5ds_9223	5D	75990	5D	9332249	85	NA	0.13	8.41
HARD_EP5_15	2781671_5ds_9223	5D	75990	5D	9332249	85	NA	0.12	8.35

Table A1 Continued

Trait_loc_Yr†	Marker	Chr	Pos	CHR‡	Mb§	QTL ID	A¶	$R^{2\#}$	-log10(p)
HARD_IRR_IRR	2781671_5ds_9223	5D	75990	5D	9332249	85	NA	0.12	7.97
HARD_BD_16	2781671_5ds_9219	5D	75989	5D	9332253	85	NA	0.11	7.34
HARD_BI_16	2781671_5ds_9219	5D	75989	5D	9332253	85	NA	0.11	7.53
HARD_CH_14	2781671_5ds_9219	5D	75989	5D	9332253	85	NA	0.11	7.43
HARD_CLI_16	2781671_5ds_9219	5D	75989	5D	9332253	85	NA	0.12	8.04
HARD_DRY_DRY	2781671_5ds_9219	5D	75989	5D	9332253	85	NA	0.11	7.54
HARD_EP3_15	2781671_5ds_9219	5D	75989	5D	9332253	85	NA	0.12	8.01
HARD_EP4_14	2781671_5ds_9219	5D	75989	5D	9332253	85	NA	0.13	8.42
HARD_EP4_15	2781671_5ds_9219	5D	75989	5D	9332253	85	NA	0.14	9.20
HARD_EP5_14	2781671_5ds_9219	5D	75989	5D	9332253	85	NA	0.11	7.39
HARD_EP5_15	2781671_5ds_9219	5D	75989	5D	9332253	85	NA	0.14	9.30
HARD_IRR_IRR	2781671_5ds_9219	5D	75989	5D	9332253	85	NA	0.13	8.85
HARD_BD_16	2781671_5ds_9179	5D	75987	5D	9332293	85	NA	0.11	7.34
HARD_BI_16	2781671_5ds_9179	5D	75987	5D	9332293	85	NA	0.11	7.53
HARD_CH_14	2781671_5ds_9179	5D	75987	5D	9332293	85	NA	0.11	7.43
HARD_CLI_16	2781671_5ds_9179	5D	75987	5D	9332293	85	NA	0.12	8.04
HARD_DRY_DRY	2781671_5ds_9179	5D	75987	5D	9332293	85	NA	0.11	7.54
HARD_EP3_15	2781671_5ds_9179	5D	75987	5D	9332293	85	NA	0.12	8.01
HARD_EP4_14	2781671_5ds_9179	5D	75987	5D	9332293	85	NA	0.13	8.42
HARD_EP4_15	2781671_5ds_9179	5D	75987	5D	9332293	85	NA	0.14	9.20
HARD_EP5_14	2781671_5ds_9179	5D	75987	5D	9332293	85	NA	0.11	7.39
HARD_EP5_15	2781671_5ds_9179	5D	75987	5D	9332293	85	NA	0.14	9.30
HARD_IRR_IRR	2781671_5ds_9179	5D	75987	5D	9332293	85	NA	0.13	8.85
HARD_CLI_16	2781671_5ds_9157	5D	75986	5D	9332315	85	NA	0.11	7.22
HARD_EP3_15	2781671_5ds_9157	5D	75986	5D	9332315	85	NA	0.11	7.30
HARD_EP4_14	2781671_5ds_9157	5D	75986	5D	9332315	85	NA	0.11	7.38
HARD_EP4_15	2781671_5ds_9157	5D	75986	5D	9332315	85	NA	0.13	8.41
HARD_EP5_15	2781671_5ds_9157	5D	75986	5D	9332315	85	NA	0.12	8.35
HARD_IRR_IRR	2781671_5ds_9157	5D	75986	5D	9332315	85	NA	0.12	7.97
HARD_EP3_15	2739401_5ds_20579	5D	76380	5D	11421190	85	-6.50	0.12	7.12
HARD_EP4_15	2242858_5ds_843	5D	76537	5D	21256151	85	NA	0.11	7.31
HARD_CH_14	2614662_5ds_579	5D	76397	5D	23058289	85	NA	0.11	7.50
HARD_CLI_16	2614662_5ds_579	5D	76397	5D	23058289	85	NA	0.10	7.08
HARD_EP4_14	2614662_5ds_579	5D	76397	5D	23058289	85	NA	0.11	7.64
HARD_EP4_15	2614662_5ds_579	5D	76397	5D	23058289	85	NA	0.10	7.05
HARD_EP5_15	2614662_5ds_579	5D	76397	5D	23058289	85	NA	0.11	7.38
HARD_IRR_IRR	2614662_5ds_579	5D	76397	5D	23058289	85	NA	0.12	7.90
HARD_CLI_16	2748871_5ds_2822	UKN	129709	5D	23346667	85	4.50	0.12	7.02
HARD_IRR_IRR	2748871_5ds_2822	UKN	129709	5D	23346667	85	4.47	0.12	7.03
HARD_BD_16	3169317_7bs_6045	7B	106340	7B	156437593	113	1.88	0.13	8.02
HARD_BI_16	3169317_7bs_6045	7B	106340	7B	156437593	113	2.85	0.15	8.81
HARD_EP5_15	3169317_7bs_6045	7B	106340	7B	156437593	113	2.60	0.12	7.28
HARD_IRR_IRR	3169317_7bs_6045	7B	106340	7B	156437593	113	2.89	0.13	7.80
MLPH_EP5_15	10560024_3b_8154	3B	46264	3B	626368663	52	-1.70	0.12	7.23
MLRS_EP5_14	3976624_1al_4871	UKN	133073	1A	563337674	5	0.16	0.15	8.06
MLRS_EP5_14	2755762_1bs_446	1B	6180	1B	15393391	6	-0.05	0.13	7.90
MLRS_EP4_14	2715434_2as_1190	UKN	125190	2A	163468275	20	0.15	0.15	8.81
MLRS_EP5_14	6416031_2al_726	2A	22559	2A	689804623	24	-0.07	0.16	9.69
MLRS_EP4_14	6415092_2al_1762	2A	21970	2A	700980102	24	0.00	0.15	8.53
MLRS_EP4_14	6415092_2al_1688	2A	21962	2A	700980176	24	0.00	0.15	8.53
MLRS_EP5_14	5246892_2bs_1581	2B	24440	2B	9127312	26	-0.09	0.13	8.02
MLRS_EP5_14	5176564_2bs_847	UKN	123971	2B	38620602	27	-0.18	0.15	8.81
MLRS_EP5_14	5192097_2bs_4621	2B	26002	2B	63820373	27	0.00	0.13	7.85
MLRS_BD_16	5244816_2bs_10170	2B	26109	2B	72938260	27	-0.14	0.11	7.20
MLRS_EP4_14	8020386_2bl_973	2B	28014	2B	415059969	28	-0.05	0.15	8.64
MLRS_EP4_14	8002564_2bl_4534	2B	32112	2B	656976741	31	-0.02	0.15	8.60
MLRS_EP4_14	8002564_2bl_4533	2B	32111	2B	656976742	31	-0.04	0.15	8.63
MLRS_EP5_14	7953703_2bl_4726	2B	31389	2B	657071400	31	0.10	0.13	8.00
MLRS_EP5_14	7953703_2bl_4718	2B	31387	2B	657071408	31	-0.02	0.13	7.89
MLRS_EP5_14	7953703_2bl_4692	2B	31384	2B	657071434	31	0.02	0.13	7.88
MLRS_EP5_14	8006724_2bl_4660	2B	33033	2B	735404943	32	0.04	0.13	7.91
MLRS_EP5_14	8088961_2bl_3997	2B	33671	2B	774682954	32	-0.13	0.13	8.04
MLRS_EP5_14	5388307_2ds_14890	2D	35318	2D	56254163	34	0.19	0.13	8.10
MLRS_EP5_14	5391007_2ds_4367	2D	36416	2D	116764802	35	-0.20	0.14	8.35
MLRS_EP5_14	9833177_2dl_16160	2D	35537	2D	527921804	37	-0.01	0.13	7.89
MLRS_EP5_14	9858970_2dl_3219	2D	38469	2D	601965671	38	0.03	0.13	7.89
MLRS_EP5_14	9858970_2dl_3228	2D	38473	2D	601965680	38	-0.09	0.13	8.04
MLRS_EP5_14	3331403_3as_17138	3A	40067	3A	28146043	39	-0.03	0.13	7.68
MLRS_EP4_14	3447514_3as_343	3A	40651	3A	85272189	40	-0.12	0.15	8.87
MLRS_EP4_14	4326927_3al_462	3A	41057	3A	430959405	42	0.17	0.14	8.29

Table A1 Continued

Trait_loc_Yr[†]	Marker	Chr	Pos	CHR[‡]	Mb[§]	QTL ID	A[¶]	R^{2}[#]	-log10(p)
MLRS_EP5_14	10762578_3b_6885	UKN	134993	3B	2164045	45	0.27	0.18	8.58
MLRS_EP5_14	10705157_3b_753	3B	44454	3B	66887150	46	0.28	0.16	9.54
MLRS_EP5_14	10705597_3b_1425	3B	45387	3B	409529033	50	0.13	0.14	8.16
MLRS_EP5_14	10580786_3b_4786	UKN	132947	3B	418748348	50	-0.08	0.16	9.74
MLRS_EP4_14	10760636_3b_4215	3B	47079	3B	769543611	54	-0.10	0.16	8.98
MLRS_EP5_14	10425662_3b_3428	3B	47289	3B	798205862	54	0.03	0.13	7.90
MLRS_EP5_14	2603046_3ds_1335	3D	47614	3D	8561225	55	-0.14	0.13	8.04
MLRS_EP5_14	6953993_3dl_1165	3D	48858	3D	528623288	57	-0.07	0.13	7.98
MLRS_EP5_14	6012949_4as_v2_9009	4A	50695	4A	67414835	58	-0.08	0.13	7.95
MLRS_EP4_14	7110987_4al_3876	4A	51052	4A	476134651	60	0.03	0.15	8.58
MLRS_EP5_14	7145077_4al_19258	4A	54649	4A	707246102	63	-0.04	0.13	7.91
MLRS_EP5_14	7022490_4bl_1414	4B	59890	4B	524603106	66	-0.02	0.13	7.90
MLRS_EP5_14	6965059_4bl_4331	4B	59698	4B	608056018	67	-0.12	0.13	8.05
MLRS_EP5_14	2275446_4ds_19878	UKN	137738	4D	7096132	69	0.08	0.14	7.87
MLRS_EP5_14	2325871_4ds_12910	4D	61537	4D	16813690	69	0.17	0.14	8.37
MLRS_EP5_14	2316586_4ds_4113	4D	61687	4D	26205822	69	0.00	0.13	7.88
MLRS_EP5_14	14377340_4dl_v2_17679	4D	63465	4D	496139310	73	-0.02	0.13	7.90
MLRS_EP5_14	14377340_4dl_v2_17626	4D	63461	4D	496139363	73	0.02	0.13	7.90
MLRS_EP5_14	14377340_4dl_v2_17615	4D	63459	4D	496139374	73	0.02	0.13	7.90
MLRS_EP4_14	14320034_4dl_v2_2527	UKN	128940	5A	414046997	72?	-0.03	0.17	8.53
MLRS_EP4_14	14320034_4dl_v2_2536	UKN	128971	5A	414047006	72?	0.17	0.18	9.09
MLRS_EP5_14	2257417_5bs_15959	5B	70107	5B	121185149	78	-0.10	0.14	8.12
MLRS_EP5_14	2257417_5bs_15958	5B	70106	5B	121185150	78	0.10	0.14	8.12
MLRS_EP5_14	2257417_5bs_15913	5B	70105	5B	121185195	78	0.08	0.15	7.99
MLRS_EP5_15	10925497_5bl_8503	5B	69123	5B	307003599	79	-0.23	0.13	7.02
MLRS_EP5_14	10882853_5bl_3768	5B	67832	5B	359486768	79	0.05	0.13	7.91
MLRS_EP5_14	10910228_5bl_7379	UKN	135253	5B	523932477	82	0.03	0.15	7.84
MLRS_EP5_14	10910228_5bl_7370	UKN	135249	5B	523932486	82	-0.03	0.15	7.84
MLRS_EP5_14	10910228_5bl_7366	UKN	135244	5B	523932490	82	-0.04	0.15	7.86
MLRS_EP5_14	10910228_5bl_7364	UKN	135242	5B	523932492	82	-0.03	0.15	7.84
MLRS_BD_16	10890478_5bl_16094	UKN	137597	5B	528563376	82	-0.33	0.16	9.11
MLRS_EP5_14	10919338_5bl_1478	5B	75350	5B	686433888	84	0.01	0.13	7.89
MLRS_EP5_14	10919338_5bl_1486	5B	75351	5B	686433896	84	0.11	0.13	7.97
MLRS_EP4_14	4503898_5dl_1782	5D	77180	5D	276671889	87	-0.01	0.15	8.57
MLRS_EP5_14	4488923_5dl_4410	5D	81451	5D	511948668	90	-0.21	0.14	8.25
MLRS_EP5_14	4429106_6as_3390	6A	83059	6A	3705808	92	0.01	0.13	7.89
MLRS_EP5_14	4429106_6as_3396	6A	83060	6A	3705814	92	-0.01	0.13	7.89
MLRS_EP4_14	5806319_6al_1934	6A	85822	6A	442085721	95	0.20	0.16	9.10
MLRS_EP4_14	5745805_6al_1075	6A	87221	6A	552828358	96	0.02	0.15	8.59
MLRS_EP5_15	5692765_6al_1356	6A	87704	6A	594960290	96	-0.27	0.13	7.41
MLRS_EP4_14	5819489_6al_18687	6A	87766	6A	595061050	96	0.01	0.15	8.57
MLRS_EP5_14	5835370_6al_17148	6A	88223	6A	612113836	97	0.08	0.13	7.98
MLRS_EP5_14	5835370_6al_17142	6A	88222	6A	612113842	97	0.22	0.12	7.05
MLRS_EP4_14	2943095_6bs_552	6B	89018	6B	27126339	98	0.05	0.15	8.64
MLRS_EP4_14	4345576_6bl_497	6B	92365	6B	681901174	100	0.03	0.12	7.28
MLRS_EP4_14	4345576_6bl_537	6B	92366	6B	681901214	100	0.03	0.12	7.28
MLRS_EP4_14	4261361_6bl_2114	6B	92571	6B	706582549	100	-0.09	0.15	8.74
MLRS_EP5_14	2116712_6ds_6275	6D	94035	6D	22182783	101	-0.04	0.13	7.91
MLRS_EP5_14	2124102_6ds_225	6D	94342	6D	60383430	101	-0.15	0.14	8.29
MLRS_EP5_14	3295766_6dl_4239	6D	97211	6D	435306987	103	0.04	0.13	7.92
MLRS_EP4_14	4190671_7as_2139	UKN	128032	7A	38749287	104	-0.04	0.17	8.52
MLRS_EP5_14	4047115_7as_639	7A	100568	7A	94913347	105	0.13	0.14	8.17
MLRS_EP5_14	4446000_7al_2788	7A	102512	7A	540909569	109	-0.08	0.13	7.97
MLRS_EP5_14	4446000_7al_2731	7A	102511	7A	540909626	109	0.08	0.13	7.97
MLRS_EP5_14	4446000_7al_2729	7A	102510	7A	540909628	109	-0.08	0.13	7.97
MLRS_EP5_14	4455276_7al_1712	UKN	126707	7A	723388881	111	-0.23	0.14	8.42
MLRS_EP5_14	6670865_7bl_689	7B	107934	7B	562992216	115	0.14	0.13	8.05
MLRS_EP5_14	3919807_7ds_190	7D	111330	7D	60148204	116	0.02	0.13	7.90
MLRS_EP5_14	3314448_7dl_1711	7D	113315	7D	461403554	120	0.10	0.13	8.06
MLRS_EP5_14	3314448_7dl_1518	7D	113312	7D	461403747	120	0.09	0.13	8.02
MLRS_EP4_14	1277312_7dl_526	UKN	122449	7D	488050396	121	-0.01	0.16	8.46
MLRS_EP5_14	3331788_7dl_1409	7D	115946	7D	547276474	122	-0.21	0.14	8.20
MLRS_EP5_14	339577_7dl_1102	UKN	124912	7D	594987964	123	0.04	0.16	7.99
MLRS_EP5_14	3342062_7dl_680	UKN	123182	7D	615915739	123	-0.09	0.15	7.92
MLRS_EP5_14	3348754_7dl_4968	7D	118998	7D	623156542	123	0.04	0.13	7.90
MLRS_EP5_14	3348754_7dl_4926	7D	118996	7D	623156584	123	0.04	0.13	7.90
MLRS_EP5_14	3387155_7dl_1367	7D	118688	7D	626231720	123	0.14	0.14	8.29
MLRS_EP5_14	3334708_7dl_3503	7D	118491	7D	634376273	123	-0.16	0.14	8.24
MLRS_EP5_14	7012446_4al_76	4A	52159	Un	244927138	60?	0.04	0.13	7.92
MLRW_IRR_IRR	3453826_1bs_3226	1B	5932	1B	17145962	6	-1.29	0.12	7.57

Table A1 Continued

Trait_loc_Yr[†]	Marker	Chr	Pos	CHR[‡]	Mb[§]	QTL ID	A[¶]	R^2[#]	-log10(p)
MLRW_IRR_IRR	3453826_1bs_3043	1B	5926	1B	17146145	6	-1.30	0.13	7.71
MLRW_IRR_IRR	3453826_1bs_3023	1B	5923	1B	17146165	6	1.26	0.13	7.71
MLRW_BI_16	3451628_1bs_1524	1B	6336	1B	25899498	6	-3.15	0.12	7.64
MLRW_BI_16	3451628_1bs_1476	1B	6334	1B	25899546	6	3.15	0.12	7.64
MLRW_BI_16	3451628_1bs_1473	1B	6333	1B	25899549	6	3.15	0.12	7.64
MLTW_EP5_15	3921954_1al_1101	UKN	124909	1A	521991074	5	-0.31	0.12	7.53
MLTW_EP5_15	3921954_1al_1141	UKN	125052	1A	521991114	5	0.06	0.12	7.40
MLTW_EP5_15	3971867_1al_22696	1A	4680	1A	547901775	5	-0.37	0.19	12.05
MLTW_EP5_15	3869500_1al_16071	1A	4720	1A	564603615	5	-0.44	0.14	8.52
MLTW_EP5_15	3869500_1al_16060	1A	4718	1A	564603626	5	-0.44	0.14	8.52
MLTW_BI_16	3453826_1bs_3226	1B	5932	1B	17145962	6	-2.78	0.12	8.02
MLTW_BI_16	3453826_1bs_3043	1B	5926	1B	17146145	6	-2.71	0.11	7.70
MLTW_BI_16	3453826_1bs_3023	1B	5923	1B	17146165	6	2.69	0.12	8.01
MLTW_EP5_15	3482438_1bs_1714	1B	6425	1B	21367114	6	1.66	0.12	7.92
MLTW_BI_16	3451172_1bs_433	1B	6326	1B	21443789	6	NA	0.09	7.32
MLTW_EP5_15	3422647_1bs_7183	1B	6268	1B	22824562	6	-0.49	0.11	7.14
MLTW_BD_16	3434158_1bs_9081	1B	6314	1B	30403173	6	NA	0.12	8.25
MLTW_EP5_15	3475565_1bs_1037	UKN	124703	1B	32817045	6	-0.05	0.19	11.78
MLTW_EP5_15	3470361_1bs_739	1B	8175	1B	171106182	8	-0.67	0.11	7.50
MLTW_EP5_15	3433385_1bs_2429	1B	7694	1B	202758082	8	-0.57	0.19	12.09
MLTW_EP5_15	3433385_1bs_2460	1B	7695	1B	202758113	8	-0.11	0.19	11.87
MLTW_EP5_15	3895037_1bl_2485	1B	11987	1B	653081906	13	0.18	0.19	11.88
MLTW_EP5_15	1910681_1ds_1845	1D	14416	1D	67443132	14	-1.04	0.11	7.09
MLTW_EP5_15	2290615_1dl_3201	1D	14205	1D	295402927	15	0.01	0.19	11.86
MLTW_EP5_15	2284405_1dl_7872	1D	15917	1D	462718121	17	-0.66	0.15	9.43
MLTW_EP5_15	2284405_1dl_7840	1D	15914	1D	462718153	17	-0.59	0.20	12.36
MLTW_EP5_15	2284405_1dl_7834	1D	15913	1D	462718159	17	-0.58	0.20	12.34
MLTW_EP5_15	2284405_1dl_7833	1D	15912	1D	462718160	17	0.59	0.20	12.36
MLTW_EP5_15	2284405_1dl_7596	1D	15904	1D	462718397	17	-0.63	0.15	9.67
MLTW_EP5_15	2266038_1dl_884	1D	16428	1D	474983270	17	-0.22	0.19	11.90
MLTW_EP5_15	2266038_1dl_688	1D	16422	1D	474983466	17	0.39	0.19	12.01
MLTW_EP5_15	2266038_1dl_672	1D	16421	1D	474983482	17	-0.35	0.19	12.01
MLTW_EP5_15	5274853_2as_1597	2A	17595	2A	23497175	18	0.30	0.12	7.08
MLTW_EP5_15	5274853_2as_1583	2A	17593	2A	23497189	18	-0.30	0.12	7.08
MLTW_EP5_15	5197325_2as_765	2A	18383	2A	49884137	18	0.55	0.19	12.00
MLTW_EP5_15	6335763_2al_578	UKN	122745	2A	588215121	22	0.20	0.13	7.75
MLTW_EP5_15	6335763_2al_574	UKN	122727	2A	588215125	22	-0.14	0.21	11.46
MLTW_EP5_15	6434376_2al_9024	2A	19021	2A	597215006	22	0.20	0.19	11.88
MLTW_EP5_15	6380908_2al_4964	2A	22895	2A	728813485	24	-0.68	0.20	12.37
MLTW_EP5_15	6362950_2al_3896	2A	23459	2A	748682248	25	0.15	0.19	11.90
MLTW_EP5_15	6362950_2al_3887	2A	23457	2A	748682257	25	-0.36	0.19	11.95
MLTW_EP5_15	8075293_2bl_9728	2B	28825	2B	436242677	28	0.00	0.19	11.91
MLTW_EP5_15	7987244_2bl_3643	2B	29223	2B	436412383	28	0.51	0.11	7.22
MLTW_EP5_15	8090690_2bl_14565	2B	29636	2B	524235209	29	-1.22	0.11	7.29
MLTW_EP5_15	8062742_2bl_977	UKN	124480	2B	552338802	29	0.38	0.11	7.09
MLTW_EP5_15	6983730_2bl_1537	2B	30388	2B	598961876	30	-0.15	0.19	11.77
MLTW_EP5_15	7942088_2bl_3961	UKN	131689	2B	667417891	31	-0.18	0.20	11.58
MLTW_EP5_15	8085346_2bl_8079	2B	32832	2B	699288270	31	0.30	0.12	8.04
MLTW_EP5_15	5372804_2ds_1471	UKN	126072	2D	44894650	33	0.05	0.19	11.73
MLTW_EP5_15	5331953_2ds_4427	2D	35468	2D	61024791	34	0.34	0.11	7.15
MLTW_EP5_15	5330991_2ds_5096	2D	35466	2D	73583923	34	-0.30	0.19	11.90
MLTW_EP5_15	5388470_2ds_592	2D	37758	2D	261987621	36	-0.30	0.11	7.05
MLTW_EP5_15	3284444_3as_3787	3A	40143	3A	23908087	39	0.68	0.11	7.17
MLTW_EP5_15	3439719_3as_124	3A	41188	3A	129893201	40	0.44	0.15	9.74
MLTW_EP5_15	3354266_3as_54	3A	41312	3A	135590589	40	-0.13	0.19	11.88
MLTW_EP5_15	3354266_3as_104	3A	41313	3A	135590592	40	0.13	0.19	11.88
MLTW_EP5_15	3441353_3as_768	UKN	123623	3A	212196873	41	-0.43	0.12	7.20
MLTW_EP5_15	4338188_3al_5343	3A	41475	3A	440027969	42	-0.80	0.11	7.29
MLTW_EP5_15	4343024_3al_33	UKN	119548	3A	684521615	44	0.13	0.20	11.70
MLTW_EP5_15	4343024_3al_38	UKN	119567	3A	684521615	44	0.12	0.20	11.69
MLTW_EP5_15	4233820_3al_4642	3A	43010	3A	706202437	44	0.02	0.19	11.86
MLTW_EP5_15	4233820_3al_4641	3A	43009	3A	706202438	44	-0.56	0.19	12.19
MLTW_EP5_15	4108010_3b_247	3B	45020	3B	245911025	48	-0.01	0.19	11.85
MLTW_EP5_15	10751565_3b_2623	UKN	129207	3B	739339484	53	1.37	0.24	13.01
MLTW_EP5_15	10774300_3b_13150	3B	47429	3B	815050498	54	0.35	0.19	12.05
MLTW_EP5_15	10757127_3b_4836	UKN	133025	3B	821046179	54	-0.55	0.21	11.39
MLTW_EP5_15	10757127_3b_4802	UKN	132973	3B	821046213	54	0.00	0.13	7.64
MLTW_EP5_15	6955423_3dl_274	3D	48129	3D	347562978	56	-0.11	0.19	11.89
MLTW_EP5_15	6952453_3dl_47	3D	48587	3D	495921615	57	-0.60	0.19	12.13
MLTW_EP5_15	5898011_4as_v2_1139	4A	50560	4A	100668627	59	0.25	0.19	11.92

