

QTL mapping for bread making quality and agronomic traits in a winter wheat mapping population



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Introduction

Both bread making quality and high productivity are critically important for U.S. hard winter wheat (*Triticum aestivum* L.). Bread making quality traits are influenced by both genotype and environment, but the effects of specific loci and their interactions with the environment are not completely understood. Knowledge of quantitative trait loci (QTL) for quality and agronomic traits in different environments will improve understanding of the genetic control of those traits, and may increase the efficiency of selection. Of the many procedures used to evaluate bread making quality, the Mixograph is preferred by many U.S. breeding programs for its ability to evaluate dough functional properties relevant to the milling and baking industry.

Objectives

- To evaluate a doubled haploid mapping population in multiple environments for agronomic and bread making quality traits.
- To develop genome-wide molecular marker linkage maps based on DNA and protein markers.
- To conduct QTL analysis to determine the location and size of QTLs and their stability across environments.

Materials and Methods

- A doubled haploid (DH) population of 186 lines was produced from a cross of the parents CO940610 and 'Platte'.
- CO940610 is an experimental hard white winter line developed by the CSU Wheat Breeding Program. It has excellent dryland yield and pre-harvest sprouting tolerance, but poor bread making quality. Platte is a hard white winter cultivar developed by Agripro (Junction City, KS) and is known for its excellent bread making quality.
- Lines were grown in two replications of a row-column design at Fort Collins and Greeley, Colorado in 2008 and 2009, respectively. At each site, trials were grown under moderate moisture stress ("dry") and fully irrigated ("wet") conditions, giving a total of four environments.
- Quality traits were evaluated with a 10-g Mixograph (National Manufacturing Division, TMCO, Lincoln, NE), single kernel characterization system (Perten Instruments, Springfield, IL), and near infrared spectroscopy (Foss-Tecator NIR systems Model 6500, Foss North America, Eden Prairie, MN).
- For the Mixograph evaluation, higher values of peak time, peak height, right width, and right slope are considered favorable (Fig. 1).

