Genetic mapping of quantitative trait loci associated with end-use quality traits in the spring wheat (*Triticum aestivum* L.) cross 'Louise' by 'Penawawa'

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Table 1. Means, ranges, and heritabilities of 18 end-use quality traits among 188 recombinant inbred lines from the Louise by Penawawa soft white wheat population using data combined across three locations.

Traits	Parental Lines		RIL Population				Heritability (h^2)	Confidence interval (h^2)
	Louise	Penawawa	Mean	Min	Max	Mean		
Test Weight (lb/bu)	61.0	59.0	60.0	55.0	62.9	59.6	0.64	0.61-0.67
Protein Content (%)	10.5	10.8	10.6	10.4	12.3	11.1	0.23	0.18-0.28
Wheat Protein (%)	10.3	11.3	10.8	10.2	12.8	11.0	0.19	0.10-0.28
SKCS Hardness (1-100)	18.9	13.1	16.0	2.4	36.9	16.7	0.63	0.60-0.66
Kernel Weight (mg)	37.0	30.5	33.8	29.7	39.1	34.1	0.69	0.66-0.72
Kernel Size (mm)	2.6	2.5	2.5	2.3	2.8	2.6	0.62	0.58-0.66
Flour Protein (%)	8.9	9.2	9.1	8.3	9.8	9.1	0.25	0.20-0.30
Flour Ash (%)	0.35	0.45	0.40	0.33	0.50	0.39	0.20	0.15-0.25
SDS Sedimentation (mm)	135.2	161.6	148.4	46.4	118.9	86.4	ND[1]	ND
SRC Carbonate (%)	71.9	78.8	75.3	68.0	83.9	74.9	0.68	0.65-0.71
SRC Lactic Acid (%)	127.3	136.9	132.1	109.8	149.0	131.1	ND	ND
SRC Water (%)	53.7	54.9	54.3	50.0	58.3	53.7	0.66	0.63-0.69
SRC Sucrose (%)	94.0	111.3	102.6	86.1	114.3	100.3	0.73	0.70-0.76
Flour Yield (%)	72.3	68.7	70.5	65.7	73.8	70.4	0.82	0.80-0.84
Milling Score	91.1	80.0	85.6	77.1	93.3	86.5	0.69	0.66-0.72
Break Flour Yield (%)	50.9	48.7	49.8	42.2	53.7	49.4	0.91	0.90-0.92
Flour Swelling Volume (mm)	19.6	25.1	22.3	18.4	26.2	22.4	0.82	0.80-0.84
Cookie Diameter (cm)	9.5	9.1	9.3	8.8	9.7	9.3	0.49	0.45-0.53

[1] ND data not calculated due to missing environments.

Introduction

Wheat (*Triticum aestivum* L.) is an important food source globally, and due to this importance, genetic improvements of wheat have focused on three main areas: yield enhancement, biotic and abiotic stress tolerance, and improvement of end-use quality (Mann et al., 2009). Enhanced milling and baking quality is essential for improving the marketability of wheat produced in the United States as well as around the world. New tools that accurately predict processing and end-use quality of wheat would be useful for increasing the rate of progress for expanding food uses for wheat. Many end-use quality tests have been developed to evaluate wheat germplasm for superior end-use quality performance such as protein quality, starch quality, and milling extraction rates (AACCI 2008). Knowledge concerning genetic factors controlling end-use quality traits in wheat aids in the selection of lines having enhanced quality, thereby improving the chances of meeting the strict end-use quality parameters needed to successfully market a wheat cultivar (Wheat Marketing Center, 2007). Coupling the knowledge of genetic control of end-use quality traits with protocols to rapidly measure the potential of individual lines to meet required end-use quality specifications will allow breeders to make gains from both direct and indirect selection, thereby facilitating the improvement of complex traits in regionally adapted wheat cultivars. The objective of this study was to identify DNA markers associated with QTL for important end-use quality traits for use in marker-assisted selection programs.