Table A1 Continued

Trait_loc_Yr[†]	Marker	Chr	Pos	CHR[‡]	Mb[§]	QTL ID	A[¶]	R[2#]	-log10(p)
MLTW_EP5_15	5927344_4as_v2_3198	4A	50482	4A	120340689	59	1.13	0.12	7.63
MLTW_EP5_15	3922577_7ds_700	UKN	123258	4A	729442112	63	0.35	0.25	11.84
MLTW_EP5_15	3922577_7ds_694	UKN	123235	4A	729442116	63	-0.31	0.24	11.80
MLTW_EP5_15	4864066_4bs_4860	4B	57580	4B	117092437	64	-0.24	0.19	11.92
MLTW_EP5_15	4890458_4bs_3401	4B	58888	4B	167373704	64	-0.04	0.19	11.86
MLTW_EP5_15	4880127_4bs_1078	4B	58666	4B	213097236	65	-0.22	0.19	11.90
MLTW_EP5_15	6972744_4bl_154	4B	59736	4B	534660990	66	0.14	0.19	11.88
MLTW_EP5_15	6890178_4bl_557	UKN	122641	4B	615383932	67	0.18	0.12	7.55
MLTW_EP5_15	6890178_4bl_539	UKN	122521	4B	615383950	67	-0.15	0.13	8.00
MLTW_EP5_15	6890178_4bl_498	UKN	122270	4B	615383991	67	-0.15	0.13	8.00
MLTW_EP5_15	14381009_4dl_v2_287	UKN	120995	4D	401566773	72	-0.34	0.17	8.98
MLTW_EP5_15	14381009_4dl_v2_263	UKN	120834	4D	401566797	72	-0.35	0.17	8.99
MLTW_EP5_15	14381009_4dl_v2_248	UKN	120702	4D	401566812	72	-0.34	0.17	8.98
MLTW_EP5_15	1517889_5as_12083	5A	64145	5A	6627042	74	0.12	0.19	11.88
MLTW_EP5_15	1539578_5as_2723	UKN	129425	5A	12667826	74	-0.12	0.23	11.64
MLTW_EP5_15	2804003_5al_1159	5A	63879	5A	280524196	75	-0.64	0.20	12.28
MLTW_EP5_15	2805435_5al_10340	5A	65511	5A	606358734	76	0.21	0.19	11.91
MLTW_EP5_15	1615135_5bs_6987	5B	66703	5B	6601302	77	0.24	0.19	11.91
MLTW_EP5_15	1615135_5bs_6996	5B	66705	5B	6601311	77	0.09	0.19	11.87
MLTW_EP5_15	10925497_5bl_8503	5B	69123	5B	307003599	79	0.34	0.19	12.01
MLTW_EP5_15	10918258_5bl_2861	5B	69038	5B	322877015	79	-0.69	0.20	12.36
MLTW_EP5_15	10874919_5bl_19095	5B	70838	5B	473888733	81	-1.08	0.11	7.42
MLTW_EP5_15	10789285_5bl_1125	5B	71348	5B	497845690	81	-0.04	0.19	11.86
MLTW_EP5_15	10789285_5bl_1190	5B	71352	5B	497845755	81	0.63	0.19	12.18
MLTW_EP5_15	10789285_5bl_1399	5B	71353	5B	497845964	81	0.36	0.19	11.84
MLTW_EP5_15	10820340_5bl_743	5B	71653	5B	497905885	81	-0.35	0.11	7.03
MLTW_EP5_15	10713906_5bl_3165	5B	73131	5B	580426190	83	-0.58	0.20	12.27
MLTW_EP5_15	10878230_5bl_14895	5B	73254	5B	587120949	83	-0.12	0.19	11.87
MLTW_EP5_15	10887191_5bl_781	5B	73364	5B	590737126	83	0.13	0.19	11.88
MLTW_EP5_15	10840148_5bl_5172	5B	73954	5B	610369884	83	0.28	0.19	11.93
MLTW_EP5_15	1451356_5ds_1126	5D	76642	5D	34888016	85	-0.09	0.19	11.90
MLTW_EP5_15	4600039_5dl_719	UKN	123371	5D	375579358	88	0.40	0.22	11.68
MLTW_EP5_15	4600039_5dl_718	UKN	123364	5D	375579359	88	-0.10	0.21	11.44
MLTW_EP5_15	4590311_5dl_2239	5D	81195	5D	491845992	90	-0.18	0.19	11.88
MLTW_EP5_15	4350665_6as_530	6A	83308	6A	12213963	92	-0.39	0.19	11.97
MLTW_EP5_15	4377011_6as_2697	6A	84059	6A	39460963	92	0.35	0.13	8.47
MLTW_EP5_15	4385583_6as_630	6A	84811	6A	86383939	93	-0.48	0.19	12.07
MLTW_EP5_15	4352420_6as_2972	UKN	130086	6A	182664762	94	-0.12	0.20	11.87
MLTW_EP5_15	5692765_6al_1356	6A	87704	6A	594960290	96	-0.56	0.12	7.57
MLTW_EP5_15	5833404_6al_16346	6A	88286	6A	617804657	97	-0.58	0.11	7.43
MLTW_EP5_15	5833404_6al_16345	6A	88285	6A	617804658	97	-0.39	0.11	7.13
MLTW_EP5_15	4275962_6bl_1951	6B	91361	6B	511387953	99	-0.64	0.11	7.05
MLTW_EP5_15	4291994_6bl_6847	6B	92430	6B	687299185	100	0.52	0.19	12.05
MLTW_EP5_15	4291994_6bl_6839	6B	92429	6B	687299193	100	0.52	0.19	12.05
MLTW_EP5_15	2122083_6ds_4026	UKN	131794	6D	45486337	101	0.14	0.22	11.71
MLTW_EP5_15	2072646_6ds_14285	6D	94290	6D	46845804	101	0.02	0.19	11.63
MLTW_EP5_15	2058228_6ds_5139	6D	94864	6D	169592240	102	-0.57	0.19	12.08
MLTW_EP5_15	3248171_6dl_5095	6D	97080	6D	418887706	103	-0.10	0.19	11.87
MLTW_EP5_15	3291528_6dl_2437	6D	98530	6D	462275105	103	0.69	0.21	12.61
MLTW_EP5_15	3291528_6dl_2429	6D	98529	6D	462275113	103	0.56	0.20	12.27
MLTW_EP5_15	3291528_6dl_2425	6D	98528	6D	462275117	103	0.56	0.20	12.25
MLTW_EP5_15	3291528_6dl_2418	6D	98527	6D	462275124	103	0.54	0.20	12.22
MLTW_EP5_15	3291528_6dl_2417	6D	98526	6D	462275125	103	-0.69	0.21	12.61
MLTW_EP5_15	4249975_7as_1439	7A	100340	7A	65563625	104	-0.48	0.19	12.00
MLTW_EP5_15	4438833_7al_10700	UKN	136796	7A	428810677	108	-0.27	0.22	11.66
MLTW_EP5_15	4553164_7al_163	7A	101829	7A	501077934	109	0.50	0.11	7.09
MLTW_EP5_15	4536065_7al_716	7A	104347	7A	708435298	111	-0.76	0.11	7.42
MLTW_EP5_15	4551774_7al_1331	7A	104655	7A	725159844	111	-0.48	0.11	7.06
MLTW_EP5_15	3089883_7bs_247	UKN	120699	7B	131177775	113	-0.42	0.11	7.10
MLTW_EP5_15	3162004_7bs_1655	7B	106452	7B	182597172	113	-0.11	0.12	7.77
MLTW_EP5_15	3162004_7bs_1649	7B	106451	7B	182597178	113	0.18	0.19	11.89
MLTW_EP5_15	3922577_7ds_742	UKN	123507	7D	8746640	116	0.29	0.24	11.73
MLTW_EP5_15	3922577_7ds_748	UKN	123537	7D	8746646	116	0.29	0.24	11.80
MLTW_EP5_15	3922577_7ds_754	UKN	123561	7D	8746652	116	0.21	0.24	11.64
MLTW_EP5_15	3897318_7ds_1059	UKN	124771	7D	111274244	117	-0.06	0.19	11.58
MLTW_EP5_15	3891832_7ds_3364	7D	112292	7D	126674519	117	0.42	0.19	12.05
MLTW_EP5_15	2168702_7ds_2893	7D	112716	7D	213786834	118	-0.52	0.19	12.12
MLTW_EP5_15	3348127_7dl_6011	7D	113727	7D	376956870	119	-0.37	0.19	11.96
MLTW_EP5_15	1946986_7dl_869	7D	116130	7D	538370629	122	0.17	0.19	11.64
MLTW_EP5_15	3393906_7dl_8792	7D	116543	7D	560913296	122	0.51	0.11	7.24

Table A1 Continued

Trait_loc_Yr[†]	Marker	Chr	Pos	CHR[‡]	Mb[§]	QTL ID	A[¶]	R^2[#]	-log10(p)
MLTW_EP5_15	3393906_7dl_8559	7D	116541	7D	560913529	122	0.40	0.11	7.05
MLTW_EP5_15	3381023_7dl_12349	7D	116547	7D	562408177	122	0.33	0.19	11.98
MLTW_EP5_15	3323237_7dl_1129	7D	117276	7D	585453840	122	0.62	0.11	7.27
MLTW_EP5_15	3286355_7dl_826	7D	117448	7D	593405649	123	-0.16	0.19	11.86
MLTW_EP5_15	3391603_7dl_4388	7D	118746	7D	631694003	123	0.64	0.20	12.30
MLTW_EP5_15	5240618_2as_725	UKN	123408	Un	248330867	?	0.30	0.13	7.19
gMOIST_CLI_16	10530372_3b_2952	UKN	130040	3B	149455112	47	-0.34	0.17	8.79
gMOIST_CLI_16	10530372_3b_2948	UKN	130028	3B	149455116	47	0.34	0.17	8.79
gMOIST_CLI_16	10530372_3b_2905	UKN	129931	3B	149455159	47	-0.34	0.17	8.79
gMOIST_CLI_16	10530372_3b_2902	UKN	129922	3B	149455162	47	0.34	0.17	8.79
gMOIST_CLI_16	10530372_3b_2898	UKN	129913	3B	149455166	47	-0.33	0.17	8.53
gMOIST_BD_16	7144776_4al_1620	4A	54019	4A	662542416	62	-0.28	0.10	7.02
gMOIST_EP5_14	2946616_6bs_1121	6B	89635	6B	79304656	98	-0.14	0.11	7.13
gMOIST_CLI_16	4245739_7as_2670	7A	101173	7A	206908324	107	-0.24	0.17	9.59
gMOIST_CLI_16	4245739_7as_2674	7A	101174	7A	206908328	107	-0.23	0.17	9.56
gMOIST_CLI_16	4245739_7as_2695	7A	101175	7A	206908349	107	0.24	0.17	9.59
gMOIST_CLI_16	4245739_7as_2700	7A	101176	7A	206908354	107	-0.19	0.17	9.72
gMOIST_CLI_16	4245739_7as_2705	7A	101177	7A	206908359	107	-0.24	0.17	9.61
gMOIST_CLI_16	4245739_7as_2709	7A	101178	7A	206908363	107	-0.23	0.17	9.56
gMOIST_CLI_16	4245739_7as_2715	7A	101179	7A	206908369	107	0.22	0.16	9.39
gMOIST_CLI_16	4245739_7as_2717	7A	101180	7A	206908371	107	0.23	0.17	9.58
gMOIST_CLI_16	4245739_7as_2726	7A	101181	7A	206908380	107	-0.23	0.17	9.56
gMOIST_CLI_16	4245739_7as_2727	7A	101182	7A	206908381	107	-0.23	0.17	9.56
gMOIST_CLI_16	4245739_7as_2738	7A	101183	7A	206908392	107	0.23	0.17	9.56
gMOIST_CLI_16	4245739_7as_2893	7A	101187	7A	206908547	107	-0.22	0.17	9.75
gMOIST_CLI_16	4245739_7as_2917	7A	101188	7A	206908571	107	0.21	0.14	8.46
gMOIST_CLI_16	3162666_7bs_341	7B	106478	7B	329786542	114	0.27	0.16	8.78
gMOIST_CLI_16	3162666_7bs_336	7B	106477	7B	329786547	114	-0.33	0.20	10.77
gMOIST_CLI_16	3162666_7bs_335	7B	106476	7B	329786548	114	0.32	0.20	10.65
gMOIST_CLI_16	3162666_7bs_327	7B	106475	7B	329786556	114	0.33	0.20	10.56
gMOIST_CLI_16	3162666_7bs_156	7B	106466	7B	329786727	114	-0.32	0.21	11.63
gMOIST_CLI_16	3162666_7bs_96	7B	106462	7B	329786782	114	-0.32	0.21	11.63
gMOIST_CLI_16	3055451_7dl_3076	7D	116879	7D	574031608	122	-0.35	0.12	7.00
gMOIST_CLI_16	3055451_7dl_3085	7D	116880	7D	574031617	122	NA	0.12	7.82
PROT14_IRR_IRR	3957731_1al_521	1A	1726	1A	224099448	2	0.09	0.12	7.06
PROT14_IRR_IRR	3872634_1bl_556	1B	9410	1B	366084089	10	0.00	0.16	9.65
PROT14_IRR_IRR	3872634_1bl_716	1B	9412	1B	366084249	10	-0.01	0.17	9.70
PROT14_IRR_IRR	3872634_1bl_722	1B	9413	1B	366084255	10	-0.03	0.17	10.00
PROT14_IRR_IRR	3872634_1bl_741	1B	9414	1B	366084274	10	0.03	0.17	10.02
PROT14_IRR_IRR	3872634_1bl_743	1B	9415	1B	366084276	10	0.03	0.17	10.00
PROT14_IRR_IRR	3824183_1bl_13905	1B	11529	1B	642678416	13	0.06	0.17	10.17
PROT14_IRR_IRR	3861681_1bl_6499	1B	12232	1B	659767422	13	0.01	0.16	9.71
PROT14_IRR_IRR	2031440_1dl_6042	1D	15163	1D	376005634	16	-0.02	0.16	9.79
PROT14_IRR_IRR	2031440_1dl_6033	1D	15161	1D	376005643	16	-0.02	0.16	9.76
PROT14_IRR_IRR	2031440_1dl_6010	1D	15159	1D	376005666	16	0.00	0.16	9.67
PROT14_IRR_IRR	6339185_2al_5170	2A	22314	2A	700553145	24	0.00	0.16	9.67
PROT14_IRR_IRR	6437732_2al_18701	2A	23139	2A	745669800	25	0.02	0.16	9.72
PROT14_IRR_IRR	6411521_2al_3334	2A	23808	2A	775371134	25	0.04	0.17	9.95
PROT14_IRR_IRR	8065054_2bl_3492	2B	28185	2B	437819922	28	0.04	0.12	7.10
PROT14_IRR_IRR	7973556_2bl_11007	2B	29147	2B	485163993	29	0.00	0.16	9.67
PROT14_IRR_IRR	5331794_2ds_5579	2D	34398	2D	1521231	33	0.04	0.17	10.04
PROT14_IRR_IRR	5327449_2ds_374	2D	36548	2D	131074221	35	0.01	0.16	9.72
PROT14_IRR_IRR	3354266_3as_265	3A	41314	3A	135590753	40	0.04	0.17	9.90
PROT14_IRR_IRR	4262674_3al_3119	UKN	130379	3A	611951242	43	0.04	0.23	10.01
PROT14_IRR_IRR	10566950_3b_3367	UKN	130804	3B	31786758	45	-0.05	0.19	9.74
PROT14_IRR_IRR	10649627_3b_3458	UKN	130961	3B	34395499	45	-0.01	0.17	9.71
PROT14_IRR_IRR	10649627_3b_3426	UKN	130917	3B	34395531	45	-0.02	0.17	9.75
PROT14_IRR_IRR	10649627_3b_3420	UKN	130906	3B	34395537	45	-0.02	0.17	9.75
PROT14_IRR_IRR	10396492_3b_4060	3B	45233	3B	311134116	49	0.00	0.16	9.68
PROT14_IRR_IRR	7845406_3b_1559	UKN	126259	3B	716295361	53	0.00	0.13	7.46
PROT14_IRR_IRR	7845406_3b_1572	UKN	126282	3B	716295374	53	0.00	0.13	7.46
PROT14_IRR_IRR	7845406_3b_1586	UKN	126313	3B	716295388	53	0.00	0.13	7.46
PROT14_IRR_IRR	7845406_3b_1597	UKN	126348	3B	716295399	53	0.00	0.13	7.46
PROT14_IRR_IRR	10752832_3b_13628	UKN	137327	3B	737402674	53	0.05	0.19	9.72
PROT14_IRR_IRR	2769959_3b_2123	UKN	128001	3B	796891213	54	0.01	0.21	9.58
PROT14_IRR_IRR	7085263_4al_5413	4A	51193	4A	551396551	61	-0.01	0.16	9.69
PROT14_IRR_IRR	4860661_4bs_1872	4B	57492	4B	134987855	64	0.07	0.18	10.50
PROT14_IRR_IRR	4882160_4bs_2646	4B	57779	4B	173974116	65	0.00	0.16	9.68
PROT14_IRR_IRR	4960895_4bs_15608	4B	56724	4B	503363917	66	0.10	0.12	7.05
PROT14_IRR_IRR	10865381_5bl_2065	5B	70662	5B	393756525	80	-0.09	0.12	7.05

Table A1 Continued

Trait_loc_Yr[†]	Marker	Chr	Pos	CHR[‡]	Mb[§]	QTL ID	A[¶]	R^2[#]	-log10(p)
PROT14_IRR_IRR	4465812_5dl_2083	5D	77919	5D	300254563	87	-0.01	0.16	9.68
PROT14_IRR_IRR	4533345_5dl_2182	5D	80593	5D	470384525	89	-0.04	0.17	9.89
PROT14_IRR_IRR	4594956_5dl_12321	5D	82756	5D	560219491	91	0.02	0.16	9.76
PROT14_IRR_IRR	4404183_6as_16622	6A	83405	6A	17652228	92	0.03	0.16	9.78
PROT14_IRR_IRR	3043613_6bs_719	6B	89005	6B	22437432	98	0.02	0.16	9.73
PROT14_IRR_IRR	4207272_7as_784	7A	100028	7A	48022645	104	-0.06	0.17	9.93
PROT14_DRY_DRY	4245196_7as_594	7A	100749	7A	112440932	106	NA	0.12	8.04
PROT14_DRY_DRY	4245196_7as_363	7A	100745	7A	112441163	106	-0.18	0.12	7.25
PROT14_DRY_DRY	4245196_7as_362	7A	100744	7A	112441164	106	0.18	0.12	7.25
PROT14_DRY_DRY	4245196_7as_303	7A	100743	7A	112441223	106	NA	0.12	8.04
PROT14_DRY_DRY	4245196_7as_301	7A	100742	7A	112441225	106	NA	0.12	8.04
PROT14_IRR_IRR	4557449_7al_660	7A	102261	7A	511490747	109	0.00	0.16	9.67
PROT14_IRR_IRR	3114361_7bs_10026	7B	105832	7B	68562795	112	-0.01	0.16	9.69
PROT14_IRR_IRR	3114361_7bs_10024	7B	105830	7B	68562797	112	-0.01	0.16	9.69
PROT14_IRR_IRR	381629_7dl_243	7D	113799	7D	385718110	119	0.03	0.18	10.03
PROT14_IRR_IRR	381629_7dl_221	7D	113798	7D	385718132	119	-0.03	0.18	10.03
PROT14_IRR_IRR	381629_7dl_152	7D	113796	7D	385718201	119	-0.03	0.18	10.04
PROT14_IRR_IRR	3379317_7dl_441	7D	115141	7D	390630058	119	0.00	0.16	9.67
PROT14_IRR_IRR	3394453_7dl_9044	7D	114434	7D	419769167	119	NA	0.10	7.10
SKW_EP5_15	7130376_4al_8778	4A	53500	4A	672102841	62	NA	0.11	7.70
SKW_EP5_15	7130376_4al_8777	4A	53499	4A	672102842	62	NA	0.12	8.14
SKW_EP5_15	7130376_4al_8753	4A	53498	4A	672102866	62	NA	0.10	7.11
SKW_EP5_15	7130376_4al_8717	4A	53497	4A	672102902	62	NA	0.12	8.15
WABS_EP5_14	10770064_3b_7986	UKN	135705	3B	571455474	51	NA	0.13	7.45
WABS_DRY_DRY	4245196_7as_594	7A	100749	7A	112440932	106	NA	0.12	8.05
WABS_DRY_DRY	4245196_7as_363	7A	100745	7A	112441163	106	-0.27	0.12	7.25
WABS_DRY_DRY	4245196_7as_362	7A	100744	7A	112441164	106	0.27	0.12	7.25
WABS_DRY_DRY	4245196_7as_303	7A	100743	7A	112441223	106	NA	0.12	8.05
WABS_DRY_DRY	4245196_7as_301	7A	100742	7A	112441225	106	NA	0.12	8.05

[†] Trait_Location_year

[‡] CHR, chromosomal location of marker in IWGSC RefSeq v1.0

[§] chromosomal position of marker in IWGSC RefSeq v1.0

[¶] Additive effect of the loci

[#] phenotypic variance explained by corresponding marker loci

Table A2
Significant marker trait association detected on single traits combined across environments, chromosome, position, effect for end-use quality traits in AMPSY population