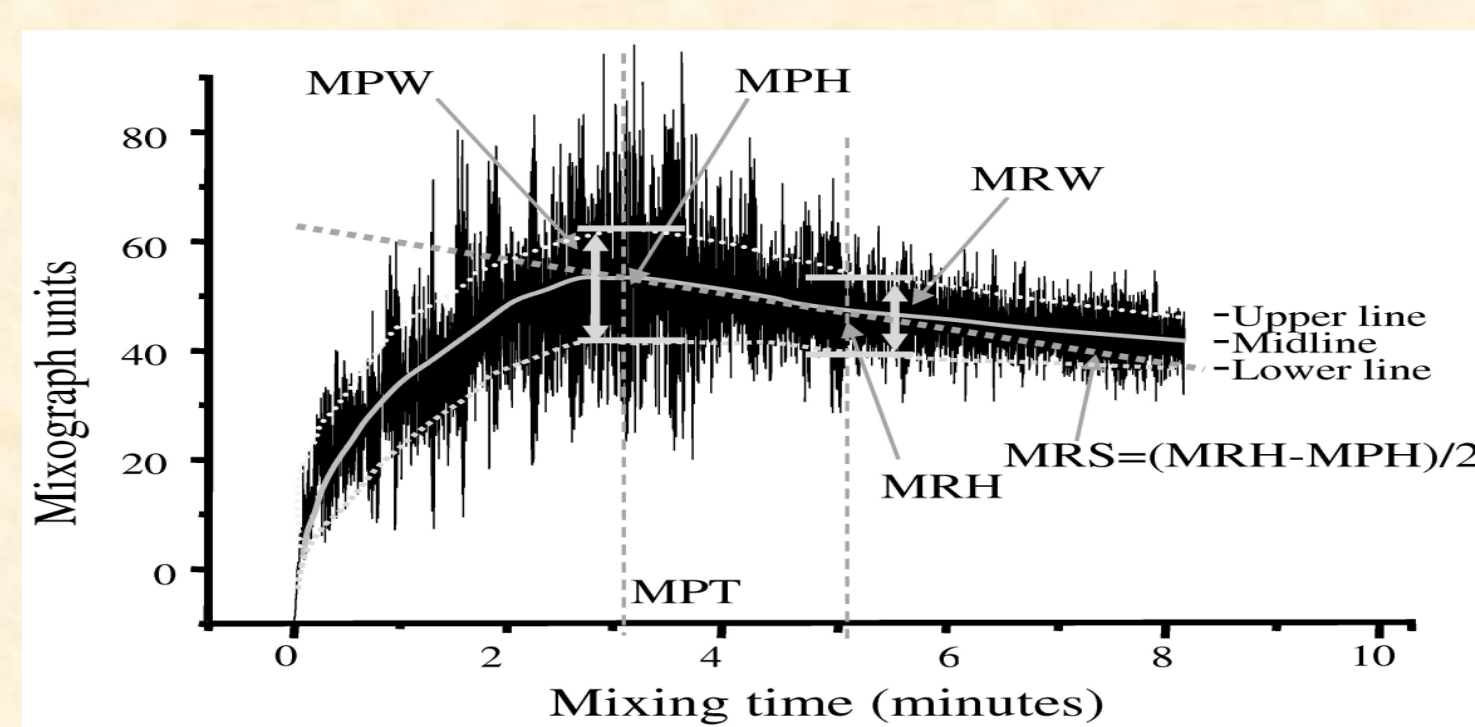


Fig. 1. Example of Mixograph output. MPT=Mixograph peak time, MPH= Mixograph peak height, MRS=Mixograph right slope, MRW=Mixograph right width.

- Above-ground biomass, grain weight, and average kernel weight were determined from 1-m lengths of row (Fig. 2).
- Pre-harvest sprouting (PHS) was evaluated with the method of Mares et al. (2005). Two replicates of 50 grains were arrayed on moist blotter paper in petri dishes, placed in a growth chamber (20°C, 12 hr light/12 hr dark), and number germinated seeds counted at daily intervals for 7 days.
- Analysis of variance was conducted with PROC MIXED of SAS 9.1 (Cary, NC) to calculate least squares means for each environment, which were then used in the QTL analyses.
- Linkage maps were constructed with JoinMap 4 software (Van Ooijen, 2006) using the Haldane mapping function.
- The composite interval mapping option of QTL Cartographer software 2.5 (Wang et al., 2007) was used in a genome-wide scan for significant (LOD ≥ 2.5) QTLs.

Results

Fig. 2. Field trials in Fort Collins, 2008 and Greeley, 2009

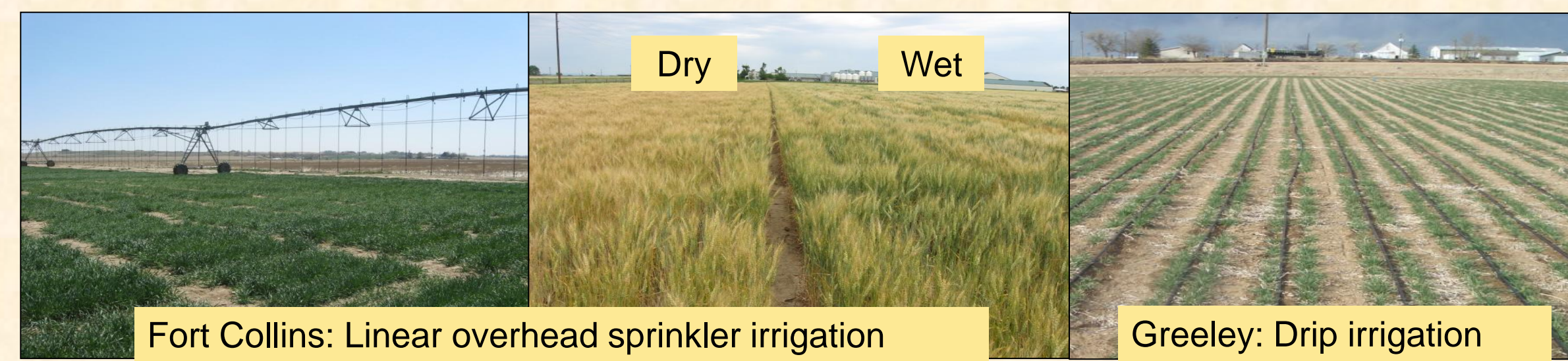


Table 1. Comparison of selected trait means in four environments.

Trait	08 dry	08 wet	09 dry	09 wet
Days to heading	152.5	156.3	143.2	144.7
Above-ground biomass, g	296.9	365.3	401.5	463.5
Grain yield, k/ha	2924	3720	3057	3761
Grain protein conc., g/kg	145.9	138.4	143.6	114.0
Kernel hardness, %	75.1	73.1	71.7	68.0
Mixograph peak time, min.	2.79	2.43	3.76	3.42
Mixograph peak ht, mixogr. units	58.2	56.6	57.2	51.1

Fig. 3. Chromosome 7B showing QTL peak positions and 1-LOD support intervals for multiple traits in four environments (El-Feki, 2010).

