

QTL Validation for Agronomic Traits on 3A Chromosome of Winter Wheat (*Triticum aestivum*) Using Recombinant Inbred Chromosome Lines

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INTRODUCTION

Quantitative trait loci (QTLs) that control agronomic traits such as grain yield and its components are the most important economic traits for wheat (*Triticum aestivum* L.) improvement. Based on a previous study conducted using reciprocal chromosome substitution lines between winter wheat cultivars 'Wichita' (WI) and 'Cheyenne' (CNN), recombinant inbred chromosome lines (RIcLs) developed for the 3A chromosome in the CNN background CNN(RIcLs-3A) indicated the presence of a major grain yield QTL that explained up to 28% of the phenotypic variance (Berke et al., 1992a, b; Campbell et al., 2003).

In the current study a population of WI(RIcLs-3A) where the RIcLs involve WI and CNN chromosome 3A in WI background was used to validate the QTLs detected in the CNN(RIcLs-3A) population. Effectively, WI(RIcLs-3A) is a mirror population to the previously studied CNN(RIcLs-3A).

Therefore, the objectives of this study were to (1) identify and map QTLs for eight agronomic traits; (2) evaluate QTL x environment interaction (QEI) by comparing the consistency of QTLs detected in individual environments and; (3) determine the presence of common QTLs between the current population, WI(RIcLs-3A), and the previous mapping population, CNN(RIcLs-3A).

MATERIALS AND METHODS

A population of 90 WI(RIcLs-3A) doubled haploid (DH) lines of the cross between cultivar Wichita (WI) and chromosome substitution line WI(CNN3A) were used to investigate QTLs for grain yield and other agronomic traits. The WI(RIcLs-3A) population, parents and checks were grown in six environments (year x location) during the 2007/2008-2008/2009 cropping season at four sites in Nebraska (Lincoln, Mead, North Platte and Sidney). The experiment was evaluated in an incomplete block design with three-replications where each replication consisted of 20 incomplete blocks of 5 plots.

The agronomic traits evaluated include days to flowering (DF), plant height (PH), grain yield (GY), grain volume weight (GVW), 1000-kernel weight (TKW), kernels per spike (KPS), kernels per square meter (KPSM), and spikes per square meter (SPSM). Phenotypic traits were analyzed following the PROC MIXED procedure of the SAS version 9.1 (SAS Institute, 2004). Prior to the combined analysis, homogeneity of error variances was checked with the Bartlett's Chi-square test as outlined by Gomez and Gomez (1984).

MAPMAKER/ EXP3.0 program (Lander et al. 1987) was used for marker diagnostics and to determine the linkage groups. The map for the QTLs analysis was constructed from a single linkage group of 26 SSR markers. Identification of QTLs was performed using WinQTL cartographer v.2.5 (Statistical Genetics, NCSU, Raleigh, NC).

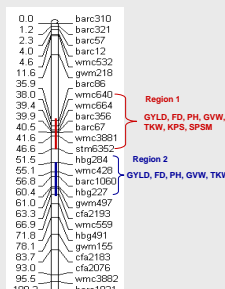


Fig. 1. Position of QTLs detected on chromosome 3A

RESULTS AND DISCUSSION

The ANOVA of all eight agronomic traits for the individual environments and for the combined analysis were highly significantly different ($P \leq 0.01$) (data not shown). Significant correlations were observed between grain yield and most of the yield components. Grain volume weight and yield component traits such as 1000-kernel weight, kernels per spike, kernels per square meter, and spikes per square meter were all positively correlated with grain yield (Table 1). The parents showed significant differences for most of the phenotypic traits (Table 2).

QTLs were detected for seven of the eight agronomic traits (Table 3, Fig. 1). These QTLs explained from 12 % (for spikes per square meter) to 53 % (for grain volume weight) of the phenotypic variance of each trait. A grain yield QTL detected in the combined analysis explained 19 % of the phenotypic variance and the substitution of CNN allele for a WI allele decreased grain yield by 86 kg ha⁻¹ (Table 3). This grain yield QTL is believed to be the major grain yield QTL detected in CNN(RIcLs-3A) population as it mapped to a similar position (Fig. 1 and Table 3). In addition, a major QTL that affected days to flowering with 23 % of R² value was identified at North Platte during the 2007/2008 cropping season (Table 3). This flowering date QTL overlapped with plant height QTL (31 % R² value on across environment) that was detected in more than two environments (Fig. 2). Also there was an observable phenotypic difference in flowering days of the two parents and cultivar Cheyenne (Fig. 3).

