

# Quantitative trait loci associated with kernel weight and test weight in durum wheat

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## ABSTRACT

Kernel weight and test weight are complex traits associated with grain yield and end use quality of durum wheat (*Triticum turgidum* L. spp. durum (Desf)Husn.). A doubled haploid population segregating for kernel weight (KW) and test weight (TW) was developed using the maize pollen method from the cross Kofa//Kyle\*2/Biodur (W9262-260D3). The Kofa parent has higher KW and lower TW compared to the other parent, W9262-260D3 (an F<sub>9</sub> selection). KW and TW were determined in replicated field trials grown at three locations in western Canada, in 2000 through 2002 (7 environments). Data were analysed using mixed-model ANOVA to assess differences among genotypes. The parents were screened for polymorphism with wheat microsatellite markers, and 208 polymorphic markers that followed a 1:1 ratio of parental bands were used to genotype the population. The QTL analysis was performed by composite interval mapping using MapQTL<sup>®</sup>5. Ten QTL affecting KW were localized on chromosomes 1A, 2A, 2B, 3B, 4B, 5B, 6B and 7B. Six QTL were associated with KW at six and seven environments, with substantial differences in phenotypic variation explained in this trait. QTLs at four loci were significantly associated with KW in five or fewer environments and tended to explain less of the variation. The two QTL on 2A and 4B were also significantly related to TW at five and seven environments and explained 5-13% and 4-45% of variation.

**Keywords:** Durum wheat, QTL, Test weight, 1000-grain weight

## INTRODUCTION

High test weight and uniform, large grain size are essential physical attributes in the Canadian durum grading system (4) due their importance in world markets because they indicate sound grain with high flour yield. Test weight is an indicator of wheat quality, and is reported to be positively correlated with milling yield and baking quality (10). Test weight provides a measurement of bulk density, an aid to grain storage and plant capacity (6). Grain weight is a component of grain yield along with spikes per unit area and grain number per spike. Large seeds may emerge more rapidly, resulting in more robust plants with more tillers (3). Kernel weight is related to semolina yield in durum and

high KW is desirable for easy processing, milling and semolina traits (5).

Both TW and KW are quantitatively inherited, and both traits are often influenced by environmental factors and exhibit high genotype–environment interaction (7), making selection difficult. Therefore, identification of microsatellite markers, which are chromosome-specific and evenly distributed along chromosomes (12, 13), would make it possible to identify quantitative trait loci (QTL) that could be used in breeding.

Elouafi and Nachit (2004) reported two QTLs on 7A and 6B for TW and five QTLs on 4B, 6A and 6B for KW in a study of a durum × *Triticum dicoccoides* backcross population. In bread wheat, QTLs have been identified on chromosomes 2B, 2D, 6B (1), 3A, 5A, 6B (2), B1, 4D (8) 6A and 7D (9) for KW. Also QTLs on chromosomes 4A, 5A, 7A, 2D, 4D (8) and, A and 6B (9) have been reported for TW. The objective of this work was to identify and determine the environmental influence on QTL associated with test weight and kernel weight in a durum wheat doubled haploid population.

## MATERIALS AND METHODS

The mapping population consisted of 155 doubled haploid durum lines developed from the cross of Kofa and Kyle\*2/ Biodur (W9262-260D3), an F<sub>9</sub> inbred selection, using the maize pollen method (11). The doubled haploid population, and 13 checks including the parents were sown in an alpha lattice design with two replications at Swift Current in 2000, and at Swift Current, Regina and Indian Head, Saskatchewan Canada in 2001 and 2002. KW was measured in grams and TW in kilograms per hectolitre for each plot. Analyses of variance were performed on each trial, and least squares means for each trait were used in subsequent analyses.

DNA was extracted from leaves of 2-week-old seedlings of lines and parents using a modified cetyltrimethylammonium bromide (CTAB) method. Parental DNA was tested with microsatellite primer pairs (12, 13). Primers that were polymorphic between the parents were tested on the entire population. The chi-square ( $\chi^2$ ) test for goodness of fit was used to determine if each marker locus in the doubled haploid population had a 1:1 ratio of parental bands. JoinMap<sup>®</sup>4 was used to determine

linkage and order of markers (14). Least square means of the trait data were used in genetic analyses. MapQTL®5 was used to identify QTLs controlling the traits (15).