Trait_loc_Yr[†]	Marker	Chr	Pos	CHR[‡]	Mb[§]	QTL ID	A[¶]	R^2[#]	-log10(p)
FYLD_CLI_16	3305478_1as_3640	1A	272	1A	12818706	1	0.17	0.13	7.88
FYLD_CLI_16	3980528_1al_5184	1A	2017	1A	301131835	3	-0.78	0.13	8.18
FYLD_CLI_16	3927067_1al_12869	1A	2977	1A	389827066	4	-0.37	0.13	7.99
FYLD_CLI_16	3902709_1al_1308	UKN	1E+05	1A	428210584	4	0.55	0.15	8.18
FYLD_CLI_16	3902709_1al_1318	UKN	1E+05	1A	428210594	4	-0.88	0.13	7.32
FYLD_CLI_16	2278844_5bs_1907	UKN	1E+05	1B	60609112	6	-0.31	0.15	7.91
FYLD_CLI_16	3466711_1bs_2061	1B	7872	1B	101628236	7	0.45	0.13	8.06
FYLD_CLI_16	3466711_1bs_2020	1B	7870	1B	101628277	7	-0.45	0.13	8.06
FYLD_BD_16	3852692_1bl_3809	1B	7220	1B	280279027	9	1.92	0.12	7.35
FYLD_CLI_16	3892149_1bl_1985	1B	9895	1B	499635782	11	-0.29	0.13	7.92
FYLD_CLI_16	3858550_1bl_14890	1B	10735	1B	570836269	12	-0.46	0.13	8.00
FYLD_CLI_16	2282749_1dl_6803	1D	13916	1D	293607345	15	0.11	0.13	7.92
FYLD_CLI_16	2282749_1dl_6810	1D	13917	1D	293607352	15	-0.11	0.13	7.93
FYLD_CLI_16	2282749_1dl_6811	1D	13918	1D	293607353	15	-0.11	0.13	7.93
FYLD_CLI_16	2291838_1dl_7209	1D	15068	1D	317186574	15	-0.03	0.13	7.87
FYLD_CLI_16	2283167_1dl_17248	UKN	1E+05	1D	471086338	17	0.27	0.13	7.91
FYLD_CLI_16	2283167_1dl_17265	UKN	1E+05	1D	471086355	17	-0.27	0.13	7.92
FYLD_CLI_16	2283167_1dl_17277	UKN	1E+05	1D	471086367	17	-0.24	0.13	7.91
FYLD_CLI_16	5309070_2as_1364	2A	20709	2A	78755910	19	-0.20	0.13	7.89
FYLD_EP5_15	6435505_2al_8117	2A	19060	2A	347820702	21	0.02	0.16	9.29
FYLD_EP5_15	6324590_2al_2660	2A	18530	2A	566862511	22	-2.24	0.18	10.60
FYLD_CLI_16	6404696_2al_13964	UKN	1E+05	2A	628677518	23	0.15	0.14	7.82
FYLD_EP5_15	2461981_2al_3009	2A	22054	2A	695467552	24	0.21	0.16	9.32
FYLD_EP5_15	5184318_2bs_5233	2B	25524	2B	50715027	27	-0.30	0.16	9.27
FYLD_EP5_15	5184318_2bs_5090	2B	25520	2B	50715170	27	-0.48	0.16	9.42
FYLD_CLI_16	8028072_2bl_3018	2B	28049	2B	411000857	28	-0.45	0.13	7.96
FYLD_BI_16	5388307_2ds_14921	2D	35320	2D	56254194	34	-0.83	0.14	8.07
FYLD_EP5_15	2260462_2ds_419	UKN	1E+05	2D	73286123	34	-0.19	0.18	9.21
FYLD_CLI_16	9909878_2dl_8779	2D	38355	2D	590338112	38	-0.81	0.13	8.24
FYLD_EP5_15	9910341_2dl_2006	UKN	1E+05	2D	641955809	38	-0.05	0.19	9.32
FYLD_EP5_15	3387459_3as_6843	3A	40273	3A	41627157	39	-0.14	0.16	9.31
FYLD_CLI_16	3413956_3as_889	3A	40791	3A	86403737	40	0.03	0.13	7.85
FYLD_CLI_16	4450272_3al_830	3A	43324	3A	715420289	44	0.14	0.16	9.79
FYLD_CLI_16	4450272_3al_835	3A	43325	3A	715420289	44	-0.14	0.16	9.79
FYLD_CLI_16	4450272_3al_1054	3A	43327	3A	715420483	44	-0.01	0.13	7.87
FYLD_CLI_16	4297373_3al_307	3A	43714	3A	736099722	44	-0.21	0.13	7.89
FYLD_EP5_15	10605995_3b_1664	UKN	1E+05	3B	29498546	45	0.40	0.18	9.10
FYLD_EP5_15	10683916_3b_2192	UKN	1E+05	3B	117555037	47	-0.01	0.16	9.21
FYLD_EP5_15	10683916_3b_2167	UKN	1E+05	3B	117555062	47	-0.46	0.16	9.31
FYLD_CLI_16	10461448_3b_557	3B	46111	3B	534828537	51	-0.03	0.13	7.85
FYLD_CLI_16	10451971_3b_7480	UKN	1E+05	3B	602586559	52	-0.13	0.13	7.83
FYLD_CLI_16	10451971_3b_7321	UKN	1E+05	3B	602586718	52	-0.54	0.14	8.11
FYLD_CLI_16	6013263_4as_v2_7346	4A	50154	4A	30155367	58	1.31	0.14	8.89
FYLD_EP5_15	7079348_4al_382	UKN	1E+05	4A	637256685	62	0.22	0.19	9.39
FYLD_CLI_16	4057017_4al_591	4A	53762	4A	646117303	62	-0.62	0.13	8.09
FYLD_CLI_16	4057017_4al_596	4A	53763	4A	646117308	62	0.62	0.13	8.09
FYLD_CLI_16	4057017_4al_613	4A	53766	4A	646117325	62	-0.62	0.13	8.09
FYLD_EP5_15	7088979_4al_3699	UKN	1E+05	4A	658897102	62	0.89	0.18	9.43
FYLD_EP5_15	7120458_4al_2339	4A	55123	4A	720204970	63	-0.25	0.16	9.33
FYLD_EP5_15	7120458_4al_2378	4A	55126	4A	720205009	63	-0.36	0.16	9.39
FYLD_EP5_15	7120458_4al_2392	4A	55129	4A	720205023	63	0.42	0.16	9.44
FYLD_CLI_16	7083149_4al_7921	4A	55523	4A	725860581	63	0.29	0.13	7.93
FYLD_EP5_15	7039666_4bl_20663	4B	60061	4B	570150846	67	0.29	0.16	9.33
FYLD_CLI_16	6975707_4bl_1506	UKN	1E+05	4B	649679461	68	0.01	0.14	7.75
FYLD_CLI_16	1380443_4ds_2087	4D	62092	4D	94263283	70	0.54	0.14	8.87
FYLD_EP5_15	2309923_4ds_2070	4D	62838	4D	164595143	71	NA	0.13	8.74
FYLD_CLI_16	14304468_4dl_v2_1665	UKN	1E+05	4D	413041988	72	-0.06	0.16	9.24
FYLD_EP5_15	1506586_5as_5534	UKN	1E+05	5A	10213724	74	-1.43	0.18	10.23
FYLD_EP5_15	2476331_5al_1297	5A	63913	5A	279102105	75	-1.56	0.17	10.14
FYLD_EP5_15	10905888_5bl_8545	5B	70646	5B	399777517	80	0.40	0.16	9.50
FYLD_EP5_15	10905888_5bl_8543	5B	70645	5B	399777519	80	-0.40	0.16	9.50
FYLD_EP5_15	10905888_5bl_8533	5B	70642	5B	399777529	80	-0.39	0.16	9.49
FYLD_EP5_15	10905888_5bl_8523	5B	70641	5B	399777539	80	-0.39	0.16	9.48
FYLD_EP5_15	10905888_5bl_8511	5B	70640	5B	399777551	80	0.39	0.16	9.49
FYLD_CLI_16	10906178_5bl_4128	5B	70984	5B	445444817	81	-0.21	0.13	7.90
FYLD_CLI_16	10906178_5bl_4143	5B	70985	5B	445444832	81	-0.27	0.13	7.96
FYLD_CLI_16	10906178_5bl_4144	5B	70986	5B	445444833	81	-0.25	0.13	7.94
FYLD_CLI_16	10906178_5bl_4445	5B	70989	5B	445445134	81	0.26	0.13	7.95

Table A2 Continued

Trait_loc_Yr†	Marker	Chr	Pos	CHR‡	Mb§	QTL ID	A¶	R2#	-log10(p)
FYLD_CLI_16	10807425_5bl_10093	5B	71312	5B	447844705	81	-0.56	0.13	8.07
FYLD_CLI_16	10847251_5bl_499	5B	71161	5B	463923822	81	0.15	0.12	7.09
FYLD_BD_16	10833329_5bl_3165	5B	73601	5B	595287398	83	-0.96	0.12	7.17
FYLD_BD_16	10833329_5bl_3193	5B	73603	5B	595287426	83	-1.03	0.12	7.33
FYLD_BD_16	10833329_5bl_3385	5B	73611	5B	595287618	83	-0.98	0.12	7.19
FYLD_BD_16	10833329_5bl_3390	5B	73613	5B	595287623	83	-1.03	0.12	7.33
FYLD_BD_16	10833329_5bl_3402	5B	73614	5B	595287635	83	-0.97	0.12	7.19
FYLD_EP5_15	10806569_5bl_2517	5B	74549	5B	636930195	83	-0.22	0.16	9.25
FYLD_EP5_15	10806569_5bl_2468	5B	74548	5B	636930244	83	-0.36	0.16	9.35
FYLD_EP5_15	10809422_5bl_3717	5B	75382	5B	684607248	84	-0.25	0.16	9.32
FYLD_CLI_16	10824756_5bl_1863	5B	75732	5B	703306588	84	-0.22	0.13	7.93
FYLD_EP4_14	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.18	11.92
FYLD_EP5_14	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.20	12.93
FYLD_EP3_15	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.14	9.15
FYLD_EP5_15	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.13	8.55
FYLD_BD_16	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.11	7.69
FYLD_BI_16	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.12	7.99
FYLD_EP4_14	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.22	14.13
FYLD_EP5_14	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.19	12.34
FYLD_EP3_15	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.14	9.66
FYLD_BI_16	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.11	7.37
FYLD_CLI_16	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.12	8.36
FYLD_EP4_14	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.27	16.45
FYLD_EP5_14	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.25	15.32
FYLD_EP3_15	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.18	11.45
FYLD_EP5_15	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.23	11.97
FYLD_BI_16	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.14	8.90
FYLD_CLI_16	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.20	12.50
FYLD_EP4_14	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.19	12.42
FYLD_EP5_14	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.24	15.05
FYLD_EP3_15	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.14	9.32
FYLD_EP5_15	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.16	10.74
FYLD_EP4_14	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.20	12.85
FYLD_EP5_14	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.26	15.78
FYLD_EP3_15	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.15	10.24
FYLD_EP5_15	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.13	8.78
FYLD_BD_16	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.11	7.78
FYLD_BI_16	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.11	7.64
FYLD_EP4_14	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.19	12.42
FYLD_EP5_14	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.24	15.05
FYLD_EP3_15	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.14	9.32
FYLD_EP5_15	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.16	10.74
FYLD_EP4_14	2770151_5ds_4035	5D	75899	5D	7257066	85	NA	0.11	7.98
FYLD_EP5_14	2739337_5ds_2304	5D	75953	5D	7485266	85	NA	0.11	7.12
FYLD_EP4_14	2781025_5ds_24425	5D	76006	5D	8018752	85	NA	0.10	7.15
FYLD_EP5_14	2781025_5ds_24425	5D	76006	5D	8018752	85	NA	0.13	8.91
FYLD_EP4_14	2781025_5ds_24421	5D	76005	5D	8018756	85	NA	0.10	7.15
FYLD_EP5_14	2781025_5ds_24421	5D	76005	5D	8018756	85	NA	0.13	8.91
FYLD_EP4_14	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.11	7.67
FYLD_EP5_14	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.15	9.99
FYLD_EP3_15	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.14	9.44
FYLD_EP5_15	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.11	7.47
FYLD_CLI_16	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.10	7.23
FYLD_EP4_14	2781671_5ds_9461	5D	75993	5D	9332011	85	NA	0.10	7.03
FYLD_EP4_14	2781671_5ds_9443	5D	75992	5D	9332029	85	NA	0.10	7.03
FYLD_EP4_14	2781671_5ds_9235	5D	75991	5D	9332237	85	NA	0.10	7.03
FYLD_EP4_14	2781671_5ds_9219	5D	75989	5D	9332253	85	NA	0.10	7.03
FYLD_EP4_14	2781671_5ds_9179	5D	75987	5D	9332293	85	NA	0.10	7.03
FYLD_EP5_15	2739401_5ds_20579	5D	76380	5D	11421190	85	-2.74	0.12	7.00
FYLD_CLI_16	2760386_5ds_1248	UKN	1E+05	5D	14719288	85	0.02	0.15	7.80
FYLD_CLI_16	2770949_5ds_845	5D	77116	5D	70819097	86	-0.35	0.13	7.94
FYLD_CLI_16	2783341_5ds_8399	5D	77064	5D	72551106	86	-0.16	0.13	7.88
FYLD_EP5_14	4599562_5dl_5399	5D	78574	5D	298137698	87	NA	0.10	7.22
FYLD_EP5_15	4590136_5dl_3635	5D	78026	5D	345935291	88	0.28	0.16	9.34
FYLD_CLI_16	4504942_5dl_1247	5D	78305	5D	346502034	88	-0.48	0.13	7.97
FYLD_EP5_15	4514657_5dl_1632	5D	79259	5D	385511140	88	-0.51	0.16	9.50
FYLD_CLI_16	4605319_5dl_3048	5D	79877	5D	434399580	89	0.11	0.13	7.87
FYLD_CLI_16	4544938_5dl_5497	5D	80179	5D	453882685	89	0.05	0.13	7.87
FYLD_CLI_16	4534695_5dl_15341	5D	81712	5D	526417202	90	0.13	0.13	7.89
FYLD_CLI_16	4412722_6as_11506	6A	82894	6A	1679610	92	0.01	0.13	7.87
FYLD_CLI_16	4429138_6as_4885	6A	84761	6A	81300931	93	0.33	0.13	7.95
FYLD_CLI_16	5779119_6al_30	6A	87072	6A	550280481	96	-0.28	0.13	7.95
FYLD_EP5_15	2104944_6ds_1907	6D	93021	6D	4373904	101	-0.41	0.16	9.43
FYLD_EP5_15	3241616_6dl_343	6D	95722	6D	225477162	102	-0.36	0.16	9.36
FYLD_CLI_16	4188922_7as_8493	UKN	1E+05	7A	32691576	104	-0.94	0.17	8.49

Table A2 Continued

Trait_loc_Yr†	Marker	Chr	Pos	CHR‡	Mb§	QTL ID	A¶	R^{2}#	-log10(p)
FYLD_EP5_15	4438480_7al_11172	7A	1E+05	7A	561615734	110	-0.02	0.16	9.29
FYLD_CLI_16	4556713_7al_3803	7A	1E+05	7A	581433764	110	0.36	0.13	7.94
FYLD_EP5_15	4466982_7al_4013	7A	1E+05	7A	733969740	111	0.00	0.16	9.28
FYLD_EP5_15	4466982_7al_4163	7A	1E+05	7A	733969890	111	-0.22	0.16	9.29
FYLD_CLI_16	3156753_7bs_820	7B	1E+05	7B	134714902	113	-0.09	0.13	7.87
FYLD_CLI_16	3856934_7ds_2095	7D	1E+05	7D	9376388	116	-0.54	0.13	8.00
FYLD_CLI_16	3856934_7ds_2056	7D	1E+05	7D	9376427	116	-0.20	0.12	7.68
FYLD_EP5_15	3898730_7ds_1216	7D	1E+05	7D	18207787	116	0.72	0.16	9.50
FYLD_EP5_15	5389722_2ds_5977	2D	34903	Un	24970654	33?	1.18	0.17	9.99
FYLD_CLI_16	3418003_3as_1194	3A	39385	Un	32236572	39?	-0.06	0.13	7.87
FYLD_CLI_16	5744793_6al_520	6A	88417	Un	75261141	92?	-0.23	0.13	7.91
FYLD_CLI_16	5744793_6al_542	6A	88418	Un	75261163	92?	0.11	0.13	7.87
HARD_BD_16	5176564_2bs_647	UKN	1E+05	2B	38620402	27	-0.70	0.12	7.11
HARD_BD_16	5176564_2bs_662	UKN	1E+05	2B	38620417	27	0.82	0.12	7.18
HARD_CH_14	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.17	11.09
HARD_EP4_14	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.21	12.68
HARD_EP5_14	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.21	13.32
HARD_EP3_15	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.23	13.87
HARD_EP4_15	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.25	15.19
HARD_EP5_15	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.24	14.63
HARD_BD_16	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.18	11.70
HARD_BI_16	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.16	10.37
HARD_CLI_16	1477005_5ds_2010	5D	75878	5D	344579	85	NA	0.22	13.47
HARD_EP4_14	1477005_5ds_2278	5D	75884	5D	344847	85	NA	0.11	7.27
HARD_CLI_16	1477005_5ds_2278	5D	75884	5D	344847	85	7.63	0.13	7.83
HARD_CH_14	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.20	12.79
HARD_EP4_14	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.23	13.72
HARD_EP5_14	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.23	14.13
HARD_EP3_15	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.29	17.28
HARD_EP4_15	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.33	18.93
HARD_EP5_15	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.28	16.77
HARD_BD_16	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.21	13.14
HARD_BI_16	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.18	11.78
HARD_CLI_16	2745573_5ds_3677	5D	75978	5D	554980	85	NA	0.25	15.23
HARD_CH_14	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.24	14.78
HARD_EP4_14	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.28	16.20
HARD_EP5_14	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.27	15.99
HARD_EP3_15	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.31	17.83
HARD_EP4_15	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.32	18.23
HARD_EP5_15	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.31	17.75
HARD_BD_16	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.26	15.51
HARD_BI_16	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.23	13.82
HARD_CLI_16	2736392_5ds_5233	5D	75917	5D	934031	85	NA	0.26	15.46
HARD_EP3_15	2765676_5ds_2839	5D	75901	5D	1344429	85	-8.56	0.13	7.86
HARD_CH_14	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.21	13.55
HARD_EP4_14	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.24	14.27
HARD_EP5_14	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.24	14.56
HARD_EP3_15	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.28	16.92
HARD_EP4_15	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.26	15.90
HARD_EP5_15	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.28	16.86
HARD_BD_16	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.24	14.88
HARD_BI_16	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.19	12.43
HARD_CLI_16	2773392_5ds_1412	5D	75911	5D	2220874	85	NA	0.27	16.09
HARD_CH_14	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.23	14.48
HARD_EP4_14	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.24	14.57
HARD_EP5_14	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.26	15.60
HARD_EP3_15	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.30	17.84
HARD_EP4_15	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.29	16.97
HARD_EP5_15	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.29	17.20
HARD_BD_16	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.26	15.68
HARD_BI_16	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.20	13.02
HARD_CLI_16	2773392_5ds_1238	5D	75910	5D	2221048	85	NA	0.29	17.40
HARD_CH_14	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.21	13.55
HARD_EP4_14	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.24	14.27
HARD_EP5_14	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.24	14.56
HARD_EP3_15	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.28	16.92
HARD_EP4_15	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.26	15.90
HARD_EP5_15	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.28	16.86
HARD_BD_16	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.24	14.88
HARD_BI_16	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.19	12.43
HARD_CLI_16	2773392_5ds_1206	5D	75906	5D	2221080	85	NA	0.27	16.09
HARD_EP3_15	2770151_5ds_4035	5D	75899	5D	7257066	85	NA	0.11	7.66
HARD_EP4_14	2739337_5ds_2304	5D	75953	5D	7485266	85	NA	0.12	7.71
HARD_EP3_15	2739337_5ds_2304	5D	75953	5D	7485266	85	NA	0.11	7.27
HARD_EP4_15	2739337_5ds_2304	5D	75953	5D	7485266	85	NA	0.11	7.33

Table A2 Continued

Trait_loc_Yr†	Marker	Chr	Pos	CHR‡	Mb§	QTL ID	A¶	R^{2}#	-log10(p)
HARD_EP5_15	2739337_5ds_2304	5D	75953	5D	7485266	85	NA	0.13	8.65
HARD_BD_16	2739337_5ds_2304	5D	75953	5D	7485266	85	NA	0.10	7.10
HARD_BI_16	2739337_5ds_2304	5D	75953	5D	7485266	85	NA	0.11	7.70
HARD_CLI_16	2739337_5ds_2304	5D	75953	5D	7485266	85	NA	0.14	8.80
HARD_CH_14	2781025_5ds_24425	5D	76006	5D	8018752	85	NA	0.14	9.18
HARD_EP4_14	2781025_5ds_24425	5D	76006	5D	8018752	85	NA	0.14	8.91
HARD_EP5_14	2781025_5ds_24425	5D	76006	5D	8018752	85	NA	0.12	8.19
HARD_EP3_15	2781025_5ds_24425	5D	76006	5D	8018752	85	NA	0.16	10.09
HARD_EP4_15	2781025_5ds_24425	5D	76006	5D	8018752	85	NA	0.15	9.69
HARD_EP5_15	2781025_5ds_24425	5D	76006	5D	8018752	85	NA	0.18	11.58
HARD_BD_16	2781025_5ds_24425	5D	76006	5D	8018752	85	NA	0.15	9.86
HARD_BI_16	2781025_5ds_24425	5D	76006	5D	8018752	85	NA	0.15	10.03
HARD_CLI_16	2781025_5ds_24425	5D	76006	5D	8018752	85	NA	0.15	9.86
HARD_CH_14	2781025_5ds_24421	5D	76005	5D	8018756	85	NA	0.14	9.18
HARD_EP4_14	2781025_5ds_24421	5D	76005	5D	8018756	85	NA	0.14	8.91
HARD_EP5_14	2781025_5ds_24421	5D	76005	5D	8018756	85	NA	0.12	8.19
HARD_EP3_15	2781025_5ds_24421	5D	76005	5D	8018756	85	NA	0.16	10.09
HARD_EP4_15	2781025_5ds_24421	5D	76005	5D	8018756	85	NA	0.15	9.69
HARD_EP5_15	2781025_5ds_24421	5D	76005	5D	8018756	85	NA	0.18	11.58
HARD_BD_16	2781025_5ds_24421	5D	76005	5D	8018756	85	NA	0.15	9.86
HARD_BI_16	2781025_5ds_24421	5D	76005	5D	8018756	85	NA	0.15	10.03
HARD_CLI_16	2781025_5ds_24421	5D	76005	5D	8018756	85	NA	0.15	9.86
HARD_EP4_14	2745020_5ds_15344	5D	76053	5D	8419265	85	7.25	0.13	7.73
HARD_EP5_14	2745020_5ds_15344	5D	76053	5D	8419265	85	6.51	0.12	7.17
HARD_EP3_15	2745020_5ds_15344	5D	76053	5D	8419265	85	7.39	0.12	7.36
HARD_EP4_15	2745020_5ds_15344	5D	76053	5D	8419265	85	7.74	0.13	8.01
HARD_BD_16	2745020_5ds_15344	5D	76053	5D	8419265	85	6.15	0.12	7.33
HARD_EP4_14	2745020_5ds_15346	5D	76054	5D	8419267	85	7.25	0.13	7.73
HARD_EP5_14	2745020_5ds_15346	5D	76054	5D	8419267	85	6.51	0.12	7.17
HARD_EP3_15	2745020_5ds_15346	5D	76054	5D	8419267	85	7.39	0.12	7.36
HARD_EP4_15	2745020_5ds_15346	5D	76054	5D	8419267	85	7.74	0.13	8.01
HARD_BD_16	2745020_5ds_15346	5D	76054	5D	8419267	85	6.15	0.12	7.33
HARD_CH_14	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.12	8.08
HARD_EP4_14	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.14	9.19
HARD_EP5_14	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.11	7.30
HARD_EP3_15	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.15	9.98
HARD_EP4_15	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.16	10.43
HARD_EP5_15	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.19	11.80
HARD_BD_16	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.13	8.71
HARD_BI_16	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.12	8.05
HARD_CLI_16	2774182_5ds_7304	5D	76010	5D	8613963	85	NA	0.15	9.89
HARD_EP4_14	2781671_5ds_9472	5D	75997	5D	9332000	85	NA	0.11	7.33
HARD_EP3_15	2781671_5ds_9472	5D	75997	5D	9332000	85	NA	0.11	7.43
HARD_EP4_15	2781671_5ds_9472	5D	75997	5D	9332000	85	NA	0.13	8.49
HARD_EP5_15	2781671_5ds_9472	5D	75997	5D	9332000	85	NA	0.13	8.94
HARD_CLI_16	2781671_5ds_9472	5D	75997	5D	9332000	85	NA	0.11	7.47
HARD_CH_14	2781671_5ds_9461	5D	75993	5D	9332011	85	NA	0.11	7.43
HARD_EP4_14	2781671_5ds_9461	5D	75993	5D	9332011	85	NA	0.13	8.42
HARD_EP5_14	2781671_5ds_9461	5D	75993	5D	9332011	85	NA	0.11	7.39
HARD_EP3_15	2781671_5ds_9461	5D	75993	5D	9332011	85	NA	0.12	8.01
HARD_EP4_15	2781671_5ds_9461	5D	75993	5D	9332011	85	NA	0.14	9.20
HARD_EP5_15	2781671_5ds_9461	5D	75993	5D	9332011	85	NA	0.14	9.30
HARD_BD_16	2781671_5ds_9461	5D	75993	5D	9332011	85	NA	0.11	7.34
HARD_BI_16	2781671_5ds_9461	5D	75993	5D	9332011	85	NA	0.11	7.53
HARD_CLI_16	2781671_5ds_9461	5D	75993	5D	9332011	85	NA	0.12	8.04
HARD_CH_14	2781671_5ds_9443	5D	75992	5D	9332029	85	NA	0.11	7.43
HARD_EP4_14	2781671_5ds_9443	5D	75992	5D	9332029	85	NA	0.13	8.42
HARD_EP5_14	2781671_5ds_9443	5D	75992	5D	9332029	85	NA	0.11	7.39
HARD_EP3_15	2781671_5ds_9443	5D	75992	5D	9332029	85	NA	0.12	8.01
HARD_EP4_15	2781671_5ds_9443	5D	75992	5D	9332029	85	NA	0.14	9.20
HARD_EP5_15	2781671_5ds_9443	5D	75992	5D	9332029	85	NA	0.14	9.30
HARD_BD_16	2781671_5ds_9443	5D	75992	5D	9332029	85	NA	0.11	7.34
HARD_BI_16	2781671_5ds_9443	5D	75992	5D	9332029	85	NA	0.11	7.53
HARD_CLI_16	2781671_5ds_9443	5D	75992	5D	9332029	85	NA	0.12	8.04
HARD_CH_14	2781671_5ds_9235	5D	75991	5D	9332237	85	NA	0.11	7.43
HARD_EP4_14	2781671_5ds_9235	5D	75991	5D	9332237	85	NA	0.13	8.42
HARD_EP5_14	2781671_5ds_9235	5D	75991	5D	9332237	85	NA	0.11	7.39
HARD_EP3_15	2781671_5ds_9235	5D	75991	5D	9332237	85	NA	0.12	8.01
HARD_EP4_15	2781671_5ds_9235	5D	75991	5D	9332237	85	NA	0.14	9.20
HARD_EP5_15	2781671_5ds_9235	5D	75991	5D	9332237	85	NA	0.14	9.30
HARD_BD_16	2781671_5ds_9235	5D	75991	5D	9332237	85	NA	0.11	7.34
HARD_BI_16	2781671_5ds_9235	5D	75991	5D	9332237	85	NA	0.11	7.53
HARD_CLI_16	2781671_5ds_9235	5D	75991	5D	9332237	85	NA	0.12	8.04