Table 2. Mean phenotypic values for parents and RIcLs-3A in individual and across environments

Trait name	Environment	Parents		RIcLs3A					
		WI	WI(CNN3A)	Estimate	Standard Error	Pr > R	Mean	Range	Standard deviation
Days to flowering	LNK_08	152.9	154.8	-2.0	0.46	<.0001	152.9	150.0 - 155.0	1.31
	NP_08	151.5	155.1	-2.1	0.46	<.0001	153.8	152.0 - 156.8	0.98
	LNK_09	142.8	144.5	-1.7	0.45	<.0001	145.0	140.2 - 145.0	1.10
	MD_09	144.8	147.5	-2.7	0.47	<.0001	146.7	141.9 - 146.7	1.28
	NP_09	145.6	148.3	-2.7	0.40	<.0001	147.7	145.2 - 149.9	0.94
	Combined	148.1	150.15	-2.1	0.35	<.0001	148.5	139.0 - 158.0	4.46
	SD_09	106.6	116.8	-10.2	1.89	<.0001	104.4	97.0 - 110.0	4.82
Plant height (cm)	LNK_08	119.3	123.5	-5.3	2.42	<.0017	117.5	104.0 - 123.3	3.63
	LNK_09	83.9	98.0	-14.1	2.22	<.0001	90.7	82.6 - 105.0	4.00
	MD_09	96.8	101.4	-4.6	2.40	0.056	97.9	89.2 - 110.0	4.74
	NP_09	113.0	123.7	-10.8	2.17	<.0001	118.7	109.5 - 127.6	3.96
	SD_09	94.1	100.5	-6.4	2.18	0.0039	91.3	75.1 - 104.4	4.84
	Combined	102.1	110.6	-8.4	1.93	<.0001	104.1	73.7 - 129.5	11.80
	LNK_08	278.7	219.9	58.8	346.24	0.0002	266.4	129.0 - 362.0	48.39
Grain yield (kg ha ⁻¹)	NP_08	4759.8	4378.1	421.8	251.74	<.0001	4670.5	2344.5 - 4903.3	419.71
	LNK_09	4147.5	3500.3	647.2	263.75	0.0164	3967.7	3332.8 - 4522.2	317.86
	MD_09	4073.7	3510.9	562.8	288.02	0.0528	3584.8	2476.6 - 4388.5	387.64
	NP_09	3518.9	3062.1	456.8	211.37	0.0034	3660.9	2664.2 - 3931.1	260.03
	SD_09	3812.9	3285.1	527.8	179.93	0.0039	4053.8	2912.8 - 4058.4	221.42
	Combined	3863.2	3319.2	543.9	186.06	0.0016	3612.0	1201.0 - 6929.0	770.60
	LNK_08	74.6	72.7	1.9	0.279	0.0038	73.7	71.0 - 75.0	0.87
Grain volume weight (kg HL ⁻¹)	NP_08	76.8	74.9	1.9	0.98	0.0578	76.3	69.9 - 79.5	1.28
	LNK_09	82.1	80.6	1.5	0.51	0.0045	81.9	79.2 - 82.6	0.67
	MD_09	74.8	73.5	1.4	0.86	0.0983	75.2	70.1 - 76.1	1.08
	NP_09	74.2	73.8	0.4	0.66	0.5354	74.7	71.8 - 75.7	0.76
	SD_09	75.6	74.1	1.5	0.50	0.004	76.7	74.3 - 77.6	0.74