Materials and Methods

Plant materials: A RIL population of 188 individuals from a cross between 'Louise' (Kidwell et al. 2006; PI 634865) and 'Penawawa' (PI 495916) was selected for phenotypic and genotypic analyses. Louise, a soft white spring wheat released in 2005, has moderate grain volume weight, low grain protein concentration, and excellent end-use quality characteristics. Penawawa, a soft white spring wheat released in 1985, has moderate grain volume weight, moderate grain protein concentration, and average end-use quality characteristics.

Field experiment and data collection: Field trials were conducted in Genesee, ID (latitude 46° 35' N, longitude 116° 56' W, elevation 864.7 meters), and Pullman, WA (latitude 46° 41' N, longitude 117° 08' W, elevation 776.3 meters), in 2007, and in Moscow, ID (latitude 46° 43' N, longitude 116° 57' W, elevation 796.1 meters), and again in Pullman, WA, in 2008. End-use quality analysis was performed by blending 200 g from each replicated field plot for each line at each location (600 g total). All quality analyses were conducted at the USDA-ARS Western Wheat Quality Laboratory in Pullman, WA. Samples were tempered to 14% moisture and milled on a Quadrumat system as modified by Jeffers and Rubenthaler (1979). Approved methods of the AACCI (2008) were used to determine end-use quality traits. Milling score was calculated as: 100 – [(80 – flour yield) + 50*(flour ash – 0.30) + 0.48*(milling time – 12.5) + 0.5*(65 – per cent long patent) + 0.5*(16 – first tempering moisture)]. Kernel hardness, size, and weight were obtained using the SKCS 4100 (Perten Instruments, Springfield, IL). Solvent retention capacity was conducted on straight grade flour (Approved Method 56-11.02).

DNA isolation and marker analysis: Fresh leaf tissue of three individuals from each $F_{5:6}$ RIL or parent was collected at the five leaf stage, and used to extract genomic DNA using the method described by Anderson et al. (1992). The genetic linkage map described by Carter et al. (2009) was used for QTL analysis. An additional 40 markers located on chromosome 3B and 4D were screened for polymorphism between the parents. Sequences of available SSR markers along with their previously determined chromosomal locations were obtained from Graingenes (http://wheat.pw.usda.gov/). SSR marker analysis was conducted using the PCR conditions described by Röder et al. (1998) except that primers were synthesized to include the M13-tail (Oetting et al. 1995). New markers were added using the 'try' and 'ripple' command using Mapmaker V3.0 (Lander et al. 1987). The Kosambi map function was applied to calculate genetic distances in centiMorgans (cM) between the ordered markers (Kosambi 1944). The software WinQTLCart V2.5 (Basten et al. 1997) was used for QTL analysis. Composite interval mapping was used to identify markers with significant effects on associated end-use quality traits (Zeng 1994). Heritability estimates were calculated using a SAS code provided by Dr. Jim Holland (Holland 2003).