Table A2 Continued

Trait_loc_Yr[†]	Marker	Chr	Pos	CHR[‡]	Mb[§]	QTL ID	A[¶]	$R^{2\#}$	-log10(p)
HARD_EP4_14	2781671_5ds_9223	5D	75990	5D	9332249	85	NA	0.11	7.38
HARD_EP3_15	2781671_5ds_9223	5D	75990	5D	9332249	85	NA	0.11	7.30
HARD_EP4_15	2781671_5ds_9223	5D	75990	5D	9332249	85	NA	0.13	8.41
HARD_EP5_15	2781671_5ds_9223	5D	75990	5D	9332249	85	NA	0.12	8.35
HARD_CLI_16	2781671_5ds_9223	5D	75990	5D	9332249	85	NA	0.11	7.22
HARD_CH_14	2781671_5ds_9219	5D	75989	5D	9332253	85	NA	0.11	7.43
HARD_EP4_14	2781671_5ds_9219	5D	75989	5D	9332253	85	NA	0.13	8.42
HARD_EP5_14	2781671_5ds_9219	5D	75989	5D	9332253	85	NA	0.11	7.39
HARD_EP3_15	2781671_5ds_9219	5D	75989	5D	9332253	85	NA	0.12	8.01
HARD_EP4_15	2781671_5ds_9219	5D	75989	5D	9332253	85	NA	0.14	9.20
HARD_EP5_15	2781671_5ds_9219	5D	75989	5D	9332253	85	NA	0.14	9.30
HARD_BD_16	2781671_5ds_9219	5D	75989	5D	9332253	85	NA	0.11	7.34
HARD_BI_16	2781671_5ds_9219	5D	75989	5D	9332253	85	NA	0.11	7.53
HARD_CLI_16	2781671_5ds_9219	5D	75989	5D	9332253	85	NA	0.12	8.04
HARD_CH_14	2781671_5ds_9179	5D	75987	5D	9332293	85	NA	0.11	7.43
HARD_EP4_14	2781671_5ds_9179	5D	75987	5D	9332293	85	NA	0.13	8.42
HARD_EP5_14	2781671_5ds_9179	5D	75987	5D	9332293	85	NA	0.11	7.39
HARD_EP3_15	2781671_5ds_9179	5D	75987	5D	9332293	85	NA	0.12	8.01
HARD_EP4_15	2781671_5ds_9179	5D	75987	5D	9332293	85	NA	0.14	9.20
HARD_EP5_15	2781671_5ds_9179	5D	75987	5D	9332293	85	NA	0.14	9.30
HARD_BD_16	2781671_5ds_9179	5D	75987	5D	9332293	85	NA	0.11	7.34
HARD_BI_16	2781671_5ds_9179	5D	75987	5D	9332293	85	NA	0.11	7.53
HARD_CLI_16	2781671_5ds_9179	5D	75987	5D	9332293	85	NA	0.12	8.04
HARD_EP4_14	2781671_5ds_9157	5D	75986	5D	9332315	85	NA	0.11	7.38
HARD_EP3_15	2781671_5ds_9157	5D	75986	5D	9332315	85	NA	0.11	7.30
HARD_EP4_15	2781671_5ds_9157	5D	75986	5D	9332315	85	NA	0.13	8.41
HARD_EP5_15	2781671_5ds_9157	5D	75986	5D	9332315	85	NA	0.12	8.35
HARD_CLI_16	2781671_5ds_9157	5D	75986	5D	9332315	85	NA	0.11	7.22
HARD_EP3_15	2739401_5ds_20579	5D	76380	5D	11421190	85	-6.50	0.12	7.12
HARD_EP4_15	2242858_5ds_843	5D	76537	5D	21256151	85	NA	0.11	7.31
HARD_CH_14	2614662_5ds_579	5D	76397	5D	23058289	85	NA	0.11	7.50
HARD_EP4_14	2614662_5ds_579	5D	76397	5D	23058289	85	NA	0.11	7.64
HARD_EP4_15	2614662_5ds_579	5D	76397	5D	23058289	85	NA	0.10	7.05
HARD_EP5_15	2614662_5ds_579	5D	76397	5D	23058289	85	NA	0.11	7.38
HARD_CLI_16	2614662_5ds_579	5D	76397	5D	23058289	85	NA	0.10	7.08
HARD_CLI_16	2748871_5ds_2822	UKN	1E+05	5D	23346667	85	4.50	0.12	7.02
HARD_EP5_15	3169317_7bs_6045	7B	1E+05	7B	156437593	113	2.60	0.12	7.28
HARD_BD_16	3169317_7bs_6045	7B	1E+05	7B	156437593	113	1.88	0.13	8.02
HARD_BI_16	3169317_7bs_6045	7B	1E+05	7B	156437593	113	2.85	0.15	8.81
MLPH_EP5_15	10560024_3b_8154	3B	46264	3B	626368663	52	-1.70	0.12	7.23
MLRS_EP5_14	3976624_1al_4871	UKN	1E+05	1A	563337674	5	0.16	0.15	8.06
MLRS_EP5_14	2755762_1bs_446	1B	6180	1B	15393391	6	-0.05	0.13	7.90
MLRS_EP4_14	2715434_2as_1190	UKN	1E+05	2A	163468275	20	0.15	0.15	8.81
MLRS_EP5_14	6416031_2al_726	2A	22559	2A	689804623	24	-0.07	0.16	9.69
MLRS_EP4_14	6415092_2al_1762	2A	21970	2A	700980102	24	0.00	0.15	8.53
MLRS_EP4_14	6415092_2al_1688	2A	21962	2A	700980176	24	0.00	0.15	8.53
MLRS_EP5_14	5246892_2bs_1581	2B	24440	2B	9127312	26	-0.09	0.13	8.02
MLRS_EP5_14	5176564_2bs_847	UKN	1E+05	2B	38620602	27	-0.18	0.15	8.81
MLRS_EP5_14	5192097_2bs_4621	2B	26002	2B	63820373	27	0.00	0.13	7.85
MLRS_BD_16	5244816_2bs_10170	2B	26109	2B	72938260	27	-0.14	0.11	7.20
MLRS_EP4_14	8020386_2bl_973	2B	28014	2B	415059969	28	-0.05	0.15	8.64
MLRS_EP4_14	8002564_2bl_4534	2B	32112	2B	656976741	31	-0.02	0.15	8.60
MLRS_EP4_14	8002564_2bl_4533	2B	32111	2B	656976742	31	-0.04	0.15	8.63
MLRS_EP5_14	7953703_2bl_4726	2B	31389	2B	657071400	31	0.10	0.13	8.00
MLRS_EP5_14	7953703_2bl_4718	2B	31387	2B	657071408	31	-0.02	0.13	7.89
MLRS_EP5_14	7953703_2bl_4692	2B	31384	2B	657071434	31	0.02	0.13	7.88
MLRS_EP5_14	8006724_2bl_4660	2B	33033	2B	735404943	32	0.04	0.13	7.91
MLRS_EP5_14	8088961_2bl_3997	2B	33671	2B	774682954	32	-0.13	0.13	8.04
MLRS_EP5_14	5388307_2ds_14890	2D	35318	2D	56254163	34	0.19	0.13	8.10
MLRS_EP5_14	5391007_2ds_4367	2D	36416	2D	116764802	35	-0.20	0.14	8.35
MLRS_EP5_14	9833177_2dl_16160	2D	35537	2D	527921804	37	-0.01	0.13	7.89
MLRS_EP5_14	9858970_2dl_3219	2D	38469	2D	601965671	38	0.03	0.13	7.89
MLRS_EP5_14	9858970_2dl_3228	2D	38473	2D	601965680	38	-0.09	0.13	8.04
MLRS_EP5_14	3331403_3as_17138	3A	40067	3A	28146043	39	-0.03	0.13	7.68
MLRS_EP4_14	3447514_3as_343	3A	40651	3A	85272189	40	-0.12	0.15	8.87
MLRS_EP4_14	4326927_3al_462	3A	41057	3A	430959405	42	0.17	0.14	8.29
MLRS_EP5_14	10762578_3b_6885	UKN	1E+05	3B	2164045	45	0.27	0.18	8.58
MLRS_EP5_14	10705157_3b_753	3B	44454	3B	66887150	46	0.28	0.16	9.54
MLRS_EP5_14	10705597_3b_1425	3B	45387	3B	409529033	50	0.13	0.14	8.16
MLRS_EP5_14	10580786_3b_4786	UKN	1E+05	3B	418748348	50	-0.08	0.16	9.74
MLRS_EP4_14	10760636_3b_4215	3B	47079	3B	769543611	54	-0.10	0.16	8.98
MLRS_EP5_14	10425662_3b_3428	3B	47289	3B	798205862	54	0.03	0.13	7.90
MLRS_EP5_14	2603046_3ds_1335	3D	47614	3D	8561225	55	-0.14	0.13	8.04
MLRS_EP5_14	6953993_3dl_1165	3D	48858	3D	528623288	57	-0.07	0.13	7.98
MLRS_EP5_14	6012949_4as_v2_9009	4A	50695	4A	67414835	58	-0.08	0.13	7.95

Table A2 Continued

Trait_loc_Yr†	Marker	Chr	Pos	CHR‡	Mb§	QTL ID	A¶	R^{2}#	-log10(p)
MLRS_EP4_14	7110987_4al_3876	4A	51052	4A	476134651	60	0.03	0.15	8.58
MLRS_EP5_14	7145077_4al_19258	4A	54649	4A	707246102	63	-0.04	0.13	7.91
MLRS_EP5_14	7022490_4bl_1414	4B	59890	4B	524603106	66	-0.02	0.13	7.90
MLRS_EP5_14	6965059_4bl_4331	4B	59698	4B	608056018	67	-0.12	0.13	8.05
MLRS_EP5_14	2275446_4ds_19878	UKN	1E+05	4D	7096132	69	0.08	0.14	7.87
MLRS_EP5_14	2325871_4ds_12910	4D	61537	4D	16813690	69	0.17	0.14	8.37
MLRS_EP5_14	2316586_4ds_4113	4D	61687	4D	26205822	69	0.00	0.13	7.88
MLRS_EP5_14	14377340_4dl_v2_17679	4D	63465	4D	496139310	73	-0.02	0.13	7.90
MLRS_EP5_14	14377340_4dl_v2_17626	4D	63461	4D	496139363	73	0.02	0.13	7.90
MLRS_EP5_14	14377340_4dl_v2_17615	4D	63459	4D	496139374	73	0.02	0.13	7.90
MLRS_EP4_14	14320034_4dl_v2_2527	UKN	1E+05	5A	414046997	72?	-0.03	0.17	8.53
MLRS_EP4_14	14320034_4dl_v2_2536	UKN	1E+05	5A	414047006	72?	0.17	0.18	9.09
MLRS_EP5_14	2257417_5bs_15959	5B	70107	5B	121185149	78	-0.10	0.14	8.12
MLRS_EP5_14	2257417_5bs_15958	5B	70106	5B	121185150	78	0.10	0.14	8.12
MLRS_EP5_14	2257417_5bs_15913	5B	70105	5B	121185195	78	0.08	0.15	7.99
MLRS_EP5_15	10925497_5bl_8503	5B	69123	5B	307003599	79	-0.23	0.13	7.02
MLRS_EP5_14	10882853_5bl_3768	5B	67832	5B	359486768	79	0.05	0.13	7.91
MLRS_EP5_14	10910228_5bl_7379	UKN	1E+05	5B	523932477	82	0.03	0.15	7.84
MLRS_EP5_14	10910228_5bl_7370	UKN	1E+05	5B	523932486	82	-0.03	0.15	7.84
MLRS_EP5_14	10910228_5bl_7366	UKN	1E+05	5B	523932490	82	-0.04	0.15	7.86
MLRS_EP5_14	10910228_5bl_7364	UKN	1E+05	5B	523932492	82	-0.03	0.15	7.84
MLRS_BD_16	10890478_5bl_16094	UKN	1E+05	5B	528563376	82	-0.33	0.16	9.11
MLRS_EP5_14	10919338_5bl_1478	5B	75350	5B	686433888	84	0.01	0.13	7.89
MLRS_EP5_14	10919338_5bl_1486	5B	75351	5B	686433896	84	0.11	0.13	7.97
MLRS_EP4_14	4503898_5dl_1782	5D	77180	5D	276671889	87	-0.01	0.15	8.57
MLRS_EP5_14	4488923_5dl_4410	5D	81451	5D	511948668	90	-0.21	0.14	8.25
MLRS_EP5_14	4429106_6as_3390	6A	83059	6A	3705808	92	0.01	0.13	7.89
MLRS_EP5_14	4429106_6as_3396	6A	83060	6A	3705814	92	-0.01	0.13	7.89
MLRS_EP4_14	5806319_6al_1934	6A	85822	6A	442085721	95	0.20	0.16	9.10
MLRS_EP4_14	5745805_6al_1075	6A	87221	6A	552828358	96	0.02	0.15	8.59
MLRS_EP5_15	5692765_6al_1356	6A	87704	6A	594960290	96	-0.27	0.13	7.41
MLRS_EP4_14	5819489_6al_18687	6A	87766	6A	595061050	96	0.01	0.15	8.57
MLRS_EP5_14	5835370_6al_17148	6A	88223	6A	612113836	97	0.08	0.13	7.98
MLRS_EP5_14	5835370_6al_17142	6A	88222	6A	612113842	97	0.22	0.12	7.05
MLRS_EP4_14	2943095_6bs_552	6B	89018	6B	27126339	98	0.05	0.15	8.64
MLRS_EP4_14	4345576_6bl_497	6B	92365	6B	681901174	100	0.03	0.12	7.28
MLRS_EP4_14	4345576_6bl_537	6B	92366	6B	681901214	100	0.03	0.12	7.28
MLRS_EP4_14	4261361_6bl_2114	6B	92571	6B	706582549	100	-0.09	0.15	8.74
MLRS_EP5_14	2116712_6ds_6275	6D	94035	6D	22182783	101	-0.04	0.13	7.91
MLRS_EP5_14	2124102_6ds_225	6D	94342	6D	60383430	101	-0.15	0.14	8.29
MLRS_EP5_14	3295766_6dl_4239	6D	97211	6D	435306987	103	0.04	0.13	7.92
MLRS_EP4_14	4190671_7as_2139	UKN	1E+05	7A	38749287	104	-0.04	0.17	8.52
MLRS_EP5_14	4047115_7as_639	7A	1E+05	7A	94913347	105	0.13	0.14	8.17
MLRS_EP5_14	4446000_7al_2788	7A	1E+05	7A	540909569	109	-0.08	0.13	7.97
MLRS_EP5_14	4446000_7al_2731	7A	1E+05	7A	540909626	109	0.08	0.13	7.97
MLRS_EP5_14	4446000_7al_2729	7A	1E+05	7A	540909628	109	-0.08	0.13	7.97
MLRS_EP5_14	4455276_7al_1712	UKN	1E+05	7A	723388881	111	-0.23	0.14	8.42
MLRS_EP5_14	6670865_7bl_689	7B	1E+05	7B	562992216	115	0.14	0.13	8.05
MLRS_EP5_14	3919807_7ds_190	7D	1E+05	7D	60148204	116	0.02	0.13	7.90
MLRS_EP5_14	3314448_7dl_1711	7D	1E+05	7D	461403554	120	0.10	0.13	8.06
MLRS_EP5_14	3314448_7dl_1518	7D	1E+05	7D	461403747	120	0.09	0.13	8.02
MLRS_EP4_14	1277312_7dl_526	UKN	1E+05	7D	488050396	121	-0.01	0.16	8.46
MLRS_EP5_14	3331788_7dl_1409	7D	1E+05	7D	547276474	122	-0.21	0.14	8.20
MLRS_EP5_14	339577_7dl_1102	UKN	1E+05	7D	594987964	123	0.04	0.16	7.99
MLRS_EP5_14	3342062_7dl_680	UKN	1E+05	7D	615915739	123	-0.09	0.15	7.92
MLRS_EP5_14	3348754_7dl_4968	7D	1E+05	7D	623156542	123	0.04	0.13	7.90
MLRS_EP5_14	3348754_7dl_4926	7D	1E+05	7D	623156584	123	0.04	0.13	7.90
MLRS_EP5_14	3387155_7dl_1367	7D	1E+05	7D	626231720	123	0.14	0.14	8.29
MLRS_EP5_14	3334708_7dl_3503	7D	1E+05	7D	634376273	123	-0.16	0.14	8.24
MLRS_EP5_14	7012446_4al_76	4A	52159	Un	244927138	60?	0.04	0.13	7.92
MLRW_BI_16	3451628_1bs_1524	1B	6336	1B	25899498	6	-3.15	0.12	7.64
MLRW_BI_16	3451628_1bs_1476	1B	6334	1B	25899546	6	3.15	0.12	7.64
MLRW_BI_16	3451628_1bs_1473	1B	6333	1B	25899549	6	3.15	0.12	7.64
MLTW_EP5_15	3921954_1al_1101	UKN	1E+05	1A	521991074	5	-0.31	0.12	7.53
MLTW_EP5_15	3921954_1al_1141	UKN	1E+05	1A	521991114	5	0.06	0.12	7.40
MLTW_EP5_15	3971867_1al_22696	1A	4680	1A	547901775	5	-0.37	0.19	12.05
MLTW_EP5_15	3869500_1al_16071	1A	4720	1A	564603615	5	-0.44	0.14	8.52
MLTW_EP5_15	3869500_1al_16060	1A	4718	1A	564603626	5	-0.44	0.14	8.52
MLTW_BI_16	3453826_1bs_3226	1B	5932	1B	17145962	6	-2.78	0.12	8.02
MLTW_BI_16	3453826_1bs_3043	1B	5926	1B	17146145	6	-2.71	0.11	7.70
MLTW_BI_16	3453826_1bs_3023	1B	5923	1B	17146165	6	2.69	0.12	8.01
MLTW_EP5_15	3482438_1bs_1714	1B	6425	1B	21367114	6	1.66	0.12	7.92
MLTW_BI_16	3451172_1bs_433	1B	6326	1B	21443789	6	NA	0.09	7.32
MLTW_EP5_15	3422647_1bs_7183	1B	6268	1B	22824562	6	-0.49	0.11	7.14