## RESULTS AND DISCUSSION

The ANOVA for genotype effects revealed variation ( $P < 0.01$ ) among the lines. Kofa showed greater KW and lower TW compared to W9262-260D3. The mean of the DH population fell within the range of the parental values, but some of the lines showed considerable transgressive segregation for both traits, indicating quantitative inheritance.

Environment has an important influence on loci involved in the control of KW. Table 1 shows that some QTL,

**Table 1. QTL for Kernel Weight, level of significance, additive effect, percent of variation explained by the QTL and marker interval.**

QTL	Env.	Sig.	Add <sup>a</sup> (g)	% Expl.	Marker Interval
<b>QGw.spa-1AS</b>					
SC00	*		1.14	7.6	Xwmc95-Xbarc148
SC01	***		1.15	13.3	Xbarc197-Xbarc83
SC02	*		0.98	8.1	Xwmc95-Xbarc148
<b>QGw.spa-2AS</b>					
IH01	***		1.06	14.1	Xbarc10-Xwmc114
IH02	***		1.35	13	Xbarc10-Xwmc114
RG01	*		0.88	7.2	Xbarc10-Xwmc601
RG02	**		0.98	6.7	Xbarc10-Xwmc114
SC00	***		1.54	13.9	Xbarc10-Xwmc114
SC01	*		0.81	6.5	Xwmc601-Xgwm425
<b>QGw.spa-2BL</b>					
IH01	*		-0.83	8.6	Xwmc586-Xbarc101
IH02	*		-1.14	9.4	Xwmc586-Xbarc101
RG01	*		-0.88	7.1	Xwmc586-Xbarc101
RG02	*		-1.25	10.8	Xwmc586-Xbarc101
SC00	***		-1.81	19.3	Xbarc361-Xgwm47
SC01	***		-1.39	19.5	Xbarc361-Xwmc332
SC02	**		-1.2	12.1	Xwmc586-Xwmc175
<b>QGw.spa-3BL1</b>					
IH01	***		0.8	8	Xbarc1152-Xbarc218
IH02	*		0.87	5.5	Xbarc1152-Xbarc164
RG01	**		0.99	9	Xbarc1152-Xbarc164
RG02	**		1.01	7	Xbarc1152-Xbarc164
SC00	**		1.21	8.5	Xbarc1152-Xbarc218
SC02	*		0.92	7.2	Xbarc1152-Xbarc164
<b>QGw.spa-3BL2</b>					
SC01	*		-0.68	4.7	Xgwm114-Xgwm247
SC02	**		-0.86	6.3	Xgwm114-Xgwm247
<b>QGw.spa-4BL</b>					
IH01	**		-0.9	10.2	Rht-B1b-Xgwm251
IH02	***		-2.06	30.6	Rht-B1b-Xgwm251
RG01	***		-1.42	18.7	Rht-B1b-Xgwm251
RG02	***		-2.45	42	Rht-B1b-Xgwm251
SC00	***		-2.17	27.5	Rht-B1b-Xgwm251
SC01	*		-0.87	7.5	Rht-B1b-Xgwm251
SC02	***		-1.8	27.3	Rht-B1b-Xgwm251

Table 1 continued.

<b>QGw.spa-5B</b>					
IH01	*		0.89	10	OPC20-Xwmc415
IH02	**		1.23	10.8	Cdu1-Xwmc415
RG02	***		1.55	16.8	Cdu1-Xwmc415
SC00	**		1.44	12.1	Cdu1-Xwmc415
SC01	**		1.08	11.7	Cdu1-Xwmc415
SC02	**		1.14	11	Xbarc337-Xwmc415
<b>QGw.spa-6B1</b>					
IH01	***		0.85	9	Xgwm88-Xbarc79
IH02	*		0.93	6	Xgwm88-Xbarc79
RG02	**		0.99	6.6	Xgwm88-Xbarc79
SC00	***		1.38	10.9	Xbarc129.2-Xbarc79
SC01	***		1.03	10.4	Xbarc14-Xbarc79
SC02	*		0.75	4.7	Xbarc125
<b>QGw.spa-6B2</b>					
IH01	**		0.79	7.8	Xgwm5-Xgwm133
RG02	**		1.08	8.2	Xgwm5-Xgwm133
SC02	*		0.69	4.1	Xbarc306
<b>QGw.spa-7B</b>					
RG01	*		0.81	6.1	Xbarc172-Xgwm537
RG02	**		1	6.9	Xbarc72-Xgwm537