	Combined	76.3	75.0	1.4	0.45	0.0025	76.0	67.1 - 85.8	2.96
	LNK_08	39.2	33.9	5.3	2.10	0.0049	36.5	29.9 - 37.0	1.98
100-kernel weight (gram)	NP_08	38.5	38.5	0.0	1.11	0.9915	38.0	34.4 - 41.1	1.41
	LNK_09	38.0	39.6	-1.7	1.37	0.2291	38.3	34.3 - 41.5	1.31
	MD_09	39.4	37.1	2.2	1.59	0.1596	38.2	32.3 - 41.4	1.71
	NP_09	31.6	31.8	-0.2	1.92	0.9165	34.7	28.7 - 35.0	1.49
	SD_09	34.2	35.7	-1.4	1.22	0.2403	36.5	31.8 - 37.3	1.25
	Combined	35.7	36.1	-0.4	0.74	0.0057	35.8	17.5 - 45.4	3.62
	LNK_08	28.2	22.2	6.0	2.12	0.0063	23.1	17.7 - 29.1	2.98
Kernels per spike	NP_08	21.7	23.4	-1.7	1.59	0.2785	23.1	19.7 - 25.9	1.34
	LNK_09	32.7	34.9	-2.2	2.10	0.2898	36.1	28.0 - 39.4	2.31
	MD_09	32.2	31.1	1.2	1.91	0.5446	31.2	28.5 - 36.7	1.77
	NP_09	25.4	22.7	2.7	1.65	0.1063	23.3	19.6 - 27.2	1.55
	SD_09	19.5	21.9	-2.3	1.80	0.138	24.3	20.6 - 28.8	1.48
	Combined	29.3	29.3	0.0	2.84	0.9916	26.4	15.2 - 45.0	5.59
	LNK_08	8504.6	6697.8	1806.7	1212.32	0.0184	6918.2	5142.0 - 12097.0	1574.01
Kernels per square meter	NP_08	12472.0	11317.0	1155.0	763.93	0.0328	12028.0	6864.1 - 13019.0	954.80
	LNK_09	10665.0	8835.5	2111.5	739.39	0.005	10367.0	8189.0 - 12417.0	861.31
	MD_09	10465.0	9472.1	992.9	830.21	0.2337	9344.1	6847.9 - 11379.0	909.61
	NP_09	11131.0	9663.6	1467.4	924.45	0.1147	11024.0	8150.1 - 12573.0	875.09
	SD_09	11148.0	9196.2	1948.8	629.99	0.0024	11083.0	8489.2 - 11917.0	650.34
	Combined	10779.0	9196.4	1600.6	504.50	0.0016	10112.0	3864.0 - 21728.0	2017.00
	LNK_08	330.9	302.1	28.8	69.04	0.0772	281.1	194.5 - 564.7	80.82
Spikes per square meter	NP_08	578.2	493.7	84.5	52.02	0.1064	522.3	323.6 - 616.0	51.56
	LNK_09	337.4	253.7	83.6	30.90	0.0076	290.0	244.6 - 422.9	33.80
	MD_09	326.7	314.2	12.5	28.46	0.6611	302.5	191.2 - 376.8	33.33
	NP_09	431.9	418.1	13.8	49.06	0.3716	479.2	375.6 - 555.0	48.44
	SD_09	575.9	426.8	148.2	47.01	0.0019	456.4	337.9 - 529.9	38.36
	Combined	431.9	368.4	63.5	24.26	0.0001	356.7	143.9 - 656.5	109.84