Table A2 Continued

Trait_loc_Yr†	Marker	Chr	Pos	CHR‡	Mb§	QTL ID	A¶	$R^{2\#}$	-log10(p)
MLTW_BD_16	3434158_1bs_9081	1B	6314	1B	30403173	6	NA	0.12	8.25
MLTW_EP5_15	3475565_1bs_1037	UKN	1E+05	1B	32817045	6	-0.05	0.19	11.78
MLTW_EP5_15	3470361_1bs_739	1B	8175	1B	171106182	8	-0.67	0.11	7.50
MLTW_EP5_15	3433385_1bs_2429	1B	7694	1B	202758082	8	-0.57	0.19	12.09
MLTW_EP5_15	3433385_1bs_2460	1B	7695	1B	202758113	8	-0.11	0.19	11.87
MLTW_EP5_15	3895037_1bl_2485	1B	11987	1B	653081906	13	0.18	0.19	11.88
MLTW_EP5_15	1910681_1ds_1845	1D	14416	1D	67443132	14	-1.04	0.11	7.09
MLTW_EP5_15	2290615_1dl_3201	1D	14205	1D	295402927	15	0.01	0.19	11.86
MLTW_EP5_15	2284405_1dl_7872	1D	15917	1D	462718121	17	-0.66	0.15	9.43
MLTW_EP5_15	2284405_1dl_7840	1D	15914	1D	462718153	17	-0.59	0.20	12.36
MLTW_EP5_15	2284405_1dl_7834	1D	15913	1D	462718159	17	-0.58	0.20	12.34
MLTW_EP5_15	2284405_1dl_7833	1D	15912	1D	462718160	17	0.59	0.20	12.36
MLTW_EP5_15	2284405_1dl_7596	1D	15904	1D	462718397	17	-0.63	0.15	9.67
MLTW_EP5_15	2266038_1dl_884	1D	16428	1D	474983270	17	-0.22	0.19	11.90
MLTW_EP5_15	2266038_1dl_688	1D	16422	1D	474983466	17	0.39	0.19	12.01
MLTW_EP5_15	2266038_1dl_672	1D	16421	1D	474983482	17	-0.35	0.19	12.01
MLTW_EP5_15	5274853_2as_1597	2A	17595	2A	23497175	18	0.30	0.12	7.08
MLTW_EP5_15	5274853_2as_1583	2A	17593	2A	23497189	18	-0.30	0.12	7.08
MLTW_EP5_15	5197325_2as_765	2A	18383	2A	49884137	18	0.55	0.19	12.00
MLTW_EP5_15	6335763_2al_578	UKN	1E+05	2A	588215121	22	0.20	0.13	7.75
MLTW_EP5_15	6335763_2al_574	UKN	1E+05	2A	588215125	22	-0.14	0.21	11.46
MLTW_EP5_15	6434376_2al_9024	2A	19021	2A	597215006	22	0.20	0.19	11.88
MLTW_EP5_15	6380908_2al_4964	2A	22895	2A	728813485	24	-0.68	0.20	12.37
MLTW_EP5_15	6362950_2al_3896	2A	23459	2A	748682248	25	0.15	0.19	11.90
MLTW_EP5_15	6362950_2al_3887	2A	23457	2A	748682257	25	-0.36	0.19	11.95
MLTW_EP5_15	8075293_2bl_9728	2B	28825	2B	436242677	28	0.00	0.19	11.91
MLTW_EP5_15	7987244_2bl_3643	2B	29223	2B	436412383	28	0.51	0.11	7.22
MLTW_EP5_15	8090690_2bl_14565	2B	29636	2B	524235209	29	-1.22	0.11	7.29
MLTW_EP5_15	8062742_2bl_977	UKN	1E+05	2B	552338802	29	0.38	0.11	7.09
MLTW_EP5_15	6983730_2bl_1537	2B	30388	2B	598961876	30	-0.15	0.19	11.77
MLTW_EP5_15	7942088_2bl_3961	UKN	1E+05	2B	667417891	31	-0.18	0.20	11.58
MLTW_EP5_15	8085346_2bl_8079	2B	32832	2B	699288270	31	0.30	0.12	8.04
MLTW_EP5_15	5372804_2ds_1471	UKN	1E+05	2D	44894650	33	0.05	0.19	11.73
MLTW_EP5_15	5331953_2ds_4427	2D	35468	2D	61024791	34	0.34	0.11	7.15
MLTW_EP5_15	5330991_2ds_5096	2D	35466	2D	73583923	34	-0.30	0.19	11.90
MLTW_EP5_15	5388470_2ds_592	2D	37758	2D	261987621	36	-0.30	0.11	7.05
MLTW_EP5_15	3284444_3as_3787	3A	40143	3A	23908087	39	0.68	0.11	7.17
MLTW_EP5_15	3439719_3as_124	3A	41188	3A	129893201	40	0.44	0.15	9.74
MLTW_EP5_15	3354266_3as_54	3A	41312	3A	135590589	40	-0.13	0.19	11.88
MLTW_EP5_15	3354266_3as_104	3A	41313	3A	135590592	40	0.13	0.19	11.88
MLTW_EP5_15	3441353_3as_768	UKN	1E+05	3A	212196873	41	-0.43	0.12	7.20
MLTW_EP5_15	4338188_3al_5343	3A	41475	3A	440027969	42	-0.80	0.11	7.29
MLTW_EP5_15	4343024_3al_33	UKN	1E+05	3A	684521615	44	0.13	0.20	11.70
MLTW_EP5_15	4343024_3al_38	UKN	1E+05	3A	684521615	44	0.12	0.20	11.69
MLTW_EP5_15	4233820_3al_4642	3A	43010	3A	706202437	44	0.02	0.19	11.86
MLTW_EP5_15	4233820_3al_4641	3A	43009	3A	706202438	44	-0.56	0.19	12.19
MLTW_EP5_15	4108010_3b_247	3B	45020	3B	245911025	48	-0.01	0.19	11.85
MLTW_EP5_15	10751565_3b_2623	UKN	1E+05	3B	739339484	53	1.37	0.24	13.01
MLTW_EP5_15	10774300_3b_13150	3B	47429	3B	815050498	54	0.35	0.19	12.05
MLTW_EP5_15	10757127_3b_4836	UKN	1E+05	3B	821046179	54	-0.55	0.21	11.39
MLTW_EP5_15	10757127_3b_4802	UKN	1E+05	3B	821046213	54	0.00	0.13	7.64
MLTW_EP5_15	6955423_3dl_274	3D	48129	3D	347562978	56	-0.11	0.19	11.89
MLTW_EP5_15	6952453_3dl_47	3D	48587	3D	495921615	57	-0.60	0.19	12.13
MLTW_EP5_15	5898011_4as_v2_1139	4A	50560	4A	100668627	59	0.25	0.19	11.92
MLTW_EP5_15	5927344_4as_v2_3198	4A	50482	4A	120340689	59	1.13	0.12	7.63
MLTW_EP5_15	3922577_7ds_700	UKN	1E+05	4A	729442112	63	0.35	0.25	11.84
MLTW_EP5_15	3922577_7ds_694	UKN	1E+05	4A	729442116	63	-0.31	0.24	11.80
MLTW_EP5_15	4864066_4bs_4860	4B	57580	4B	117092437	64	-0.24	0.19	11.92
MLTW_EP5_15	4890458_4bs_3401	4B	58888	4B	167373704	64	-0.04	0.19	11.86
MLTW_EP5_15	4880127_4bs_1078	4B	58666	4B	213097236	65	-0.22	0.19	11.90
MLTW_EP5_15	6972744_4bl_154	4B	59736	4B	534660990	66	0.14	0.19	11.88
MLTW_EP5_15	6890178_4bl_557	UKN	1E+05	4B	615383932	67	0.18	0.12	7.55
MLTW_EP5_15	6890178_4bl_539	UKN	1E+05	4B	615383950	67	-0.15	0.13	8.00
MLTW_EP5_15	6890178_4bl_498	UKN	1E+05	4B	615383991	67	-0.15	0.13	8.00
MLTW_EP5_15	14381009_4dl_v2_287	UKN	1E+05	4D	401566773	72	-0.34	0.17	8.98
MLTW_EP5_15	14381009_4dl_v2_263	UKN	1E+05	4D	401566797	72	-0.35	0.17	8.99
MLTW_EP5_15	14381009_4dl_v2_248	UKN	1E+05	4D	401566812	72	-0.34	0.17	8.98
MLTW_EP5_15	1517889_5as_12083	5A	64145	5A	6627042	74	0.12	0.19	11.88
MLTW_EP5_15	1539578_5as_2723	UKN	1E+05	5A	12667826	74	-0.12	0.23	11.64
MLTW_EP5_15	2804003_5al_1159	5A	63879	5A	280524196	75	-0.64	0.20	12.28
MLTW_EP5_15	2805435_5al_10340	5A	65511	5A	606358734	76	0.21	0.19	11.91
MLTW_EP5_15	1615135_5bs_6987	5B	66703	5B	6601302	77	0.24	0.19	11.91
MLTW_EP5_15	1615135_5bs_6996	5B	66705	5B	6601311	77	0.09	0.19	11.87
MLTW_EP5_15	10925497_5bl_8503	5B	69123	5B	307003599	79	0.34	0.19	12.01

Table A2 Continued

Trait_loc_Yr[†]	Marker	Chr	Pos	CHR[‡]	Mb[§]	QTL ID	A[¶]	R^{2}[#]	-log10(p)
MLTW_EP5_15	10918258_5bl_2861	5B	69038	5B	322877015	79	-0.69	0.20	12.36
MLTW_EP5_15	10874919_5bl_19095	5B	70838	5B	473888733	81	-1.08	0.11	7.42
MLTW_EP5_15	10789285_5bl_1125	5B	71348	5B	497845690	81	-0.04	0.19	11.86
MLTW_EP5_15	10789285_5bl_1190	5B	71352	5B	497845755	81	0.63	0.19	12.18
MLTW_EP5_15	10789285_5bl_1399	5B	71353	5B	497845964	81	0.36	0.19	11.84
MLTW_EP5_15	10820340_5bl_743	5B	71653	5B	497905885	81	-0.35	0.11	7.03
MLTW_EP5_15	10713906_5bl_3165	5B	73131	5B	580426190	83	-0.58	0.20	12.27
MLTW_EP5_15	10878230_5bl_14895	5B	73254	5B	587120949	83	-0.12	0.19	11.87
MLTW_EP5_15	10887191_5bl_781	5B	73364	5B	590737126	83	0.13	0.19	11.88
MLTW_EP5_15	10840148_5bl_5172	5B	73954	5B	610369884	83	0.28	0.19	11.93
MLTW_EP5_15	1451356_5ds_1126	5D	76642	5D	34888016	85	-0.09	0.19	11.90
MLTW_EP5_15	4600039_5dl_719	UKN	1E+05	5D	375579358	88	0.40	0.22	11.68
MLTW_EP5_15	4600039_5dl_718	UKN	1E+05	5D	375579359	88	-0.10	0.21	11.44
MLTW_EP5_15	4590311_5dl_2239	5D	81195	5D	491845992	90	-0.18	0.19	11.88
MLTW_EP5_15	4350665_6as_530	6A	83308	6A	12213963	92	-0.39	0.19	11.97
MLTW_EP5_15	4377011_6as_2697	6A	84059	6A	39460963	92	0.35	0.13	8.47
MLTW_EP5_15	4385583_6as_630	6A	84811	6A	86383939	93	-0.48	0.19	12.07
MLTW_EP5_15	4352420_6as_2972	UKN	1E+05	6A	182664762	94	-0.12	0.20	11.87
MLTW_EP5_15	5692765_6al_1356	6A	87704	6A	594960290	96	-0.56	0.12	7.57
MLTW_EP5_15	5833404_6al_16346	6A	88286	6A	617804657	97	-0.58	0.11	7.43
MLTW_EP5_15	5833404_6al_16345	6A	88285	6A	617804658	97	-0.39	0.11	7.13
MLTW_EP5_15	4275962_6bl_1951	6B	91361	6B	511387953	99	-0.64	0.11	7.05
MLTW_EP5_15	4291994_6bl_6847	6B	92430	6B	687299185	100	0.52	0.19	12.05
MLTW_EP5_15	4291994_6bl_6839	6B	92429	6B	687299193	100	0.52	0.19	12.05
MLTW_EP5_15	2122083_6ds_4026	UKN	1E+05	6D	45486337	101	0.14	0.22	11.71
MLTW_EP5_15	2072646_6ds_14285	6D	94290	6D	46845804	101	0.02	0.19	11.63
MLTW_EP5_15	2058228_6ds_5139	6D	94864	6D	169592240	102	-0.57	0.19	12.08
MLTW_EP5_15	3248171_6dl_5095	6D	97080	6D	418887706	103	-0.10	0.19	11.87
MLTW_EP5_15	3291528_6dl_2437	6D	98530	6D	462275105	103	0.69	0.21	12.61
MLTW_EP5_15	3291528_6dl_2429	6D	98529	6D	462275113	103	0.56	0.20	12.27
MLTW_EP5_15	3291528_6dl_2425	6D	98528	6D	462275117	103	0.56	0.20	12.25
MLTW_EP5_15	3291528_6dl_2418	6D	98527	6D	462275124	103	0.54	0.20	12.22
MLTW_EP5_15	3291528_6dl_2417	6D	98526	6D	462275125	103	-0.69	0.21	12.61
MLTW_EP5_15	4249975_7as_1439	7A	1E+05	7A	65563625	104	-0.48	0.19	12.00
MLTW_EP5_15	4438833_7al_10700	UKN	1E+05	7A	428810677	108	-0.27	0.22	11.66
MLTW_EP5_15	4553164_7al_163	7A	1E+05	7A	501077934	109	0.50	0.11	7.09
MLTW_EP5_15	4536065_7al_716	7A	1E+05	7A	708435298	111	-0.76	0.11	7.42
MLTW_EP5_15	4551774_7al_1331	7A	1E+05	7A	725159844	111	-0.48	0.11	7.06
MLTW_EP5_15	3089883_7bs_247	UKN	1E+05	7B	131177775	113	-0.42	0.11	7.10
MLTW_EP5_15	3162004_7bs_1655	7B	1E+05	7B	182597172	113	-0.11	0.12	7.77
MLTW_EP5_15	3162004_7bs_1649	7B	1E+05	7B	182597178	113	0.18	0.19	11.89
MLTW_EP5_15	3922577_7ds_742	UKN	1E+05	7D	8746640	116	0.29	0.24	11.73
MLTW_EP5_15	3922577_7ds_748	UKN	1E+05	7D	8746646	116	0.29	0.24	11.80
MLTW_EP5_15	3922577_7ds_754	UKN	1E+05	7D	8746652	116	0.21	0.24	11.64
MLTW_EP5_15	3897318_7ds_1059	UKN	1E+05	7D	111274244	117	-0.06	0.19	11.58
MLTW_EP5_15	3891832_7ds_3364	7D	1E+05	7D	126674519	117	0.42	0.19	12.05
MLTW_EP5_15	2168702_7ds_2893	7D	1E+05	7D	213786834	118	-0.52	0.19	12.12
MLTW_EP5_15	3348127_7dl_6011	7D	1E+05	7D	376956870	119	-0.37	0.19	11.96
MLTW_EP5_15	1946986_7dl_869	7D	1E+05	7D	538370629	122	0.17	0.19	11.64
MLTW_EP5_15	3393906_7dl_8792	7D	1E+05	7D	560913296	122	0.51	0.11	7.24
MLTW_EP5_15	3393906_7dl_8559	7D	1E+05	7D	560913529	122	0.40	0.11	7.05
MLTW_EP5_15	3381023_7dl_12349	7D	1E+05	7D	562408177	122	0.33	0.19	11.98
MLTW_EP5_15	3323237_7dl_1129	7D	1E+05	7D	585453840	122	0.62	0.11	7.27
MLTW_EP5_15	3286355_7dl_826	7D	1E+05	7D	593405649	123	-0.16	0.19	11.86
MLTW_EP5_15	3391603_7dl_4388	7D	1E+05	7D	631694003	123	0.64	0.20	12.30
MLTW_EP5_15	5240618_2as_725	UKN	1E+05	Un	248330867	?	0.30	0.13	7.19
gMOIST_CLI_16	10530372_3b_2952	UKN	1E+05	3B	149455112	47	-0.34	0.17	8.79
gMOIST_CLI_16	10530372_3b_2948	UKN	1E+05	3B	149455116	47	0.34	0.17	8.79
gMOIST_CLI_16	10530372_3b_2905	UKN	1E+05	3B	149455159	47	-0.34	0.17	8.79
gMOIST_CLI_16	10530372_3b_2902	UKN	1E+05	3B	149455162	47	0.34	0.17	8.79
gMOIST_CLI_16	10530372_3b_2898	UKN	1E+05	3B	149455166	47	-0.33	0.17	8.53
gMOIST_BD_16	7144776_4al_1620	4A	54019	4A	662542416	62	-0.28	0.10	7.02
gMOIST_EP5_14	2946616_6bs_1121	6B	89635	6B	79304656	98	-0.14	0.11	7.13
gMOIST_CLI_16	4245739_7as_2670	7A	1E+05	7A	206908324	107	-0.24	0.17	9.59
gMOIST_CLI_16	4245739_7as_2674	7A	1E+05	7A	206908328	107	-0.23	0.17	9.56
gMOIST_CLI_16	4245739_7as_2695	7A	1E+05	7A	206908349	107	0.24	0.17	9.59
gMOIST_CLI_16	4245739_7as_2700	7A	1E+05	7A	206908354	107	-0.19	0.17	9.72
gMOIST_CLI_16	4245739_7as_2705	7A	1E+05	7A	206908359	107	-0.24	0.17	9.61
gMOIST_CLI_16	4245739_7as_2709	7A	1E+05	7A	206908363	107	-0.23	0.17	9.56
gMOIST_CLI_16	4245739_7as_2715	7A	1E+05	7A	206908369	107	0.22	0.16	9.39
gMOIST_CLI_16	4245739_7as_2717	7A	1E+05	7A	206908371	107	0.23	0.17	9.58
gMOIST_CLI_16	4245739_7as_2726	7A	1E+05	7A	206908380	107	-0.23	0.17	9.56
gMOIST_CLI_16	4245739_7as_2727	7A	1E+05	7A	206908381	107	-0.23	0.17	9.56
gMOIST_CLI_16	4245739_7as_2738	7A	1E+05	7A	206908392	107	0.23	0.17	9.56

Table A2 Continued

Trait_loc_Yr[†]	Marker	Chr	Pos	CHR[‡]	Mb[§]	QTL ID	A[¶]	R^2[#]	-log10(p)
gMOIST_CLI_16	4245739_7as_2893	7A	1E+05	7A	206908547	107	-0.22	0.17	9.75
gMOIST_CLI_16	4245739_7as_2917	7A	1E+05	7A	206908571	107	0.21	0.14	8.46
gMOIST_CLI_16	3162666_7bs_341	7B	1E+05	7B	329786542	114	0.27	0.16	8.78
gMOIST_CLI_16	3162666_7bs_336	7B	1E+05	7B	329786547	114	-0.33	0.20	10.77
gMOIST_CLI_16	3162666_7bs_335	7B	1E+05	7B	329786548	114	0.32	0.20	10.65
gMOIST_CLI_16	3162666_7bs_327	7B	1E+05	7B	329786556	114	0.33	0.20	10.56
gMOIST_CLI_16	3162666_7bs_156	7B	1E+05	7B	329786727	114	-0.32	0.21	11.63
gMOIST_CLI_16	3162666_7bs_96	7B	1E+05	7B	329786782	114	-0.32	0.21	11.63
gMOIST_CLI_16	3055451_7dl_3076	7D	1E+05	7D	574031608	122	-0.35	0.12	7.00
gMOIST_CLI_16	3055451_7dl_3085	7D	1E+05	7D	574031617	122	NA	0.12	7.82
SKW_EP5_15	7130376_4al_8778	4A	53500	4A	672102841	62	NA	0.11	7.70
SKW_EP5_15	7130376_4al_8777	4A	53499	4A	672102842	62	NA	0.12	8.14
SKW_EP5_15	7130376_4al_8753	4A	53498	4A	672102866	62	NA	0.10	7.11
SKW_EP5_15	7130376_4al_8717	4A	53497	4A	672102902	62	NA	0.12	8.15
WABS_EP5_14	10770064_3b_7986	UKN	1E+05	3B	571455474	51	NA	0.13	7.45

[†] Trait_Location_year

[‡] CHR, chromosomal location of marker in IWGSC RefSeq v1.0

[§] chromosomal position of marker in IWGSC RefSeq v1.0

[¶] Additive effect of the loci

[#] phenotypic variance explained by corresponding marker loci

Table A3

Significant marker trait association detected on multiple traits combined across environments, chromosome, position, effect for end-use quality traits in AMPSY population

Trait_loc_Yr[†]	Marker	Chr	Pos	CHR[‡]	Mb[§]	QTL ID	A[¶]	R^2[#]	-log10(p)
MLRW_COMB_COMB	3453826_1bs_3226	2	5932	1B	17145962	6	-1.58	0.12	7.38
MLTW_COMB_COMB	3453826_1bs_3226	2	5932	1B	17145962	6	-1.83	0.13	8.19
MLRW_COMB_COMB	3453826_1bs_3043	2	5926	1B	17146145	6	-1.59	0.12	7.42
MLTW_COMB_COMB	3453826_1bs_3043	2	5926	1B	17146145	6	-1.79	0.12	7.78
MLTW_COMB_COMB	3453826_1bs_3023	2	5923	1B	17146165	6	1.62	0.11	7.10
MLTW_COMB_COMB	3434158_1bs_9081	2	6314	1B	30403173	6	NA	0.10	7.10
PROT14_COMB_COMB	4860661_4bs_1872	11	57492	4B	134987855	64	0.09	0.12	7.21
FYLD_COMB_COMB	1477005_5ds_2010	15	75878	5D	344579	85	NA	0.23	14.32
HARD_COMB_COMB	1477005_5ds_2010	15	75878	5D	344579	85	NA	0.22	13.69
FYLD_COMB_COMB	2745573_5ds_3677	15	75978	5D	554980	85	NA	0.21	13.18
HARD_COMB_COMB	2745573_5ds_3677	15	75978	5D	554980	85	NA	0.29	17.38
FYLD_COMB_COMB	2736392_5ds_5233	15	75917	5D	934031	85	NA	0.26	15.92
HARD_COMB_COMB	2736392_5ds_5233	15	75917	5D	934031	85	NA	0.31	17.78
HARD_COMB_COMB	2765676_5ds_2839	15	75901	5D	1344429	85	-7.56	0.12	7.48
FYLD_COMB_COMB	2773392_5ds_1412	15	75911	5D	2220874	85	NA	0.21	13.55
HARD_COMB_COMB	2773392_5ds_1412	15	75911	5D	2220874	85	NA	0.26	15.89
FYLD_COMB_COMB	2773392_5ds_1238	15	75910	5D	2221048	85	NA	0.23	14.40
HARD_COMB_COMB	2773392_5ds_1238	15	75910	5D	2221048	85	NA	0.29	17.20
FYLD_COMB_COMB	2773392_5ds_1206	15	75906	5D	2221080	85	NA	0.21	13.55
HARD_COMB_COMB	2773392_5ds_1206	15	75906	5D	2221080	85	NA	0.26	15.89
FYLD_COMB_COMB	2770151_5ds_4035	15	75899	5D	7257066	85	NA	0.10	7.03
HARD_COMB_COMB	2770151_5ds_4035	15	75899	5D	7257066	85	NA	0.12	8.10
FYLD_COMB_COMB	2739337_5ds_2304	15	75953	5D	7485266	85	NA	0.12	7.95
HARD_COMB_COMB	2739337_5ds_2304	15	75953	5D	7485266	85	NA	0.11	7.18
HARD_COMB_COMB	2781025_5ds_24425	15	76006	5D	8018752	85	NA	0.15	9.94
HARD_COMB_COMB	2781025_5ds_24421	15	76005	5D	8018756	85	NA	0.15	9.94
HARD_COMB_COMB	2745020_5ds_15344	15	76053	5D	8419265	85	6.79	0.12	7.45
HARD_COMB_COMB	2745020_5ds_15346	15	76054	5D	8419267	85	6.79	0.12	7.45
FYLD_COMB_COMB	2774182_5ds_7304	15	76010	5D	8613963	85	NA	0.16	10.61
HARD_COMB_COMB	2774182_5ds_7304	15	76010	5D	8613963	85	NA	0.16	10.52
FYLD_COMB_COMB	2781671_5ds_9472	15	75997	5D	9332000	85	NA	0.10	7.18
HARD_COMB_COMB	2781671_5ds_9472	15	75997	5D	9332000	85	NA	0.12	8.08
FYLD_COMB_COMB	2781671_5ds_9461	15	75993	5D	9332011	85	NA	0.10	7.21
HARD_COMB_COMB	2781671_5ds_9461	15	75993	5D	9332011	85	NA	0.13	8.71
FYLD_COMB_COMB	2781671_5ds_9443	15	75992	5D	9332029	85	NA	0.10	7.21
HARD_COMB_COMB	2781671_5ds_9443	15	75992	5D	9332029	85	NA	0.13	8.71
FYLD_COMB_COMB	2781671_5ds_9235	15	75991	5D	9332237	85	NA	0.10	7.21
HARD_COMB_COMB	2781671_5ds_9235	15	75991	5D	9332237	85	NA	0.13	8.71
HARD_COMB_COMB	2781671_5ds_9223	15	75990	5D	9332249	85	NA	0.12	7.84
FYLD_COMB_COMB	2781671_5ds_9219	15	75989	5D	9332253	85	NA	0.10	7.21
HARD_COMB_COMB	2781671_5ds_9219	15	75989	5D	9332253	85	NA	0.13	8.71
FYLD_COMB_COMB	2781671_5ds_9179	15	75987	5D	9332293	85	NA	0.10	7.21
HARD_COMB_COMB	2781671_5ds_9179	15	75987	5D	9332293	85	NA	0.13	8.71
HARD_COMB_COMB	2781671_5ds_9157	15	75986	5D	9332315	85	NA	0.12	7.84

[†] Trait_Location_year

[‡] CHR, chromosomal location of marker in IWGSC RefSeq v1.0

[§] chromosomal position of marker in IWGSC RefSeq v1.0

[¶] Additive effect of the loci

[#] phenotypic variance explained by corresponding marker loci

Table A4
End-use quality average performance of the parents, RIL

Trait [†]	P1	P2	RIL mean	Min	Max	Max-Min	|P2-P1|	|Min-LP|	|Max-HP|
HARD	68.15	63.17	64.66	39.5	87.5	48	4.99	23.67	19.35
GMOIST	11.74	11.61	11.63	10.7	12.3	1.6	0.13	0.91	0.56
DIAM	2.42	2.48	2.44	2.06	2.9	0.84	0.06	0.36	0.42
SKW	25.95	27.51	26.15	18.5	39.1	20.6	1.57	7.45	11.59
FYLD	68.76	69.15	68.44	56.88	78.88	22	0.39	11.88	9.73
FMOIST	11.74	11.61	13.6	12.47	14.53	2.06	0.13	0.86	2.79
PROT14	14.63	14.04	14.29	11.28	18.53	7.25	0.58	2.76	3.9
ASH14	0.47	0.45	0.45	0.36	0.62	0.26	0.01	0.09	0.15
WABS	65.38	64.72	65.02	60.52	71.4	10.88	0.66	4.2	6.02
MLPT	4.74	3.3	3.92	1.84	8	6.16	1.44	1.46	3.26
MLPW	23.21	25.18	24.9	10.18	43.3	33.12	1.97	13.03	18.12
MLPV	60.77	62.37	59.46	44.28	86.5	42.22	1.6	16.49	24.13
MLPI	197.96	137.02	160.81	62.92	294.79	231.87	60.94	74.1	96.83
MLRS	-2.43	-3.6	-3.14	-8.21	1.19	9.4	1.17	4.61	3.62
MLRW	15.76	13.67	16.32	4.4	53.81	49.41	2.09	9.27	38.05
MLTW	13.82	8.64	10.56	2.71	27.97	25.26	5.18	5.93	14.15