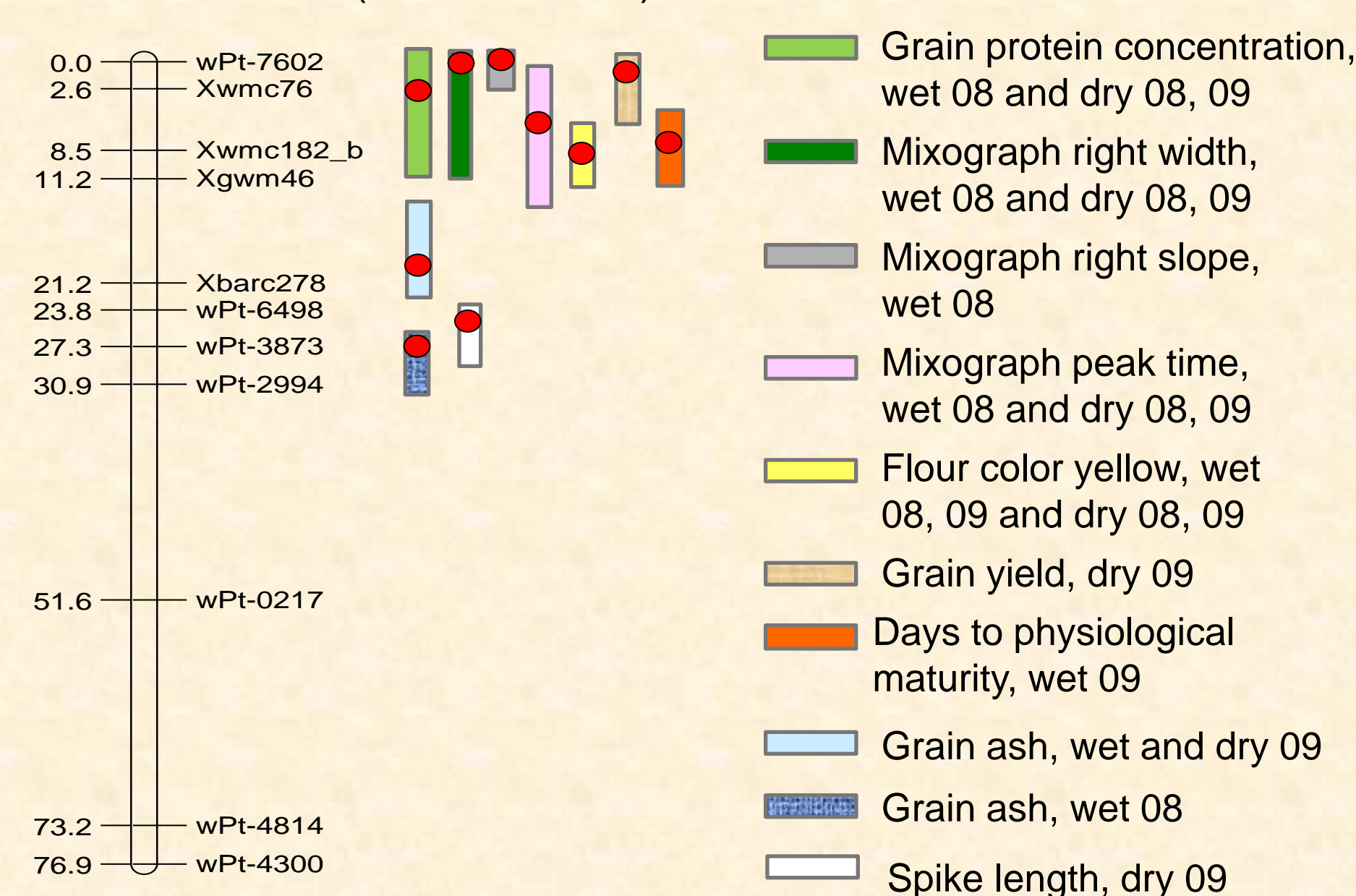


Fig. 4. Chromosome 7D showing the QTL peak positions and 1-LOD support intervals for multiple traits in four environments (El-Feki, 2010).