Table 3. Summary of QTLs detected in 90 WI(RIcLs-3A) population for agronomic, yield, and yield components traits at each environments and combined analysis

No.	QTL	Trait name	Environment	LOD score	Flanking markers	Most significant marker	% variation explained (R ²)	Additive effect	Peak position (cM)	Contributor parent
1	QTL _{neb-3A.1}	Days to flower (days)	NP08	5.1	barc06 - stm6352	wmc640	23	-0.45	38.0	CNN
2	QTL _{neb-3A.2}	Days to flower (days)	NP08	2.8	stm6352 - hbq284	hbq284	19	-0.39	51.1	CNN
3	QTL _{neb-3A.3}	Plant height (cm)	NP08	6.2	wmc218 - wmc664	wmc640	23	-1.61	38.0	CNN
4	QTL _{neb-3A.2}	Plant height (cm)	NP08	3.9	stm6352 - hbq284	hbq284	19	-1.45	51.1	CNN
5	QTL _{neb-3A.3}	Plant height (cm)	LNK09	3.9	stm6352 - wmc559	barc1090	18	-1.96	56.8	CNN
6	QTL _{neb-3A.4}	Plant height (cm)	MD09	3.1	wmc388.1 - gwm497	wmc428	15	-1.76	55.6	CNN
7	QTL _{neb-3A.5}	Plant height (cm)	NP09	5.5	wmc218 - wmc664	wmc640	25	-1.87	39.0	CNN
8	QTL _{neb-3A.6}	Plant height (cm)	SD09	5.3	hbq284 - gwm497	barc1090	26	-2.20	57.8	CNN
9	QTL _{neb-3A.7}	Plant height (cm)	Combined	7.1	barc06 - barc67	wmc640	31	-1.62	38.0	CNN
10	QTL _{neb-3A.8}	Plant height (cm)	Combined	6.3	stm6352 - hbq284	stm6352	28	-1.55	50.1	CNN
11	Oytl _{neb-3A.1}	Grain yield (kg ha ⁻¹)	LNK08	2.8	barc06 - wmc388.1	wmc640	13	173.00	38.0	WI
12	Oytl _{neb-3A.2}	Grain yield (kg ha ⁻¹)	NP09	3.4	stm6352 - ct2193	barc1090	17	101.00	58.8	WI
13	Oytl _{neb-3A.3}	Grain yield (kg ha ⁻¹)	Combined	4.0	barc06 - stm6352	wmc640	19	86.60	38.0	WI
14	Oytl _{neb-3A.4}	Grain yield (kg ha ⁻¹)	Combined	3.6	stm6352 - hbq284	hbq284	17	82.40	51.1	WI
15	OGw _{neb-3A.1}	Grain volume weight (kg HL ⁻¹)	LNK08	8.9	barc06 - stm6352	wmc388.1	39	0.52	42.6	WI
16	OGw _{neb-3A.2}	Grain volume weight (kg HL ⁻¹)	NP08	3.8	wmc664 - stm6352	wmc388.1	18	0.45	41.6	WI
17	OGw _{neb-3A.3}	Grain volume weight (kg HL ⁻¹)	LNK09	13.5	barc06 - stm6352	wmc388.1	49	0.44	41.6	WI
18	OGw _{neb-3A.4}	Grain volume weight (kg HL ⁻¹)	MD09	8.4	gwm218 - wmc640	barc06	35	0.58	35.6	WI
19	OGw _{neb-3A.5}	Grain volume weight (kg HL ⁻¹)	NP09	8.2	barc06 - stm6352	wmc640	35	0.42	36.9	WI
20	OGw _{neb-3A.6}	Grain volume weight (kg HL ⁻¹)	NP09	7.6	stm6352 - wmc428	hbq284	32	0.40	51.1	WI
21	OGw _{neb-3A.7}	Grain volume weight (kg HL ⁻¹)	Combined	14.9	barc06 - stm6352	wmc388.1	53	0.39	41.6	WI
22	OGw _{neb-3A.8}	Grain volume weight (kg HL ⁻¹)	Combined	14.0	stm6352 - wmc428	hbq284	50	0.39	51.1	WI
23	OTg _{wneb-3A.1}	Thousand-kernel weight (gm)	LNK08	4.1	barc07 - stm6352	wmc388.1	19	0.80	41.6	WI
24	OTg _{wneb-3A.2}	Thousand-kernel weight (gm)	NP08	3.4	stm6352 - wmc559	gwm497	16	0.53	61.0	WI
25	OTg _{wneb-3A.3}	Thousand-kernel weight (gm)	Combined	4.9	barc06 - wmc664	wmc640	21	0.43	38.0	WI
26	OTg _{wneb-3A.4}	Thousand-kernel weight (gm)	Combined	4.3	stm6352 - hbq284	hbq284	19	0.41	51.1	WI
27	OKps _{neb-3A}	Kernel per spike (number)	SD09	2.8	wmc640 - barc356	wmc664	13</			