Min., minimum; Max., maximum; LP, Low parent; HP, high parent

[†] HARD, hardness index; GMOIST, grain moisture; DIAM, kernel diameter; SKW, single kernel weight; FYLD, flour yield %; FMOIST, flour moisture; PROT14, flour protein at 14% moisture basis; ASH14, flour ash content at 14% moisture; WABS, water absorption; MLPT, midline peak time; MLPW, midline peak width; MLPV, midline peak value; MLPI, midline peak integral; MLRS, midline right slope; MLRW, midline right width; MLTW, midline tail width

Table A5
Additive-by-environment effects detected in multi-environment for single trait analysis

Traits[†]	QTL name	QTL ID	Position	Mbp[‡]	LeftMarker	LOD (AbyE)[§]	PVE (AbyE)[¶]	AbyE 13EP2[#]	AbyE 13EP3	AbyE 13EP4	AbyE 13EP5	AbyE 14CH	AbyE 14EP4	AbyE 14EP5
HARD	Qhard.tamu.1A	1	10	13.8	IWB55537	15.40	16.95	-1.1497	-1.16	-1.07	-1.05	-0.98	2.56	2.85
HARD	Qhard.tamu.1A	4	55	393.8	3928641_1al_1202	8.10	1.95	-0.3101	-0.29	1.42	-0.23	-0.12	-0.30	-0.17
HARD	Qhard.tamu.1A	5	62	475.6	3974856_1al_3401	6.79	12.91	-0.7314	-0.67	-0.62	-0.52	3.66	-0.49	-0.62
HARD	Qhard.tamu.1B	7	3	0.6	3473141_1bs_756	5.51	2.53	1.3482	-0.32	-0.44	-0.44	0.66	-0.34	-0.46
HARD	Qhard.tamu.1B	7	6	7.2	3285535_1bs_1678	15.49	4.72	-1.9345	0.12	0.48	0.45	-0.62	0.75	0.75
HARD	Qhard.tamu.2B	18	14	16.9	IWA2303	43.35	43.08	-0.7603	-1.54	-1.21	6.67	-1.21	-0.94	-1.02
HARD	Qhard.tamu.2B	20	107	578.7	8086989_2bl_2189	0.15	0.45	-0.032	-0.11	-0.33	-0.16	0.56	-0.17	0.24
HARD	Qhard.tamu.2D	22	21	1.7	IWB34642	1.84	1.16	-0.3232	-0.08	-0.41	-0.58	0.23	0.75	0.41
HARD	Qhard.tamu.4D	39	11	62.8	2305880_4ds_1018	5.91	2.44	1.215	0.05	-0.73	-0.10	-0.01	-0.87	0.44
HARD	Qhard.tamu.4D	42	22	366.3	IWB10053	2.69	0.91	-0.4377	0.24	0.20	0.04	0.22	-0.74	0.48
HARD	Qhard.tamu.5A	48	187	688.3	IWA2947	0.30	0.35	0.1713	0.08	0.38	0.00	-0.38	0.05	-0.31
HARD	Qhard.tamu.7D	72	95	84.3	3938880_7ds_2029	4.47	4.58	1.1574	0.80	-0.11	0.67	-1.55	-0.13	-0.84
GMOIST	Qgmoist.tamu.1B	7	3	0.6	3473141_1bs_756	1.55	2.23	-0.0121	-0.02	0.00	0.03	0.03	0.00	-0.02
GMOIST	Qgmoist.tamu.4D	39	10	62.8	2305880_4ds_1018	10.33	12.45	-0.0306	0.00	-0.02	-0.03	0.09	0.04	-0.04
GMOIST	Qgmoist.tamu.7B	70	2	709.6	IWB5306	1.35	1.29	-0.004	-0.02	-0.01	0.00	0.03	0.01	-0.01
GMOIST	Qgmoist.tamu.7D	72	79	60.6	IWB35446	1.25	1.66	0.0035	0.00	0.00	0.02	0.02	-0.02	-0.02
DIAM	Qdiam.tamu.1A	1	1	3.4	IWB47522	1.43	0.11	-0.0021	0.00	0.00	0.01	0.00	0.00	0.00
DIAM	Qdiam.tamu.1A	1	9	11.8	IWB46642	1.27	0.12	-0.0011	0.00	0.00	0.01	0.00	0.00	0.00
DIAM	Qdiam.tamu.1A	1	11	13.8	IWB63611	1.30	0.11	-0.0011	0.00	0.00	0.01	0.00	0.00	0.00
DIAM	Qdiam.tamu.1A	2	22	232.6	3877153_1al_1567	1.33	0.12	-0.0012	0.00	0.00	0.01	0.00	0.00	0.00
DIAM	Qdiam.tamu.1A	2	26	263.5	846120_1al_517	1.30	0.12	-0.0009	0.00	0.00	0.01	0.00	0.00	0.00
DIAM	Qdiam.tamu.1A	2	28	289.2	3968338_1al_936	1.20	0.12	-0.0007	0.00	0.00	0.01	0.00	0.00	0.00
DIAM	Qdiam.tamu.1A	3	34	304.1	3916820_1al_4455	1.27	0.12	-0.0007	0.00	0.00	0.01	0.00	0.00	0.00
DIAM	Qdiam.tamu.1A	3	37	316.6	3871107_1al_72	1.08	0.10	-0.0009	0.00	0.00	0.01	0.00	0.00	0.00
DIAM	Qdiam.tamu.1A	3	40	347.8	3871937_1al_2041	1.51	0.17	-0.0011	0.00	0.00	0.01	0.00	0.00	0.00
DIAM	Qdiam.tamu.1A	4	48	364.7	3976654_1al_3742	1.56	0.21	-0.0023	0.00	-0.01	0.01	0.00	-0.01	0.00
DIAM	Qdiam.tamu.1A	4	53	390.1	IWB31924	1.45	0.17	-0.0016	0.00	0.00	0.01	0.00	-0.01	0.00
DIAM	Qdiam.tamu.1A	5	59	458.4	IWB74868	1.31	0.23	-0.0023	0.00	0.00	0.01	0.00	-0.01	0.00
DIAM	Qdiam.tamu.1A	5	64	485.2	3894604_1al_116	0.91	0.13	0	0.00	0.00	0.01	0.00	-0.01	0.00
DIAM	Qdiam.tamu.1D	11	26	12.3	IWB14343	0.73	0.22	-0.0015	0.00	-0.01	0.00	0.01	0.00	0.00
DIAM	Qdiam.tamu.2D	24	113	531.4	9852937_2dl_2983	2.89	0.61	0.0071	-0.01	0.01	0.01	-0.01	0.00	-0.01
DIAM	Qdiam.tamu.4B	38	117	671.7	IWB9483	0.52	0.34	0.0018	0.01	0.00	0.00	0.00	-0.01	0.00
DIAM	Qdiam.tamu.4D	39	6	29.0	IWB30733	5.74	1.01	0.006	0.00	0.00	0.01	0.01	-0.02	-0.01
DIAM	Qdiam.tamu.5D	52	21	385.6	4522185_5dl_458	4.29	0.44	0.002	-0.01	0.00	0.00	0.00	0.01	0.00
DIAM	Qdiam.tamu.6A	54	87	104.4	IWB23452	4.09	0.47	-0.0001	-0.01	0.00	0.00	-0.01	0.01	0.00
DIAM	Qdiam.tamu.7D	71	65	38.5	IWB60795	0.44	0.13	-0.0016	-0.01	0.00	0.01	0.00	0.00	0.00
DIAM	Qdiam.tamu.7D	73	126	123.3	10396674_3b_3606	1.02	0.07	-0.002	0.00	0.00	0.00	0.00	0.00	0.00
SKW	Qskw.tamu.2D	24	114	531.4	9852937_2dl_2983	6.16	5.10	0.0229	-0.08	0.14	0.50	-0.37	0.04	-0.25
SKW	Qskw.tamu.4D	42	22	366.3	IWB10053	5.13	8.94	0.2145	0.33	0.15	0.15	0.21	-0.66	-0.40
SKW	Qskw.tamu.5B	51	153	704.8	IWB53784	1.87	3.25	-0.16	-0.20	-0.08	0.43	0.01	-0.16	0.16
SKW	Qskw.tamu.7D	71	59	38.5	IWB60795	1.19	1.34	-0.1231	-0.23	0.01	-0.02	0.03	0.17	0.16
SKW	Qskw.tamu.7D	72	91	78.5	IWB44453	1.90	3.37	-0.2612	-0.05	-0.20	-0.05	-0.01	0.16	0.42
FYLD	Qfyld.tamu.1A	6	88	533.4	IWA4536	2.67	6.06	-0.7939	0.25	0.15	0.19	0.05	0.23	-0.08
FYLD	Qfyld.tamu.1B	9	74	430.3	3884244_1al_6978	3.08	2.61	0.2898	-0.26	0.08	-0.28	-0.03	0.31	-0.11

Table A5 Continued

Traits†	QTL name	QTL ID	Position	Mbp‡	LeftMarker	LOD (AbyE) §	PVE (AbyE) ¶	AbyE 13EP2$^{\#}$	AbyE 13EP3	AbyE 13EP4	AbyE 13EP5	AbyE 14CH	AbyE 14EP4	AbyE 14EP5
FYLD	Qfyld.tamu.2B	21	135	734.4	7939581_2bl_9591	1.25	1.17	0.0331	-0.03	0.24	-0.01	-0.30	-0.03	0.08
FYLD	Qfyld.tamu.4D	40	13	109.8	2279925_4ds_1008	7.52	22.05	0.2996	-0.38	-0.11	-0.37	1.47	-0.51	-0.40
FMOIST	Qfmoist.tamu.2D	23	103	82.0	5329935_2ds_3804	7.14	177.67	0.0553	0.03	-0.03	-0.01	-0.02	-0.01	-0.02
PROT14	Qprot14.tamu.4B	34	32	47.4	4962193_4bs_3020	0.92	0.39	-0.0039	-0.01	0.02	0.00	0.02	-0.05	0.03
PROT14	Qprot14.tamu.4B	35	36	181.4	4909258_4bs_448	0.72	0.46	-0.0089	0.00	0.02	-0.02	0.01	-0.04	0.05
PROT14	Qprot14.tamu.4B	37	51	404.0	7040005_4bl_5774	1.51	0.28	0.0102	0.01	0.00	0.03	0.01	0.00	-0.05
PROT14	Qprot14.tamu.4D	39	5	29.0	IWB30733	8.95	9.74	-0.139	-0.05	-0.02	-0.05	-0.06	0.29	0.03
PROT14	Qprot14.tamu.4D	40	13	109.8	2279925_4ds_1008	28.56	43.22	-0.1953	-0.11	-0.06	-0.13	-0.10	-0.04	0.64
PROT14	Qprot14.tamu.4D	41	18	182.6	2273804_4ds_1113	14.37	14.14	-0.0159	0.06	0.10	0.04	0.10	0.08	-0.36
PROT14	Qprot14.tamu.4D	43	28	445.5	IWB3336	9.19	6.42	-0.0461	-0.18	0.06	0.12	-0.10	0.08	0.07
PROT14	Qprot14.tamu.5B	50	74	588.2	IWB36196	2.75	3.31	-0.0283	0.05	0.09	-0.03	0.06	-0.14	-0.01
ASH14	Qash14.tamu.2A	16	93	684.1	6337088_2al_8303	4.41	1.94	0.0022	0.00	0.00	0.00	-0.01	0.00	0.00
ASH14	Qash14.tamu.3D	32	69	573.6	6936842_3dl_1518	0.36	0.94	0.0026	0.00	0.00	0.00	0.00	0.00	0.00
ASH14	Qash14.tamu.6B	58	20	662.3	3252764_6dl_2803	4.91	3.78	0.0027	0.00	0.00	-0.01	0.01	-0.01	0.00
WABS	Qwabs.tamu.4B	37	53	404.0	7040005_4bl_5774	2.61	0.93	0.0096	0.00	-0.01	0.07	0.00	0.03	-0.10
WABS	Qwabs.tamu.4D	39	6	29.0	IWB30733	7.70	14.97	-0.2155	-0.08	0.01	-0.09	-0.08	0.42	0.04
WABS	Qwabs.tamu.4D	40	13	109.8	2279925_4ds_1008	28.74	66.91	-0.2922	-0.16	-0.09	-0.19	-0.15	-0.08	0.96
WABS	Qwabs.tamu.4D	41	18	182.6	2273804_4ds_1113	14.97	22.53	-0.0311	0.09	0.16	0.06	0.14	0.12	-0.55
WABS	Qwabs.tamu.4D	43	28	445.5	IWB3336	8.62	9.77	-0.0887	-0.23	0.07	0.18	-0.17	0.15	0.09
MLPT	Qmlpt.tamu.1A	1	12	14.4	IWB10932	1.49	0.00	-0.0323	-0.02	0.08	-0.10	0.11	-0.01	-0.04
MLPT	Qmlpt.tamu.1A	2	22	232.6	3877153_1al_1567	1.69	0.00	-0.0314	-0.03	0.08	-0.10	0.13	-0.01	-0.03
MLPT	Qmlpt.tamu.1A	2	24	251.3	3923134_1al_161	1.74	0.00	-0.0309	-0.04	0.08	-0.11	0.13	-0.01	-0.03
MLPT	Qmlpt.tamu.1A	2	27	283.1	3922416_1al_1034	1.89	0.00	-0.0375	-0.04	0.08	-0.10	0.14	-0.01	-0.04
MLPT	Qmlpt.tamu.1A	3	34	304.1	3916820_1al_4455	1.66	0.00	-0.0319	-0.03	0.08	-0.10	0.13	-0.01	-0.04
MLPT	Qmlpt.tamu.1A	3	38	333.5	3939178_1al_9799	1.79	0.00	-0.0433	-0.03	0.08	-0.09	0.13	-0.01	-0.03
MLPT	Qmlpt.tamu.1A	3	43	357.6	3966094_1al_942	1.46	0.00	0.0017	0.02	0.14	-0.03	-0.19	0.03	0.03
MLPT	Qmlpt.tamu.1A	4	50	367.1	3900873_1al_350	2.32	0.00	-0.0495	-0.05	0.09	-0.08	0.14	-0.01	-0.04
MLPT	Qmlpt.tamu.1A	4	56	399.2	3920586_1al_9412	2.21	0.00	-0.0514	-0.04	0.09	-0.07	0.13	-0.02	-0.04
MLPT	Qmlpt.tamu.1A	5	60	465.5	IWB65944	2.27	0.00	-0.0394	-0.05	0.09	-0.07	0.13	-0.02	-0.05
MLPT	Qmlpt.tamu.1B	7	0	0.6	3473141_1bs_756	2.73	0.00	-0.1242	0.09	-0.12	0.16	0.10	-0.13	0.02
MLPT	Qmlpt.tamu.1B	7	4	1.4	3482114_1bs_10487	2.75	0.00	0.1184	0.06	-0.15	0.11	0.05	-0.16	-0.02
MLPT	Qmlpt.tamu.1B	7	6	7.2	3285535_1bs_1678	4.29	0.00	-0.1458	0.06	-0.17	0.10	0.05	0.13	-0.02
MLPT	Qmlpt.tamu.1B	10	90	570.3	IWA5160	0.72	0.00	0.0157	0.06	-0.11	0.03	0.08	-0.04	-0.03
MLPT	Qmlpt.tamu.1D	13	58	412.0	IWB58572	14.19	0.00	-0.1649	-0.15	-0.13	0.46	-0.19	0.34	-0.16
MLPT	Qmlpt.tamu.1D	13	60	413.2	2236927_1dl_656	19.96	0.00	-0.1838	0.50	-0.13	-0.18	-0.18	-0.17	0.36
MLPT	Qmlpt.tamu.5A	44	25	17.2	1514513_5as_10557	1.55	0.00	-0.0588	0.04	-0.17	0.11	0.01	0.00	0.07
MLPT	Qmlpt.tamu.7A	65	131	657.7	4557355_7al_14033	3.52	0.00	-0.0622	-0.01	0.13	0.06	0.02	-0.10	-0.04
MLPW	Qmlpw.tamu.1A	1	6	9.2	IWB33789	6.96	6.49	0.7851	0.17	0.37	-0.66	-1.56	0.52	0.38
MLPW	Qmlpw.tamu.1A	5	64	485.2	3894604_1al_116	4.20	5.84	-1.5908	0.16	0.31	-0.46	0.48	0.63	0.47
MLPW	Qmlpw.tamu.4B	34	32	47.4	4962193_4bs_3020	17.46	26.72	0.7086	-0.55	0.82	1.33	0.82	-3.59	0.46
MLPI	Qmlpi.tamu.1A	3	43	357.6	3966094_1al_942	3.42	5.89	4.3258	-2.16	3.47	-4.74	-9.81	4.57	4.34
MLPI	Qmlpi.tamu.1A	4	51	380.7	3916130_1al_8063	4.48	3.96	4.2068	-3.18	3.00	-5.35	4.10	-6.13	3.35
MLPI	Qmlpi.tamu.1A	5	61	474.6	IWB44485	4.50	3.78	3.1679	-3.18	3.06	-5.66	4.53	3.53	-5.44
MLPI	Qmlpi.tamu.1B	7	0	0.6	3473141_1bs_756	2.65	3.62	-5.1596	3.52	-4.55	4.14	5.32	-3.70	0.44
MLPI	Qmlpi.tamu.1B	7	4	1.4	3482114_1bs_10487	4.65	3.94	6.9374	4.02	-5.21	2.23	-3.51	-4.61	0.14
MLPI	Qmlpi.tamu.1B	7	6	7.2	3285535_1bs_1678	4.08	2.78	-4.4849	4.16	-4.98	2.93	-2.24	3.90	0.72

Table A5 Continued

Traits[†]	QTL name	QTL ID	Position	Mbp[‡]	LeftMarker	LOD (AbyE)[§]	PVE (AbyE)[¶]	AbyE 13EP2[#]	AbyE 13EP3	AbyE 13EP4	AbyE 13EP5	AbyE 14CH	AbyE 14EP4	AbyE 14EP5
MLPI	Qmlpi.tamu.1D	13	58	412.0	IWB58572	18.63	23.65	-6.8134	-5.87	-5.06	18.52	-8.83	-6.39	14.44
MLPI	Qmlpi.tamu.1D	13	64	416.1	IWB35348	22.61	33.87	21.4995	18.25	-6.80	-7.67	-8.72	-8.11	-8.43
MLPI	Qmlpi.tamu.3A	26	65	595.8	4308065_3al_1951	0.65	2.57	0.854	-5.91	3.54	-4.35	0.01	3.41	2.44
MLPI	Qmlpi.tamu.4B	38	78	649.5	IWB53155	4.83	3.34	-8.7887	3.00	3.54	-1.42	2.96	0.19	0.51
MLPI	Qmlpi.tamu.4B	38	88	654.3	2804533_5al_4865	10.87	8.76	14.744	1.87	-3.22	-5.61	-0.70	-3.26	-3.83
MLPI	Qmlpi.tamu.4D	39	10	62.8	2305880_4ds_1018	3.78	2.00	-1.2784	-5.20	-3.24	2.33	1.16	2.57	3.66
MLPI	Qmlpi.tamu.5A	44	25	17.2	1514513_5as_10557	3.88	2.80	-3.4035	2.78	-6.99	3.40	-0.63	1.62	3.22
MLRS	Qmlrs.tamu.1A	2	20	227.9	3904015_1al_2374	2.39	2.87	0.173	-0.21	-0.17	-0.14	0.10	0.15	0.10
MLRS	Qmlrs.tamu.1B	7	6	7.2	3285535_1bs_1678	1.94	3.15	0.3269	0.02	-0.25	0.02	-0.05	-0.05	-0.01
MLRS	Qmlrs.tamu.1D	13	60	413.2	2236927_1dl_656	3.88	8.26	0.5557	-0.30	-0.24	-0.05	0.02	-0.03	0.04
MLRS	Qmlrs.tamu.1D	13	65	418.5	2252364_1dl_16749	3.28	4.70	-0.1956	0.41	-0.18	-0.11	0.05	-0.02	0.05
MLRW	Qmlrs.tamu.1A	1	12	14.4	IWB10932	7.30	1.41	1.0095	-0.03	0.45	-0.15	-0.17	-0.14	-0.97
MLRW	Qmlrw.tamu.1D	13	58	412.0	IWB58572	33.46	8.07	-0.4666	-0.82	-1.26	-0.11	-0.39	3.14	-0.09
MLRW	Qmlrs.tamu.1D	13	60	413.2	2236927_1dl_656	27.57	10.21	1.1184	0.26	0.00	1.11	1.02	-3.50	-0.01
MLTW	Qmltw.tamu.1B	7	4	1.4	3482114_1bs_10487	2.85	6.25	1.0248	0.55	-0.32	-0.50	-0.53	-0.09	-0.14
MLTW	Qmltw.tamu.1B	7	6	7.2	3285535_1bs_1678	3.24	8.36	-0.7288	0.35	-0.62	1.08	0.53	-0.29	-0.33
MLTW	Qmltw.tamu.1D	13	64	416.1	IWB35348	5.29	7.68	-0.2466	0.19	-0.21	-0.41	1.38	-0.31	-0.39
MLTW	Qmltw.tamu.1D	13	75	433.3	IWB49445	6.31	19.32	-0.6783	2.22	-0.17	-0.75	-0.32	-0.24	-0.06
MLTW	Qmltw.tamu.7D	74	181	591.204218	IWB10006	4.51	11.47	1.7428	-0.17	-0.51	-0.44	-0.12	-0.26	-0.24

[†] HARD, hardness index; GMOIST, grain moisture; DIAM, kernel diameter; SKW, single kernel weight; FYLD, flour yield %; FMOIST, flour moisture; PROT14, flour protein at 14% moisture basis; ASH14, flour ash content at 14% moisture; WABS, water absorption; MLPT, midline peak time; MLPW, midline peak width; MLPV, midline peak value; MLPI, midline peak integral; MLRS, midline right slope; MLRW, midline right width

[‡] Chromosomal position of the corresponding marker in the IWGSC RefSeq v1.0

[§] Logarithm of odds for additive-by-environment interaction

[¶] Phenotypic variance explained by additive-by-environment interaction

[#] Additive-by-environment interaction effect of individual environments

Table A6
Pearson Correlation between grain yield, test weight, heading date and plant height in dry, irrigated and individual environment.

a) Dry Environment

Traits	Yield	TW	HD
TW	0.30458***		
HD	-0.52285***	-0.14888	
HT	0.14928	0.09319	-0.22101*

b) Irrigated Environment

Traits	Yield	TW
TW	-0.0096	
HT	-0.29602***	0.0454

c) 2011 Bushland Dry (11BD)

Traits	Yield	HD
HD	-0.35227***	
HT	0.30986***	-0.15201

d) 2011 Etter pivot 1 (11EP1)

Traits	Yield	HD
HD	-0.05	
HT	0.52***	-0.058

e) 2011 Etter pivot 2 (11EP2)

Traits	Yield	HD
HD	-0.29**	
HT	0.58***	-0.34***

f) 2011 Etter pivot 3 (11EP3)

Traits	Yield	HD
HD	-0.17	
HT	0.68***	-0.28**

g) 2011 Etter pivot 4 (11EP4)

Traits	Yield	HD
HD	0.11	
HT	0.35***	0.31***

Table A6 Continued

h) 2102 Bushland Dry (12BD)