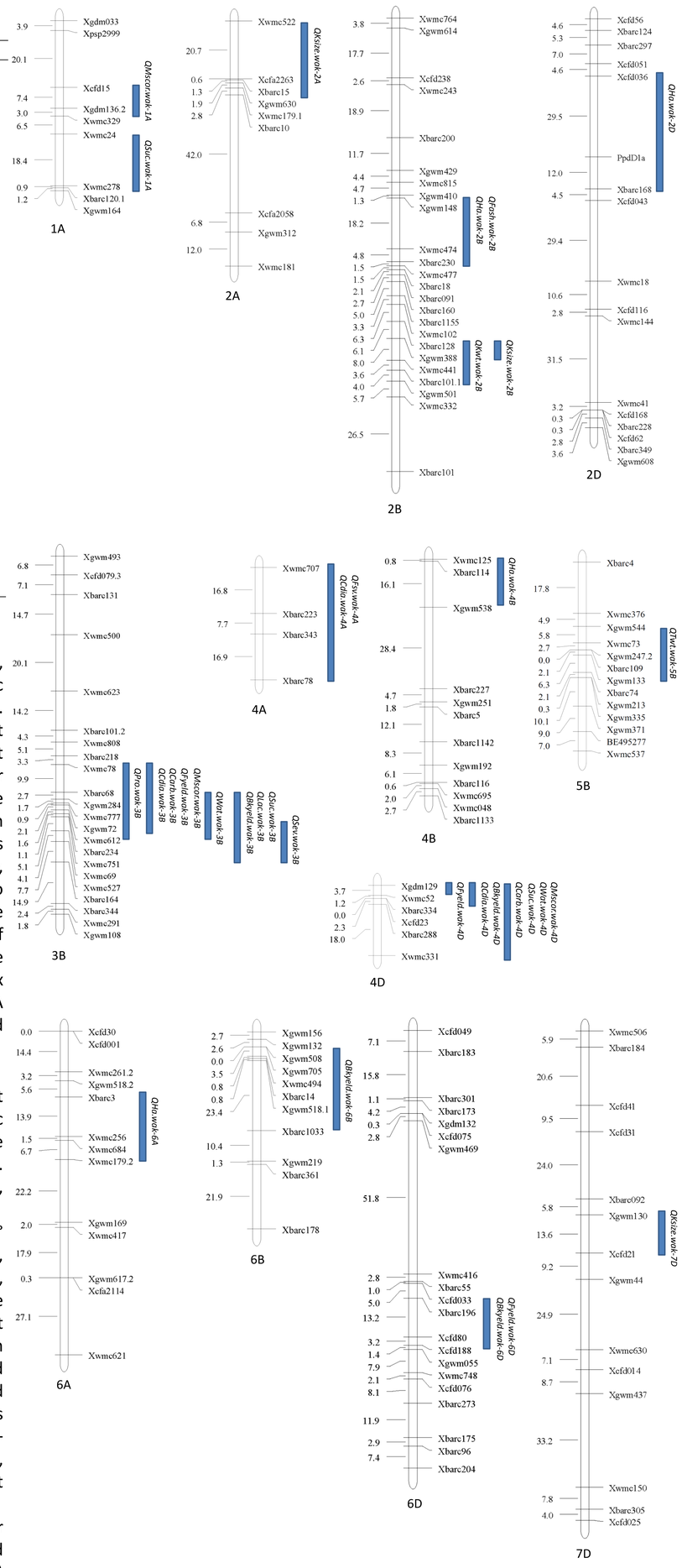

Figure 1. Partial genetic linkage map from the common wheat cross Louise by Penawawa on which 18 end-use quality trait QTL where identified on 12 chromosomes. The vertical bar indicates the QTL region with a LOD score greater than 3.0. Genetic map positions are indicated on the left of each chromosome in Kosambi centiMorgans.

Table 2. Significant quantitative trait loci (QTL) identified through composite interval mapping in a Louise by Penawawa recombinant inbred line mapping population for end-use quality traits at three locations in the Pacific Northwest.