<sup>a</sup>Additive effect: -ve associated with W9262-260D3, +ve associated with Kofa. \* $<5\%$ , \*\* $<1\%$ , \*\*\* $<0.1\%$  level of significance. SC=Swift Current, IH=Indian Head, RG=Regina, 00=2000, 01=2001 and 02=2002.

such as QGw.spa-2BL and QGw.spa-4BL, were expressed in all seven environments. However the level of KW variation explained varied from environment to environment. Other QTL, such as QGw.spa-7B, were sporadic. Some QTL, such as QGw.spa-3BL1, explain a small portion of the variation for KW. Yet QTL, such as QGw.spa-4BL, explain a substantial amount of the variation for KW. The position of a QTL for KW on chromosome 4B corresponds to a QTL detected by Elouafi and Nachit (2004). The *Rht-B1b* dwarfing allele is also known to affect KW and TW and is located on 4B. A marker for *Rht-B1b* applied in our population was coincident with the KW QTL. In all, we identified ten loci that influence KW, although QGw.spa-3BL2 and QGw.spa-7BL are more tentative QTL given they were expressed in only two environments at a lower level of statistical significance. Similar to our results, others have reported KW QTL on 6B in durum wheat (5) and bread wheat (1, 2).

We identified fewer QTL for TW than KW, but note expression also varied with environment with some QTL (Table 2). Once again the *Rht-B1b* marker was evident, appearing as a strong QTL for TW and present as a QTL marker in all environments. None of the loci reported for TW on chromosomes 7A and 6B in durum wheat (5) or on chromosomes 4A, 5A, and 7A, (8) in bread wheat were identified here. This could be due to population effects, environments, or the low density of markers on our map. Both KW and TW mapped in similar positions, which is particularly evident for chromosome 2A (Table 1 and 2), which could be a reason for the high correlation ( $r=0.56$  based on line

means) between these traits. Positive relationships between KW and TW have been reported in durum wheat (7). However the marker density in this study was not sufficient to decide whether these QTLs revealed pleiotropic effects or were due to linked QTLs.

The results demonstrate the importance of understanding which QTL function in the environment in which the QTL may be deployed. Loci that respond most consistently and to the greatest extent in the target environment are the prime candidates for marker assisted selection.

**Table 2. QTL for Test Weight, level of significance, additive effect, percent of variation explained by the QTL and marker interval.**

QTL	Env.	Sig.	Add <sup>a</sup>	% Expl.	Marker Interval
Effect			(g)		
QG vwt spa-1AL					
IH01	*	0.34	2.1	Xbarc213-Xgwm99	
RG02	**	0.42	7.3	Xbarc211-Xbarc213	
QG vwt spa-1AS					
IH02	**	0.55	8.2	Xbarc197-Xwmc95	
SC00	*	0.34	5.9	Xbarc197-Xwmc95	
SC01	*	0.34	6	Xbarc197-Xbarc148	
SC02	*	0.4	6.8	Xbarc197-Xwmc95	
QG vwt spa-2AS					
IH02	**	0.6	9.8	Xbarc10-Xgwm425	
RG01	***	0.39	11.3	Xbarc10-Xwmc114	
RG02	*	0.35	5	Xwmc601-Xgwm425	
SC00	**	0.44	9.6	Xbarc10-Xwmc51	
SC01	***	0.5	13	Xbarc10-Xgwm425	
QG vwt spa-3BL					
SC02	*	-0.3	3.9	Xgwm247	
QG vwt spa-4BL					
IH01	**	-0.47	3.9	RhtB1b-Xgwm251	
IH02	***	-1.06	30.6	RhtB1b-Xgwm251	
RG01	***	-0.6	27.1	RhtB1b-Xgwm251	
RG02	***	-0.98	39.8	RhtB1b-Xgwm251	
SC00	***	-0.95	42.9	RhtB1b-Xgwm251	
SC01	***	-0.7	25	RhtB1b-Xgwm251	
SC02	***	-1.04	45.3	RhtB1b-Xgwm251	
QG vwt spa-7B					
RG02	*	0.35	5.1	Xgwm537	

<sup>a</sup>See footnote to Table 1.

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