Traits	Yield	TW	HD
TW	0.26383**		
HD	-0.14112	0.17195	
HT	0.15093	0.11064	-0.29941***

i) 2012 Chillicothe (12CH)

Traits	Yield	TW
TW	0.53***	
HT	0.34***	0.23*

j) 2012 Etter pivot 1 (12EP1)

Traits	Yield	TW
TW	0.05	
HD	-0.18*	-0.3***

k) 2012 Etter pivot 2 (12EP2)

Traits	Yield	TW
TW	0.04	
HD	-0.07	-0.3***

l) 2012 Etter pivot 3 (12EP3)

Traits	Yield	TW
TW	0.11	
HD	-0.23**	-0.13

m) 2017 Bushland Dry (17BD)

Traits	Yield	TW	HD
TW	0.10898		
HD	-0.41242***	-0.07627	
HT	0.00672	-0.06172	0.19898*

n) 2011 Etter pivot 4 (11EP4)

Traits	Yield	HD
HD	0.1101	
HT	0.34532***	0.31443***

Table A6 Continued

o) 2011 Etter pivot 5 (11EP5)

Traits	Yield	TW	HD
TW	0.1331		
HD	0.1153	-0.44201***	
HT	0.0503	-0.42474***	0.49729***

p) 2017 Etter irrigated (17EI)

Traits	Yield	HD
TW	0.29449***	
HT	-0.22962*	-0.08325

q) 2017 Clovis irrigated (17CLI)

Traits	Yield
HT	-0.16

GY, Grain yield; HD, heading date; HT, plant height; TW, test weight
*, **, *** significance level at 5, 1, 0.1% level

Table A7
QTLs detected by individual environment, multi-environment and epistasis analysis for heading date, plant height, test weight and grain yield

QTL Analysis†	Trait ID	Trait‡	ENV§	QTL name ¶	QTL ID	LG‡‡	Chr	Pos cM	Pos Mb§§	Peak SNP	Notes¶¶
IND-ADD	1	HD	11BD	*Qhd.tamu.1D.11*	11	3	1D	68	420.92	2236906_1dl_5649	
IND-ADD	1	HD	DRY	*Qhd.tamu.1D.12*	12	3	1D	78	439.48	2262761_1dl_3962	
IND-ADD	1	HD	12EP1	*Qhd.tamu.1D.12*	12	3	1D	114	486.76	IWB41436	
IND-ADD	1	HD	12EP3	*Qhd.tamu.1D.12*	12	3	1D	114	486.76	IWB41436	
IND-ADD	1	HD	17BD	*Qhd.tamu.1D.12*	12	3	1D	114	486.76	IWB41436	
IND-ADD	1	HD	DRY	*Qhd.tamu.2A.14*	14	4	2A	64	319.05	IWB10151	
IND-ADD	1	HD	11EP5	*Qhd.tamu.2B.18*	18	5	2B	61	**39.20**	IWB22828	Ppd-B1 at 33.95 Mb
IND-ADD	1	HD	11EP1	*Qhd.tamu.2B.19*	19	5	2B	64	65.11	IWB72841	
IND-ADD	1	HD	11EP1	*Qhd.tamu.2D.21*	21	6	2D	29	**15.97**	IWB8481	Ppd-D1, 33.95 Mb
IND-ADD	1	HD	11EP2	*Qhd.tamu.3A.25*	25	7	3A	59	**507.54**	4285803_3al_628	JZ, GY, IWB21182 AT 500.97 MB
IND-ADD	1	HD	11EP2	*Qhd.tamu.4B.34*	34	12	4B	94	659.16	IWA27	
IND-ADD	1	HD	12EP3	*Qhd.tamu.7B.59*	59	23	7B	21	8.52	IWB6455	
IND-ADD	1	HD	11BD	*Qhd.tamu.7D.63*	63	25	7D	82	64.33	3950120_7ds_5316	
IND-ADD	1	HD	11EP4	*Qhd.tamu.7D.63*	63	25	7D	81	64.33	3950120_7ds_5316	
IND-ADD	1	HD	11EP5	*Qhd.tamu.7D.63*	63	25	7D	82	64.33	3950120_7ds_5316	
IND-ADD	1	HD	12BD	*Qhd.tamu.7D.63*	63	25	7D	82	64.33	3950120_7ds_5316	
IND-ADD	1	HD	12EP1	*Qhd.tamu.7D.63*	63	25	7D	81	64.33	3950120_7ds_5316	
IND-ADD	1	HD	12EP2	*Qhd.tamu.7D.63*	63	25	7D	81	64.33	3950120_7ds_5316	
IND-ADD	1	HD	12EP3	*Qht.tamu.7D.63*	63	25	7D	81	64.33	3950120_7ds_5316	
IND-ADD	1	HD	17BD	*Qyld.tamu.7D.63*	63	25	7D	80	64.33	3950120_7ds_5316	
IND-ADD	1	HD	DRY	*Qhd.tamu.7D.63*	63	25	7D	81	64.33	3950120_7ds_5316	
IND-ADD	1	HD	11EP1	*Qhd.tamu.7D.63*	63	25	7D	89	78.50	IWB44453	
IND-ADD	2	HT	12BD	*Qht.tamu.1A.3*	3	1	1A	33	296.24	3888483_1al_4013	
IND-ADD	2	HT	12BD	*Qht.tamu.1A.5*	5	1	1A	77	520.36	3904706_1al_3369	
IND-ADD	2	HT	12BD	*Qht.tamu.1D.12*	12	3	1D	80	444.01	2285810_1dl_1627	
IND-ADD	2	HT	11EP4	*Qht.tamu.1D.12*	12	3	1D	118	492.17	IWA3764	
IND-ADD	2	HT	12BD	*Qht.tamu.4D.35*	35	13	4D	0	**20.58**	IWB15038	Rht-2 at 18.7 Mb
IND-ADD	2	HT	DRY	*Qht.tamu.4D.35*	35	13	4D	0	**20.58**	IWB15038	Rht-2 at 18.7 Mb
IND-ADD	2	HT	IRR	*Qht.tamu.5A.42*	42	14	5A	119	**584.42**	IWB52657	JZ, GY, IWA4276 AT 594.57 MB JZ, GY, IWB12366 AT 595.53 MB Vrn-1, at 588.5 Mb
IND-ADD	2	HT	12BD	*Qht.tamu.6A.48*	48	17	6A	16	7.60	IWB11242	
IND-ADD	2	HT	12BD	*Qht.tamu.7A.57*	57	21	7A	90	85.78	4219271_7as_2211	
IND-ADD	2	HT	12CH	*Qht.tamu.7D.62*	62	25	7D	50	21.68	IWB21023	
IND-ADD	2	HT	17EI	*Qyld.tamu.7D.63*	63	25	7D	79	60.60	IWB35446	
IND-ADD	2	HT	11EP5	*Qhd.tamu.7D.63*	63	25	7D	80	64.33	3950120_7ds_5316	
IND-ADD	2	HT	12BD	*Qht.tamu.7D.64*	64	25	7D	126	123.27	10396674_3b_3606	
IND-ADD	3	TW	13EP5	*Qtw.tamu.1A.5*	5	1	1A	64	485.18	3894604_1al_116	
IND-ADD	3	TW	12EP3	*Qtw.tamu.1D.11*	11	3	1D	46	375.43	2263785_1dl_1257	
IND-ADD	3	TW	12CH	*Qtw.tamu.1D.11*	11	3	1D	69	421.85	2237051_1dl_3543	
IND-ADD	3	TW	DRY	*Qtw.tamu.1D.11*	11	3	1D	69	421.85	2237051_1dl_3543	
IND-ADD	3	TW	13EP5	*Qtw.tamu.2B.20*	20	5	2B	124	**708.74**	8055466_2bl_812	SOA, GY, IWB64246 AT 694.05 Mb Rht4?
IND-ADD	3	TW	12EP3	*Qtw.tamu.2B.20*	20	5	2B	141	**745.86**	8091350_2bl_6123	SOA, GY, IWB64246 AT 694.05 Mb Rht4?

Table A7 Continued

QTL Analysis†	Trait ID	Trait‡	ENV§	QTL name ¶	QTL ID	LG‡‡	Chr	Pos cM	Pos Mb§§	Peak SNP	Notes¶¶
IND-ADD	3	TW	13EP5	*Qtw.tamu.2D.22*	22	6	2D	103	**82.03**	5329935_2ds_3804	Rht8?
IND-ADD	3	TW	13EP4	*Qtw.tamu.4B.32*	32	12	4B	27	**17.04**	IWB49194	JZ, GY, IWB73353 AT 15.41 MB Rht1 at 30.86 Mb
IND-ADD	3	TW	12UV7	*Qtw.tamu.4D.35*	35	13	4D	5	28.99	IWB30733	
IND-ADD	3	TW	17BD	*Qtw.tamu.4D.35*	35	13	4D	9	35.36	2305190_4ds_510	
IND-ADD	3	TW	13EP2	*Qtw.tamu.4D.35*	35	13	4D	11	62.80	2305880_4ds_1018	
IND-ADD	3	TW	14CH	*Qtw.tamu.4D.35*	35	13	4D	11	62.80	2305880_4ds_1018	
IND-ADD	3	TW	12EP1	*Qtw.tamu.4D.35*	35	13	4D	10	62.80	2305880_4ds_1018	
IND-ADD	3	TW	12EP3	*Qtw.tamu.4D.35*	35	13	4D	10	62.80	2305880_4ds_1018	
IND-ADD	3	TW	12BD	*Qtw.tamu.4D.35*	35	13	4D	10	62.80	2305880_4ds_1018	
IND-ADD	3	TW	DRY	*Qtw.tamu.4D.35*	35	13	4D	10	62.80	2305880_4ds_1018	
IND-ADD	3	TW	12UV5	*Qtw.tamu.4D.36*	36	13	4D	13	109.80	2279925_4ds_1008	
IND-ADD	3	TW	12UVL	*Qtw.tamu.4D.37*	37	13	4D	22	366.28	IWB10053	
IND-ADD	3	TW	12BD	*Qtw.tamu.6A.48*	48	17	6A	20	12.42	4344525_6as_6773	
IND-ADD	3	TW	12UV7	*Qtw.tamu.6A.49*	49	17	6A	134	603.28	IWB11675	
IND-ADD	3	TW	13EP5	*Qtw.tamu.6A.49*	49	17	6A	139	608.50	IWB45148	
IND-ADD	3	TW	12CH	*Qtw.tamu.6A.49*	49	17	6A	144	613.48	IWB42057	
IND-ADD	3	TW	12UVL	*Qtw.tamu.6B.50*	50	19	6B	1	**130.30**	IWB38972	JZ, GY, IWB59110 AT 122.96 MB
IND-ADD	3	TW	14EP4	*Qtw.tamu.6B.50*	50	19	6B	0	**130.30**	IWB38972	JZ, GY, IWB59110 AT 122.96 MB
IND-ADD	3	TW	13EP2	*Qtw.tamu.6B.51*	51	19	6B	7	465.95	4352366_6bl_1112	
IND-ADD	3	TW	14CH	*Qtw.tamu.6B.51*	51	19	6B	7	465.95	4352366_6bl_1112	
IND-ADD	3	TW	11EP5	*Qtw.tamu.6B.51*	51	19	6B	6	465.95	4352366_6bl_1112	
IND-ADD	3	TW	12BD	*Qtw.tamu.6B.51*	51	19	6B	7	465.95	4352366_6bl_1112	
IND-ADD	3	TW	17BD	*Qtw.tamu.6B.51*	51	19	6B	6	465.95	4352366_6bl_1112	
IND-ADD	3	TW	13EP5	*Qtw.tamu.6B.52*	52	19	6B	8	559.36	IWB14861	
IND-ADD	3	TW	IRR	*Qtw.tamu.6B.52*	52	19	6B	8	559.36	IWB14861	
IND-ADD	3	TW	12BD	*Qtw.tamu.6D.56*	56	20	6D	96	458.49	3290494_6dl_50	
IND-ADD	3	TW	DRY	*Qtw.tamu.6D.56*	56	20	6D	96	458.49	3290494_6dl_50	
IND-ADD	3	TW	12UV5	*Qtw.tamu.6D.56*	56	20	6D	97	459.24	IWB24926	
IND-ADD	3	TW	13EP5	*Qtw.tamu.7D.62*	62	25	7D	206	0.00	Ksud2	
IND-ADD	3	TW	12CH	*Qtw.tamu.7D.63*	63	25	7D	79	60.60	IWB35446	
IND-ADD	3	TW	11EP5	*Qht.tamu.7D.63*	63	25	7D	79	60.60	IWB35446	
IND-ADD	3	TW	13EP2	*Qtw.tamu.7D.65*	65	25	7D	188	745.86	Gb3P4y	
IND-ADD	4	YLD	17EI	*Qyld.tamu.1A.4*	4	1	1A	58	411.66	3975933_1al_3664	
IND-ADD	4	YLD	COMB	*Qyld.tamu.1A.4*	4	1	1A	58	411.66	3975933_1al_3664	
IND-ADD	4	YLD	DRY	*Qyld.tamu.1A.6*	6	1	1A	172	585.63	3977278_1al_1171	
IND-ADD	4	YLD	DRY	*Qyld.tamu.1A.6*	6	1	1A	174	**586.95**	IWB34513	JZ, HD, IWA1644 AT 590.00 Mb Elf3/HD
IND-ADD	4	YLD	12CH	*Qyld.tamu.1D.11*	11	3	1D	69	421.85	2237051_1dl_3543	
IND-ADD	4	YLD	DRY	*Qyld.tamu.1D.11*	11	3	1D	69	421.85	2237051_1dl_3543	
IND-ADD	4	YLD	13EP3	*Qyld.tamu.2A.17*	17	4	2A	125	734.51	6415190_2al_16820	
IND-ADD	4	YLD	12UVL	*Qyld.tamu.3B.27*	27	8	3B	5	**48.56**	10435017_3b_750	SOA, GY, IWA3983 AT 42.56, Rht5?
IND-ADD	4	YLD	17CVI	*Qyld.tamu.4B.33*	33	12	4B	39	266.83	4883984_4bs_7910	
IND-ADD	4	YLD	14EP4	*Qyld.tamu.4B.34*	34	12	4B	94	659.16	IWA27	
IND-ADD	4	YLD	12UVLD	*Qyld.tamu.4B.34*	34	12	4B	99	660.94	IWB32997	
IND-ADD	4	YLD	17CVI	*Qyld.tamu.4D.35*	35	13	4D	2	**20.58**	IWB15038	Rht-2 at 18.7 Mb
IND-ADD	4	YLD	IRR	*Qyld.tamu.4D.35*	35	13	4D	0	**20.58**	IWB15038	Rht-2 at 18.7 Mb

Table A7 Continued

QTL Analysis†	Trait ID	Trait‡	ENV§	QTL name ¶	QTL ID	LG‡‡	Chr	Pos cM	Pos Mb§§	Peak SNP	Notes¶¶
IND-ADD	4	YLD	17BI	*Qyld.tamu.4D.36*	36	13	4D	13	109.80	2279925_4ds_1008	
IND-ADD	4	YLD	14CH	*Qyld.tamu.4D.38*	38	13	4D	28	445.50	IWB3336	
IND-ADD	4	YLD	17BI	*Qyld.tamu.6A.48*	48	17	6A	20	12.42	4344525_6as_6773	
IND-ADD	4	YLD	14CH	*Qyld.tamu.6D.54*	54	20	6D	1	**19.64**	2080712_6ds_6490	SOA, GY, IWB31561 AT 5.13 MB
IND-ADD	4	YLD	12CH	*Qyld.tamu.7B.59*	59	23	7B	24	15.59	IWA1089	
IND-ADD	4	YLD	DRY	*Qyld.tamu.7B.59*	59	23	7B	24	15.59	IWA1089	
IND-ADD	4	YLD	12CH	*Qyld.tamu.7B.60*	60	23	7B	100	616.96	6722360_7bl_819	
IND-ADD	4	YLD	12UVLD	*Qtw.tamu.7D.63*	63	25	7D	79	60.60	IWB35446	
IND-ADD	4	YLD	12CH	*Qhd.tamu.7D.63*	63	25	7D	80	64.33	3950120_7ds_5316	
IND-ADD	4	YLD	17BD	*Qyld.tamu.7D.63*	63	25	7D	80	64.33	3950120_7ds_5316	
IND-ADD	4	YLD	DRY	*Qyld.tamu.7D.63*	63	25	7D	80	64.33	3950120_7ds_5316	
IND-ADD	4	YLD	14CH	*Qyld.tamu.7D.63*	63	25	7D	86	72.95	IWA1247	
IND-ADD	4	YLD	17BI	*Qyld.tamu.7D.63*	63	25	7D	97	84.34	3938880_7ds_2029	
IND-ADD	4	YLD	12BD	*Qyld.tamu.7D.65*	65	25	7D	181	591.20	IWB10006	
IND-ADD	4	YLD	13EP4	*Qyld.tamu.7D.65*	65	25	7D	198	598.61	IWB45562	
MET-ADD	1	HD	MET	*Qhd.tamu.1A.1*	1	1	1A	0	1.19	IWA974	
MET-ADD	1	HD	MET	*Qhd.tamu.1A.1*	1	1	1A	9	**11.82**	IWB46642	JZ, GY, IWA2452 AT 13.67 Mb
MET-ADD	1	HD	MET	*Qhd.tamu.1A.2*	2	1	1A	19	224.21	3932290_1al_708	
MET-ADD	1	HD	MET	*Qhd.tamu.1A.2*	2	1	1A	23	238.31	3975622_1al_1296	
MET-ADD	1	HD	MET	*Qhd.tamu.1A.3*	3	1	1A	30	294.73	3915571_1al_4855	
MET-ADD	1	HD	MET	*Qhd.tamu.1D.12*	12	3	1D	114	486.76	IWB41436	
MET-ADD	1	HD	MET	*Qhd.tamu.2A.15*	15	4	2A	71	533.47	IWB24910	
MET-ADD	1	HD	MET	*Qhd.tamu.2A.16*	16	4	2A	82	635.58	IWB68780	
MET-ADD	1	HD	MET	*Qhd.tamu.2D.21*	21	6	2D	29	**15.97**	IWB8481	Ppd-D1, 33.95 Mb
MET-ADD	1	HD	MET	*Qhd.tamu.4B.34*	34	12	4B	92	657.17	IWB4448	
MET-ADD	1	HD	MET	*Qhd.tamu.4B.34*	34	12	4B	94	659.16	IWA27	
MET-ADD	1	HD	MET	*Qhd.tamu.7B.59*	59	23	7B	24	15.59	IWA1089	
MET-ADD	1	HD	MET	*Qhd.tamu.7D.63*	63	25	7D	81	64.33	3950120_7ds_5316	
MET-ADD	2	HT	MET	*Qht.tamu.1A.3*	3	1	1A	33	296.24	3888483_1al_4013	
MET-ADD	2	HT	MET	*Qht.tamu.1B.9*	9	2	1B	118	642.78	3915619_1bl_1936	
MET-ADD	2	HT	MET	*Qht.tamu.1D.12*	12	3	1D	118	492.17	IWA3764	
MET-ADD	2	HT	MET	*Qht.tamu.4D.35*	35	13	4D	0	**20.58**	IWB15038	Rht-2 at 18.7 Mb
MET-ADD	2	HT	MET	*Qht.tamu.6A.48*	48	17	6A	16	7.60	IWB11242	
MET-ADD	2	HT	MET	*Qht.tamu.7D.62*	62	25	7D	47	21.14	3916420_7ds_3323	
MET-ADD	2	HT	MET	*Qht.tamu.7D.63*	63	25	7D	80	64.33	3950120_7ds_5316	
MET-ADD	3	TW	MET	*Qtw.tamu.1A.1*	1	1	1A	9	**11.82**	IWB46642	JZ, GY, IWA2452 AT 13.67 Mb
MET-ADD	3	TW	MET	*Qtw.tamu.1A.1*	1	1	1A	13	21.04	IWB21788	
MET-ADD	3	TW	MET	*Qtw.tamu.1A.1*	1	1	1A	15	25.48	3310348_1as_2438	
MET-ADD	3	TW	MET	*Qtw.tamu.1A.2*	2	1	1A	22	232.64	3877153_1al_1567	
MET-ADD	3	TW	MET	*Qtw.tamu.1A.3*	3	1	1A	29	290.73	3909230_1al_1823	
MET-ADD	3	TW	MET	*Qtw.tamu.1A.3*	3	1	1A	34	304.11	3916820_1al_4455	
MET-ADD	3	TW	MET	*Qtw.tamu.1A.3*	3	1	1A	39	339.35	3895363_1al_1924	
MET-ADD	3	TW	MET	*Qtw.tamu.1A.4*	4	1	1A	44	**358.77**	3944816_1al_8842	JZ, GY, 355.32 IWB25391
MET-ADD	3	TW	MET	*Qtw.tamu.1A.4*	4	1	1A	51	380.65	3916130_1al_8063	
MET-ADD	3	TW	MET	*Qtw.tamu.1A.4*	4	1	1A	53	390.09	IWB31924	