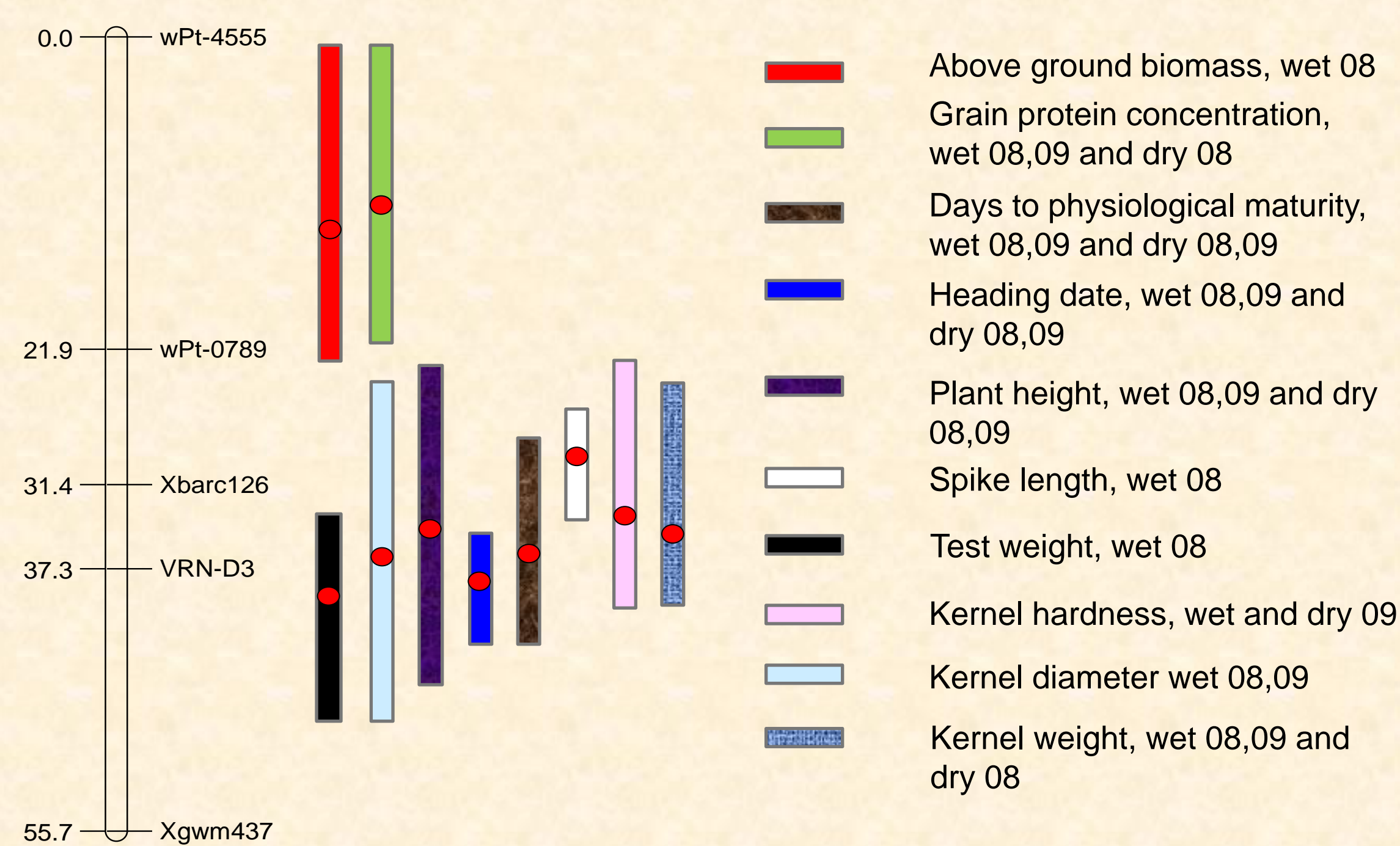


Table 2. Percent variance explained (% R²) for QTL for Mixograph peak time in four environments. ns=not significant.

Chrom.	Marker interval	08 dry	08 wet	09 dry	09 wet
1B	<i>GluB1-wPt1317</i>	4.4	6.7	3.7	3.7
2A	<i>Xgwm312-Ppo33</i>	3.7	ns	ns	4.7
2B	<i>wPt-4301 - Xgwm429</i>	24.7	21.5	20.6	21.5
3A	<i>Xwmc532 - Xbarc356</i>	4.6	5.1	ns	ns
7D	<i>wPt-0789 - Xbarc126</i>	35.9	32.1	42.6	39.3
Multiple-locus model		64.8	49.5	54.1	55.9

Table 3. Percent variance explained (% R²) for QTL for Mixograph peak time in four environments. ns=not significant.