Chromosome	Marker interval	cM	Trait	R^2	LOD	Parental allele[1]
1A	*Xcfd15-Xwmc329*	10.4	Milling score	0.06	3.7	-
	Xwmc24-Xgwm164	20.5	SRC sucrose	0.11	4.8	+
2A	*Xwmc522-Xbarc10*	27.3	Kernel size	0.10	3.4	+
2B	*Xgwm388-Xgwm501*	15.6	Kernel weight	0.11	5.1	-
	Xgwm388-Xwmc441	8.0	Kernel size	0.07	3.2	-
	Xgwm148-Xbarc230	23.0	SKCS hardness	0.13	5.2	-
			Flour ash	0.07	3.1	+
2D	*Xcfd36-Xbarc168*	41.5	SKCS hardness	0.16	7.8	+
3B	*Xwmc78-Xwmc527*	29.2	Protein content	0.14	6.8	-
	Xwmc78-Xwmc69	25.1	Cookie diameter	0.13	7.8	+
			SRC carbonate	0.13	7.2	-
			Flour yield	0.24	14.8	+
			Milling Score	0.21	13.8	+
	Xbarc68-Xbarc164	27.0	Break flour yield	0.12	7.0	+
			SRC lactic acid	0.15	7.3	-
			SRC sucrose	0.24	12.7	-
	Xbarc234-Xbarc164	18.0	SDS sedimentation	0.10	4.4	-
	Xbarc68-Xwmc527	19.3	SRC water	0.09	4.6	-
4A	*Xwmc707-Xbarc78*	41.4	Cookie diameter	0.09	4.5	+
			Flour swelling volume	0.78	67.6	-
4B	*Xwmc125-Xgwm538*	16.9	SKCS hardness	0.14	6.5	+
4D	*Xgdm129-Xwmc52*	3.7	Flour yield	0.07	3.6	+
	Xgdm129-Xbarc288	7.2	Break flour yield	0.06	3.6	+
			Cookie diameter	0.07	4.1	+
	Xgdm129-Xwmc331	25.3	SRC carbonate	0.17	6.8	-
			SRC sucrose	0.07	3.3	-
			SRC water	0.10	4.3	-
			Milling score	0.06	4.2	+
5B	*Xgwm544-Xgwm213*	19.0	Test Weight	0.11	5.2	-
6A	*Xbarc3-Xwmc179.2*	22.1	SKCS hardness	0.07	3.7	+
6B	*Xgwm508-Xbarc1033*	28.5	Break flour yield	0.12	4.6	+
6D	*Xbarc196-Xgwm55*	17.8	Break flour yield	0.10	4.3	+
			Flour yield	0.05	3.3	+
7D	*Xgwm130-Xcfd21*	13.6	Kernel size	0.10	3.7	+

[1] + indicates Louise allele, - indicates Penawawa allele

Results

- A wide range of trait values was detected between both the parental lines as well as within the RIL population (Table 1).
- All traits values had normal distributions, except flour swelling volume, which was bimodal (data not shown).
- Transgressive segregation was seen for all traits except SDS sedimentation (data not shown).
- Trait, marker interval, LOD score, percent phenotypic variation accounted for, and positive allele source are presented in Table 2 and Figure 1.
- The greatest number of traits corresponded to chromosome 3B (13 QTL; 36.9 cM region) and chromosome 4D (7 QTL; 25.3 cM region).

Discussion

- QTL were identified for all of the quality traits analyzed, and were distributed among 12 of the 21 wheat chromosomes. The majority of the positive end-use quality QTL were associated with Louise alleles.
- Both cultivars contain the *PinA* and *PinB* alleles (Girouz and Morris 1998) for grain texture; thus, the QTL for grain hardness contributed to variation within the soft wheat market class to further differentiate hardness.
- The QTL for cookie diameter and flour swelling volume identified on chromosome 4A mapped near the *Wx-B1* locus, which encodes for an important GBSS gene (Miura and Sugwara 1996). The Louise allele at this QTL increased cookie diameter by 0.14 cm and decreased flour swelling volume by four mm among RIL in this population.
- The most significant increase in break flour and flour yield occurred at the 3B locus, at which the Louise allele contributed to a 2% increase in flour yield. The QTL for break flour and flour yield appear to be additive in nature.
- A large population size would need to be sampled in order to recover progeny containing >3 QTL, the practicality of which may not be possible for many breeding programs.
- Under limited resources, the QTL on chromosome 3B and 4D would be the most useful to introgress into new soft white cultivars.
- Using molecular markers to introgress these DNA regions into new soft white wheat cultivars should enhance the efficiency of selection for improved end-use quality in soft white wheat, especially in cross-market class hybridizations.

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