Table A7 Continued

QTL Analysis†	Trait ID	Trait‡	ENV§	QTL name ¶	QTL ID	LG‡‡	Chr	Pos cM	Pos Mb§§	Peak SNP	Notes¶¶
MET-ADD	3	TW	MET	*Qtw.tamu.1A.5*	5	1	1A	64	485.18	3894604_1al_116	
MET-ADD	3	TW	MET	*Qtw.tamu.1D.11*	11	3	1D	46	375.43	2263785_1dl_1257	
MET-ADD	3	TW	MET	*Qtw.tamu.1D.11*	11	3	1D	69	421.85	2237051_1dl_3543	
MET-ADD	3	TW	MET	*Qtw.tamu.1D.12*	12	3	1D	117	489.72	IWB17626	
MET-ADD	3	TW	MET	*Qtw.tamu.2B.20*	20	5	2B	124	**708.74**	8055466_2bl_812	SOA, GY, IWB64246 AT 694.05 Mb Rht4?, Rht8?
MET-ADD	3	TW	MET	*Qtw.tamu.2D.22*	22	6	2D	103	**82.03**	5329935_2ds_3804	
MET-ADD	3	TW	MET	*Qtw.tamu.2D.23*	23	6	2D	115	532.96	9842271_2dl_198	
MET-ADD	3	TW	MET	*Qtw.tamu.3B.28*	28	8	3B	27	506.97	10680128_3b_818	
MET-ADD	3	TW	MET	*Qtw.tamu.3D.30*	30	9	3D	53	548.57	6926803_3dl_1308	
MET-ADD	3	TW	MET	*Qtw.tamu.3D.30*	30	9	3D	58	554.69	6956616_3dl_71	
MET-ADD	3	TW	MET	*Qtw.tamu.3D.30*	30	9	3D	63	562.70	IWB8129	
MET-ADD	3	TW	MET	*Qtw.tamu.4D.35*	35	13	4D	11	62.80	2305880_4ds_1018	
MET-ADD	3	TW	MET	*Qtw.tamu.5A.39*	39	14	5A	40	73.83	IWB2928	
MET-ADD	3	TW	MET	*Qtw.tamu.5A.40*	40	14	5A	43	157.32	1500192_5as_1232	
MET-ADD	3	TW	MET	*Qtw.tamu.5A.44*	44	14	5A	194	702.00	IWB28861	
MET-ADD	3	TW	MET	*Qtw.tamu.5B.45*	45	15	5B	75	**589.37**	IWB26282	JZ, SPS, IWB6746 AT 587.6 MB Vrn-1, at 573.8
MET-ADD	3	TW	MET	*Qtw.tamu.5B.45*	45	15	5B	94	645.98	10851545_5bl_762	
MET-ADD	3	TW	MET	*Qtw.tamu.6A.48*	48	17	6A	12	7.19	4348240_6as_16935	
MET-ADD	3	TW	MET	*Qtw.tamu.6A.48*	48	17	6A	17	9.89	4426950_6as_3288	
MET-ADD	3	TW	MET	*Qtw.tamu.6A.48*	48	17	6A	20	12.42	4344525_6as_6773	
MET-ADD	3	TW	MET	*Qtw.tamu.6A.49*	49	17	6A	134	603.28	IWB11675	
MET-ADD	3	TW	MET	*Qtw.tamu.6A.49*	49	17	6A	139	608.50	IWB45148	
MET-ADD	3	TW	MET	*Qtw.tamu.6A.49*	49	17	6A	143	611.57	IWB67460	
MET-ADD	3	TW	MET	*Qtw.tamu.6B.50*	50	19	6B	1	**130.30**	IWB38972	JZ, GY, IWB59110 AT 122.96 MB
MET-ADD	3	TW	MET	*Qtw.tamu.6B.51*	51	19	6B	7	465.95	4352366_6bl_1112	
MET-ADD	3	TW	MET	*Qtw.tamu.6D.56*	56	20	6D	97	459.24	IWB24926	
MET-ADD	3	TW	MET	*Qtw.tamu.6D.56*	56	20	6D	99	459.24	IWB24926	
MET-ADD	3	TW	MET	*Qtw.tamu.7B.59*	59	23	7B	19	8.52	IWB6455	
MET-ADD	3	TW	MET	*Qtw.tamu.7B.59*	59	23	7B	48	64.47	3136917_7bs_1218	
MET-ADD	3	TW	MET	*Qtw.tamu.7B.61*	61	24	7B	1	707.36	6728417_7bl_5629	
MET-ADD	3	TW	MET	*Qtw.tamu.7D.62*	62	25	7D	206	0.00	Ksud2	
MET-ADD	3	TW	MET	*Qtw.tamu.7D.63*	63	25	7D	79	60.60	IWB35446	
MET-ADD	4	YLD	MET	*Qyld.tamu.1B.8*	8	2	1B	85	556.29	3859439_1bl_2195	
MET-ADD	4	YLD	MET	*Qyld.tamu.1D.11*	11	3	1D	69	421.85	2237051_1dl_3543	
MET-ADD	4	YLD	MET	*Qyld.tamu.3A.24*	24	7	3A	8	9.60	IWB7693	
MET-ADD	4	YLD	MET	*Qyld.tamu.4B.33*	33	12	4B	39	266.83	4883984_4bs_7910	
MET-ADD	4	YLD	MET	*Qyld.tamu.4D.36*	36	13	4D	13	109.80	2279925_4ds_1008	
MET-ADD	4	YLD	MET	*Qyld.tamu.4D.38*	38	13	4D	28	445.50	IWB3336	
MET-ADD	4	YLD	MET	*Qyld.tamu.7D.63*	63	25	7D	79	60.60	IWB35446	
MET-ADD	4	YLD	MET	*Qyld.tamu.7D.63*	63	25	7D	97	84.34	3938880_7ds_2029	
MET-EPI1	1	HD	EPI	*Qhd.tamu.1A.6*	6	1	1A	175	**587.83**	3971039_1al_2867	JZ, HD, IWA1644 AT 590.00 Mb Elf3/HD
MET-EPI1	1	HD	EPI	*Qhd.tamu.1B.9*	9	2	1B	155	686.84	IWB4789	
MET-EPI1	1	HD	EPI	*Qhd.tamu.2A.13*	13	4	2A	0	**22.19**	5237958_2as_10729	Ppd-A1 at 36.9 Mb two Rht on short arm
MET-EPI1	1	HD	EPI	*Qhd.tamu.2A.17*	17	4	2A	155	755.40	6337310_2al_1925	
MET-EPI1	1	HD	EPI	*Qhd.tamu.2B.18*	18	5	2B	45	**39.20**	IWB22828	Ppd-B1? 17.3 Mb

Table A7 Continued

QTL Analysis[†]	Trait ID	Trait[‡]	ENV[§]	QTL name [¶]	QTL ID	LG[‡‡]	Chr	Pos cM	Pos Mb[§§]	Peak SNP	Notes[¶¶]
MET-EPI1	1	HD	EPI	*Qhd.tamu.2B.19*	19	5	2B	70	**69.02**	IWB61862	JZ, SPS, IWB49277 AT 68.36 Mb
MET-EPI1	1	HD	EPI	*Qhd.tamu.6A.49*	49	17	6A	140	609.00	IWA6537	
MET-EPI1	1	HD	EPI	*Qhd.tamu.6D.54*	54	20	6D	5	24.00	IWB6829	
MET-EPI1	2	HT	EPI	*Qht.tamu.1A.5*	5	1	1A	60	465.51	IWB65944	
MET-EPI1	2	HT	EPI	*Qht.tamu.1B.7*	7	2	1B	45	68.44	3432579_1bs_4957	
MET-EPI1	2	HT	EPI	*Qht.tamu.1B.8*	8	2	1B	90	570.28	IWA5160	
MET-EPI1	2	HT	EPI	*Qht.tamu.1D.10*	10	3	1D	25	**12.32**	IWB14343	JZ, GY, IWB38400 AT 10.18 Mb
MET-EPI1	2	HT	EPI	*Qht.tamu.2A.16*	16	4	2A	90	674.15	IWB20877	
MET-EPI1	2	HT	EPI	*Qht.tamu.2A.17*	17	4	2A	125	734.51	6415190_2al_16820	
MET-EPI1	2	HT	EPI	*Qht.tamu.2A.17*	17	4	2A	125	734.51	6415190_2al_16820	
MET-EPI1	2	HT	EPI	*Qht.tamu.2A.17*	17	4	2A	150	751.66	1023555_2al_3138	
MET-EPI1	2	HT	EPI	*Qht.tamu.2A.17*	17	4	2A	160	759.10	6382018_2al_8250	
MET-EPI1	2	HT	EPI	*Qht.tamu.3B.29*	29	8	3B	65	771.39	10505374_3b_18831	
MET-EPI1	2	HT	EPI	*Qht.tamu.3D.30*	30	9	3D	60	560.23	IWB32805	
MET-EPI1	2	HT	EPI	*Qht.tamu.3D.30*	30	9	3D	60	560.23	IWB32805	
MET-EPI1	2	HT	EPI	*Qht.tamu.4A.31*	31	11	4A	0	632.63	7156920_4al_5391	
MET-EPI1	2	HT	EPI	*Qht.tamu.4B.34*	34	12	4B	110	666.33	IWB55790	
MET-EPI1	2	HT	EPI	*Qht.tamu.5A.41*	41	14	5A	80	**440.77**	2774965_5al_1437	JZ, KW, IWB1040 AT 437.2MB JZ, SPS, IWB44603 AT 438.26MB
MET-EPI1	2	HT	EPI	*Qht.tamu.7B.59*	59	23	7B	45	47.29	3138767_7bs_7628	
MET-EPI1	2	HT	EPI	*Qht.tamu.7B.61*	61	24	7B	0	707.35	6550874_7bl_349	
MET-EPI1	3	TW	EPI	*Qtw.tamu.2A.16*	16	4	2A	95	**684.90**	6437445_2al_5185	YY, KPS, AT 681.1 MB
MET-EPI1	3	TW	EPI	*Qtw.tamu.2B.18*	18	5	2B	35	**29.56**	IWB47594	Ppd-B1? 17.3 Mb
MET-EPI1	3	TW	EPI	*Qtw.tamu.3A.26*	26	7	3A	115	711.69	4448357_3al_6941	
MET-EPI1	3	TW	EPI	*Qtw.tamu.7D.62*	62	25	7D	15	13.69	3933813_7ds_676	
MET-EPI1	4	YLD	EPI	*Qyld.tamu.1A.6*	6	1	1A	130	556.96	3882773_1al_4725	
MET-EPI1	4	YLD	EPI	*Qyld.tamu.1B.9*	9	2	1B	150	**675.56**	IWB73713	JZ, GY, IWB61210 AT 673.74 Mb
MET-EPI1	4	YLD	EPI	*Qyld.tamu.1B.9*	9	2	1B	155	686.84	IWB4789	
MET-EPI1	4	YLD	EPI	*Qyld.tamu.1D.10*	10	3	1D	10	**8.61**	IWA1788	JZ, GY, IWB38400 AT 10.18 Mb
MET-EPI1	4	YLD	EPI	*Qyld.tamu.2D.21*	21	6	2D	0	**0.22**	5387977_2ds_265	Ppd-D1, 33.95 Mb
MET-EPI1	4	YLD	EPI	*Qyld.tamu.3A.26*	26	7	3A	110	702.61	4365353_3al_191	
MET-EPI1	4	YLD	EPI	*Qyld.tamu.4B.32*	32	12	4B	30	**17.04**	IWB49194	JZ, GY, IWB73353 AT 15.41 MB Rht1 at 30.86 Mb
MET-EPI1	4	YLD	EPI	*Qyld.tamu.5B.46*	46	15	5B	125	680.08	10875123_5bl_6505	
MET-EPI1	4	YLD	EPI	*Qyld.tamu.6B.53*	53	19	6B	45	688.30	IWB6854	
MET-EPI1	4	YLD	EPI	*Qyld.tamu.6D.55*	55	20	6D	45	350.42	3254329_6dl_5253	
MET-EPI2	1	HD	EPI	*Qhd.tamu.6A.48*	48	17	6A	15	7.60	IWB11242	
MET-EPI2	1	HD	EPI	*Qhd.tamu.2B.20*	20	5	2B	130	**729.52**	IWB59461	SOA, GY, IWB64246 AT 694.05 Mb Rht4?,
MET-EPI2	1	HD	EPI	*Qhd.tamu.5A.43*	43	14	5A	185	682.96	2805270_5al_2730	
MET-EPI2	1	HD	EPI	*Qhd.tamu.6A.49*	49	17	6A	145	613.80	5800366_6al_6132	
MET-EPI2	1	HD	EPI	*Qhd.tamu.3B.28*	28	8	3B	55	557.99	10446102_3b_9187	
MET-EPI2	1	HD	EPI	*Qhd.tamu.7D.65*	65	25	7D	185	593.52	3356799_7dl_7319	
MET-EPI2	1	HD	EPI	*Qhd.tamu.7B.60*	60	23	7B	95	611.62	6680752_7bl_3474	
MET-EPI2	1	HD	EPI	*Qhd.tamu.7A.58*	58	21	7A	115	586.42	4445500_7al_1082	
MET-EPI2	2	HT	EPI	*Qht.tamu.6A.48*	48	17	6A	5	5.12	4427795_6as_12820	
MET-EPI2	2	HT	EPI	*Qht.tamu.5A.43*	43	14	5A	160	**633.46**	4541388_5dl_2248	JZ, KW, IWB789 AT 625.73 MB
MET-EPI2	2	HT	EPI	*Qht.tamu.3D.30*	30	9	3D	60	560.23	IWB32805	

Table A7 Continued

QTL Analysis†	Trait ID	Trait‡	ENV§	QTL name ¶	QTL ID	LG‡‡	Chr	Pos cM	Pos Mb§§	Peak SNP	Notes¶¶
MET-EPI2	2	HT	EPI	*Qht.tamu.2B.19*	19	5	2B	65	65.86	5174164_2bs_1900	
MET-EPI2	2	HT	EPI	*Qht.tamu.5B.46*	46	15	5B	155	705.89	10827029_5bl_1233	
MET-EPI2	2	HT	EPI	*Qht.tamu.7D.62*	62	25	7D	15	13.69	3933813_7ds_676	
MET-EPI2	2	HT	EPI	*Qht.tamu.6A.48*	48	17	6A	10	6.73	4354844_6as_593	
MET-EPI2	2	HT	EPI	*Qht.tamu.4B.34*	34	12	4B	65	638.12	IWA3040	
MET-EPI2	2	HT	EPI	*Qht.tamu.7B.59*	59	23	7B	25	19.11	3096912_7bs_110	
MET-EPI2	2	HT	EPI	*Qht.tamu.7D.63*	63	25	7D	80	64.33	3950120_7ds_5316	
MET-EPI2	2	HT	EPI	*Qht.tamu.7B.59*	59	23	7B	0	1.34	6380245_2al_4723	
MET-EPI2	2	HT	EPI	*Qht.tamu.5B.46*	46	15	5B	150	693.40	10848805_5bl_3948	
MET-EPI2	2	HT	EPI	*Qht.tamu.5D.47*	47	16	5D	5	349.87	IWA3429	
MET-EPI2	2	HT	EPI	*Qht.tamu.5A.41*	41	14	5A	50	**430.25**	IWB34498	JZ, KW, IWB1040 AT 437.2MB JZ, SPS, IWB44603 AT 438.26MB
MET-EPI2	2	HT	EPI	*Qht.tamu.7D.65?*	65?	25	7D	195	NA	Sec61	
MET-EPI2	2	HT	EPI	*Qht.tamu.7D.63*	63	25	7D	110	108.24	3946880_7ds_1493	
MET-EPI2	2	HT	EPI	*Qht.tamu.7B.61*	61	24	7B	10	722.20	6666775_7bl_1452	
MET-EPI2	3	TW	EPI	*Qtw.tamu.2A.17*	17	4	2A	100	**700.96**	IWB11977	YY, KPS AT 690.1 MB
MET-EPI2	3	TW	EPI	*Qtw.tamu.4D.35*	35	13	4D	0	**20.58**	IWB15038	Rht-2 at 18.7 Mb
MET-EPI2	3	TW	EPI	*Qtw.tamu.7D.62*	62	25	7D	15	13.69	3933813_7ds_676	
MET-EPI2	3	TW	EPI	*Qtw.tamu.7D.62*	62	25	7D	25	15.32	IWB12582	
MET-EPI2	4	YLD	EPI	*Qyld.tamu.2B.18*	18	5	2B	10	**8.34**	IWB9673	Ppd-B1? 17.3 Mb
MET-EPI2	4	YLD	EPI	*Qyld.tamu.6D.56*	56	20	6D	105	461.36	IWA1924	
MET-EPI2	4	YLD	EPI	*Qyld.tamu.2B.20*	20	5	2B	135	**734.41**	7939581_2bl_9591	SOA, GY, IWB64246 AT 694.05 Mb Rht4?,
MET-EPI2	4	YLD	EPI	*Qyld.tamu.7D.62*	62	25	7D	40	21.14	3916420_7ds_3323	
MET-EPI2	4	YLD	EPI	*Qyld.tamu.3B.29*	29	8	3B	70	776.95	10764714_3b_3097	
MET-EPI2	4	YLD	EPI	*Qyld.tamu.6A.48*	48	17	6A	70	23.20	IWB28195	
MET-EPI2	4	YLD	EPI	*Qyld.tamu.4D.36*	36	13	4D	15	121.61	2298011_4ds_5609	
MET-EPI2	4	YLD	EPI	*Qyld.tamu.7D.63*	63	25	7D	85	72.95	IWA1247	
MET-EPI2	4	YLD	EPI	*Qyld.tamu.6D.54*	54	20	6D	20	33.69	4251907_7as_438	
MET-EPI2	4	YLD	EPI	*Qyld.tamu.7D.65*	65	25	7D	160	568.68	3388911_7dl_2689	

† IND-ADD, individual environment QTL analysis; MET-ADD, multi-environment QTL analysis; MET-EPI1 and MET-EPI2, epistasis QTL analysis for position 1 and position 2, respectively

‡ HD, heading date; HT, plant height; TW, test weight; YLD, grain yield

§ Env, environments; 11BD, 2011 Bushland dryland; 12BD, 2012 Bushland dryland; 17BD, 2017 Bushland dryland; 17BI, 2017 Bushland irrigated; 11CH, 2011 Chillicothe, 12CH, 2012 Chillicothe; 14CH, 2014 Chillicothe; 17CVI, 2017 Clovis irrigated; 11EP1, 2011 Etter 0% ET; 11EP2, 2011 Etter 40% ET; 11EP3, 2011 Etter 60% ET; 11EP4, 2011 Etter 75% ET; 11EP5, 2011 Etter 100% ET; 12EP1, 2012 Etter 0% ET; 12EP2, 2012 Etter 40% ET; 12EP3, 2012 Etter 60% ET; 13EP2, 2013 Etter 40% ET; 13EP3, 2013 Etter 60% ET; 13EP4, 2013 Etter 75% ET; 13EP5, 2013 Etter 100% ET; 14EP4, 2014 Etter 75% ET; 14EP5, 2014 Etter 100% ET; 17EI, 2017 Etter 100% ET; 12UVLD, 2012 Uvalde dryland; 12UV5, 2012 Uvalde 50% ET; 12UV7, 2012 Uvalde 70% ET; 12UVL, 2012 Uvalde irrigated; 13UVL, 2013 Uvalde irrigated; 13UVLD, 2013 Uvalde dryland

¶ QTLs highlighted in red text were also detected by individual or multi-environment QTL analysis

\# QTLs that were stably expressed in more than a single environment

†† Multi-trait QTL cluster

Table A7 Continued

[‡‡] LG, linkage group number

[§§] Physical position of the peak marker (leftmarker) extracted from IWGSC RefSeq v 1.0; Blue text color corresponds to the peak marker previously identified presented on Notes column

[¶¶] JZ, Zhang et al., (2018); SOA, Assanga et al., (2018); YY, Yang et al., (2017); GY, grain yield; KW, kernel weight; HD, heading date; SPS, spikelets per spike, KPS, kernel per spike; Rht, height reducing gene; *Ppd*, photoperiod insensitive gene; Vrn, vernalization requirement gene, Elf3: early flowering gene

Zhang et al., (2018)

Assanga et al., (2018)

Yang, Y. 2017. Characterization of yield and yield components using bi-parental and association mapping of Texas popular cultivars and synthetic wheat. PhD Diss. Texas A&M University, College Station, TX

Table A8

Peak markers, chromosome, physical position related to yield and related traits from different study

Author	Traits†	Peak marker	Chr‡	Mbp§	Aligned length	Align similarity	Notes¶
Zhang et al., (2018)	GY	IWA2452	chr1A	13.67076	113	99.12	
Zhang et al., (2018)	GY	IWB25391	chr1A	355.324349	102	99.02	
Zhang et al., (2018)	GY	IWB38367	chr1A	505.52378	102	99.02	
Zhang et al., (2018)	GY	IWB62751	chr1A	568.01277	84	98.81	
Zhang et al., (2018)	GY	IWB26466	chr1B	7.995497	102	99.02	
Zhang et al., (2018)	GY	IWB50944	chr1B	52.899773	102	99.02	
Zhang et al., (2018)	GY	IWB61210	chr1B	673.743486	102	99.02	
Zhang et al., (2018)	GY	IWB38400	chr1D	10.180432	102	99.02	
Zhang et al., (2018)	GY	IWB15693	chr1D	20.045042	251	99.6	
Zhang et al., (2018)	GY	IWB21128	chr3A	500.976955	102	99.02	
Zhang et al., (2018)	GY	IWB11049	chr3B	819.503122	102	99.02	
Zhang et al., (2018)	GY	IWB35371	chr4A	535.427992	202	99.5	
Zhang et al., (2018)	GY	IWB73353	chr4B	15.413202	66	98.48	
Zhang et al., (2018)	GY	IWA4276	chr5A	594.57672	202	99.5	
Zhang et al., (2018)	GY	IWB12366	chr5A	595.537652	102	99.02	
Zhang et al., (2018)	GY	IWB59110	chr6B	122.96789	102	99.02	
Zhang et al., (2018)	KPS	IWB6510	chr6B	625.379773	102	98.04	
Zhang et al., (2018)	KW	IWB25267	chr2A	42.402213	102	98.04	
Zhang et al., (2018)	KW	IWB45501	chr2A	115.140873	95	98.95	
Zhang et al., (2018)	KW	**IWB35243**	chr2B	214.590768	104	99.04	TaSUS-2B
Zhang et al., (2018)	KW	**IWB29808**	chr2B	189.619237	74	98.65	TaSUS-2B
Zhang et al., (2018)	KW	IWB1356	chr6A	403.507598	100	93	
Zhang et al., (2018)	KW	IWB1040	chr5A	437.208797	102	99.02	
Zhang et al., (2018)	KW	IWB789	chr5A	625.732671	102	99.02	
Zhang et al., (2018)	KW	IWB35964	chr5B	279.097478	121	99.17	
Zhang et al., (2018)	KW	**IWB47942**	chr6A	297.714551	102	99.02	GW2
Zhang et al., (2018)	KW	IWB63290	chr6A	563.131061	91	98.9	
Zhang et al., (2018)	KW	**IWA2808**	chr6D	157.321607	202	98.51	GW2
Zhang et al., (2018)	KW	IWA604	chr7D	266.388658	122	98.36	
Zhang et al., (2018)	SPS	IWB7717	chr1A	37.501036	102	99.02	

Table A8 Continued

Author	Traits[†]	Peak marker	Chr[‡]	Mbp[§]	Aligned length	Align similarity	Notes[¶]
Zhang et al., (2018)	SPS	IWA1191	chr1B	57.713254	202	99.5	
Zhang et al., (2018)	SPS	IWB49277	chr2B	68.365388	85	98.82	
Zhang et al., (2018)	SPS	IWB26631	chr2B	158.643806	102	98.04	
Zhang et al., (2018)	SPS	IWB64813	chr2B	464.290408	102	99.02	
Zhang et al., (2018)	SPS	IWB59779	chr2B	244.572527	82	98.78	
Zhang et al., (2018)	SPS	IWB75234	chr3B	816.599798	102	99.02	
Zhang et al., (2018)	SPS	IWB44603	chr5A	438.267529	102	99.02	
Zhang et al., (2018)	SPS	IWB56233	chr5A	504.873158	102	99.02	
Zhang et al., (2018)	SPS	IWA12	chr5A	556.683952	122	99.18	
Zhang et al., (2018)	SPS	IWA2257	chr5B	315.613541	202	99.5	
Zhang et al., (2018)	SPS	IWB6746	chr5B	587.600676	77	98.7	
Zhang et al., (2018)	SPS	IWA2017	chr2B	156.918623	136	94.85	
Zhang et al., (2018)	SPS	IWB7349	chr7A	34.539424	102	99.02	
Zhang et al., (2018)	SPS	IWA5912	chr7A	674.276749	202	98.02	
Zhang et al., (2018)	HD	**IWA1644**	chr1A	590.001502	143	99.3	Elf3/HD
Zhang et al., (2018)	HD	**IWA989**	chr2D	32.792768	202	99.5	Ppd-D1/HD
Zhang et al., (2018)	KW	**IWB39422**	chr1A	168.718422	108	87.04	GW2
Assanga et al., (2018)	GY	IWB70591	chr2B	640.986765	102	99.02	
Assanga et al., (2018)	GY	IWB64246	chr2B	694.056368	102	99.02	
Assanga et al., (2018)	GY	IWB23950	chr5B	554.820366	102	97.06	
Assanga et al., (2018)	GY	IWB52093	chr5B	52.00537	83	98.8	
Assanga et al., (2018)	GY	IWA3983	chr3B	42.564588	200	99	
Assanga et al., (2018)	GY	IWB31561	chr6D	5.19597	102	99.02	
Assanga et al., (2018)	GY	IWB11000	chr7A	617.687683	102	99.02	

[†] GY, grain yield; KW, kernel weight; HD, heading date; SPS, spikelets per spike, KPS, kernel per spike; *Rht*, height reducing gene; *Ppd*, photoperiod insensitive gene; *Vrn*, vernalization requirement gene, *Elf3*: early flowering gene

[‡] Chromosome of the corresponding marker in IWGSC RefSeq v1.0

[§] position of the corresponding marker in IWGSC RefSeq v1.0

[¶] GY, grain yield; KW, kernel weight; HD, heading date; SPS, spikelets per spike, KPS, kernel per spike; *Rht*, height reducing gene; *Ppd*, photoperiod insensitive gene; *Vrn*, vernalization requirement gene, *Elf3*: early flowering gene

Zhang et al., (2018)
Assanga et al., (2018)

Table A8 Continued

Yang, Y. 2017. Characterization of yield and yield components using bi-parental and association mapping of Texas popular cultivars and synthetic wheat. PhD Diss. Texas A&M University, College Station, TX

Table A9
Physical position of different height reducing gene (*Rht*) identified by Ellis et al., (2005)

Rht gene	Linked marker	Chromosome	IWGSC position (Mb)
Rht4	wmc317	2BL	783.89
Rht5	barc102	3BS	17.57
Rht8c	wmc503	2DS	19.63
Rht9	barc151	5AL	558.34
Rht12	wmc410	5AL	678.29
Rht13	wms577	7BL	711.23

Ellis et al., (2005)