Chrom.	Marker interval	08 dry	08 wet	09 dry	09 wet
1A	<i>Xwmc312 - Glu-A1</i>	6.2	4.9	4.7	ns
1B	<i>Xcfd20a - Glu-B1</i>	25.9	22.6	26.3	24.1
1D	<i>Xcfd48 - Glu-D1</i>	27.1	29.3	28.2	25.8
2D	<i>wPt-3728 - wPt-4413</i>	ns	4.7	ns	ns
6A	<i>wPt-0357 - Xcfd1</i>	ns	ns	3.3	ns
6B	<i>wPt2587-wPt6437</i>	ns	3.0	2.3	ns
7B	<i>wPt-7602 - Xgwm46</i>	6.8	6.2	6.8	ns
7D	<i>wPt0789-Xbarc126-VrnD3</i>	ns	ns	2.7	4.7
Multiple-locus model		68.3	68.9	73.8	56.4

Results

Table 4. Percent variance explained (% R²) for QTL for grain protein concentration in four environments. ns=not significant.

Chrom.	Marker interval	08 dry	08 wet	09 dry	09 wet
1B	<i>wPt-0705-wPt-9857</i>	ns	4.8	ns	ns
2D	<i>wPt-4413-wPt-0638</i>	ns	9.4	ns	ns
5B	<i>Xgwm540-Xgwm499</i>	ns	8.0	13.6	ns
6A	<i>Xwmc256-wPt-3069</i>	7.3	12.9	9.6	5.6
6B	<i>Xwmc397-Xwmc182a</i>	ns	7.0	4.5	ns
7B	<i>wPt-7602-Xwmc76</i>	9.2	6.7	5.8	ns
7D	<i>wPt-0789-Xbarc126</i>	9.5	6.8	ns	7.9
unlinked	<i>wPt-8920</i>	8.1	7.6	ns	ns
Multiple-locus model		35.0	54.9	32.9	11.3

- The degree of moisture stress was moderate based on grain yield reduction: 21% reduction in 2008 and 19% in 2009. As expected, means for most agronomic traits in the fully irrigated treatment exceeded those in the limited irrigation treatment (Table 1).
- Grain protein concentration, kernel hardness, and Mixograph peak time and height were more favorable in the dryland environments (Table 1).
- 31 linkage groups contained 221 markers (108 SSR, 105 DArT, 5 protein, and 3 sequence-tagged site) and spanned 2,083 cM. All 21 chromosomes were represented, but some had limited coverage.
- Major QTL for some traits were detected in all environments, whether fully irrigated or moisture stressed, as shown in Tables 2 and 3. Results were less consistent for yield-related traits.
- Chromosomes 1A, 1B, and 1D contained QTL for multiple bread making quality traits, most likely indicating the effects of the *Glu-A1*, *Glu-B1*, and *Glu-D1* loci (Table 3).
- The 7BS QTL region near SSR marker *Xwmc76* may reflect a novel quality locus or loci (Fig. 3). The poor quality parent, CO940610, contributed the favorable allele in this region. Markers in the 7BS region did not show epistatic interactions with the *Glu-1* loci.
- The 7DS region near *Vrn-D3* contained QTL for multiple maturity and quality traits (Fig. 4). These results are consistent with previous studies indicating pleiotropic effects in this region (Hai et al., 2008; McCartney et al., 2005; Wang et al., 2009).
- We confirmed a QTL for PHS on chromosome 4A in one environment (Mares et al., 2005). Three other QTLs were detected on chromosomes 2B, 3B, and 4D (data not shown).

Summary

To evaluate the effects of moisture stress on genetic control of agronomic and quality traits of hard white winter wheat, we evaluated the CO940610/Platte DH population in four environments differing in level of irrigation. Our analysis revealed multiple QTL for quality traits on chromosomes 1AL, 1BL, 1DL, and 7BS. The 7BS region may reflect a novel quality locus or loci that affects kernel composition. The 7D region near *Vrn-D3* affected multiple morphological, maturity, and kernel traits.

Backcross populations are currently being developed to introgress the 7BS region from CO940610 into Platte. If confirmed, QTL in this region may be useful for marker assisted selection or high resolution mapping leading to map-based cloning.

Acknowledgements

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