

# Inheritance and QTL analysis of dough rheological parameters in wheat

Caiying ZHANG (✉)<sup>1,2\*</sup>, Changhai DONG<sup>1,2\*</sup>, Jun MA<sup>1,2,3</sup>, Guijun YAN<sup>1,2,3</sup>, Chunji LIU<sup>1,2,3</sup>, Guangmin LI<sup>1</sup>

<sup>1</sup> College of Life Sciences, Agricultural University of Hebei, Baoding 071001, China

<sup>2</sup> CSIRO Plant Industry, Brisbane 4067, Australia

<sup>3</sup> School of Plant Biology, The University of Western Australia, Perth, 6009, Australia

© Higher Education Press and Springer-Verlag Berlin Heidelberg 2011

**Abstract** A RIL population from two Australian wheats, Lang and CSCR6, was employed to evaluate the genetic variation and to detect QTL associated with dough rheological characters based on DArT and SSR markers and two environmental experiments. It was showed that the higher variation existed in the RIL for dough rheological characters, and so did much more abundant selection potentials that lacked in Chinese current commercial varieties. Nine additive QTLs for dough rheological characters were identified. Of which those for water absorption (WA) were located on chromosome 2A and 5A, stability time (ST) on 4B and 1B, breaking time (BT) on 1B, degree of softening (DS) on 1B, band width (BW) on 2B (two loci), evaluation value (EV) on 1B. And seven epistatic QTLs were screened out, and non-significant variance was found for the interaction between these epistatic QTLs and the environment. Correlation analysis indicated that there was a significantly positive relation between WA and development time (DT), and EV, whereas negatively related to BW. A significantly positive relation existed between DT, ST, BT and EV each other. They were negatively related to mixing tolerance index (MTI) and degree of softening (DS), both had a markedly positive relation.

**Keywords** dough rheological characters, quality properties, QTL, DArT, additive effect

## Introduction

Improving bread baking quality is one of the most important targets for quality breeding program in wheat. Bread baking quality is usually affected by the dough rheological parameters which are quantitatively inherited traits. There is a low efficiency for such kind of traits based on the phenotypic selection in traditional breeding. Genetic mapping and quantitative trait loci (QTL) analysis make it possible to dissect QTL controlling the quality traits and to increase the forecast feasibility of selection.

Quite a few studies have been carried out in QTL detection for quality characters by using various genetic populations and molecular markers in wheat. QTLs analysis on dough rheological characters and bread baking quality with 182 DH lines showed that the QTLs associated with dough water

absorption were detected on chromosome 1A, 1B, 2A and 2D, as well as those were linked to dough development time on chromosome 1B, dough stability on 1A, 1B and 2A, dough strength and loaf volume on chromosome 2A and 3A (Kuchel et al., 2006). Eight QTLs associated with dough rheological parameters were identified by using 165 RILs, which gave 5.4%–26.6% explanation of phenotypic variance. Those on chromosome 3A and 5B also affected the grain hardness and protein content (Groos et al., 2004). Ninety-nine QTLs controlling 47 quality characters, including milling, dough rheological, baking, starch and noodle color etc., were screened out by McCartney et al. (2006) using 182 DH lines. They were located on 18 chromosomes, and of which, 44 were mapped to three major QTL clusters on chromosomes 1B, 4D and 7D. Major-effect QTLs were detected for grain and flour protein content, farinograph absorption, mixograph parameters and dietary fiber on chromosome 2BS. In another research, the dough properties of 204 RILs from a cross between wheat and spelt assessed in different environments indicated that nine QTLs were found for Zeleny sedimentation values explaining 47% of the phenotypic variance. For the alveograph parameters, 10 QTLs were

Received October 10, 2010; accepted November 8, 2010

Correspondence: Caiying ZHANG

E-mail: Zhangcaiying@hebau.edu.cn

\*These authors contributed equally to this work.

found for baking strength, nine for tenacity, seven for configuration ratio, and four for elasticity index and extensibility (Zanetti et al., 2001). Also, analysis of dough rheological parameters with 165 DH lines found that the main additive QTL for dough rheological properties were located at the high- and low-molecular-weight glutenin loci. A new QTL on chromosome 5A for M-extensibility was detected, and the genotypic factors were the major determinants of dough strength (Ma et al., 2005).

The objectives of this study were to evaluate the genetic bases of an RIL population from wheat and spelt, and to identify QTLs controlling wheat dough rheological characters using SSR and DArT markers.

## Materials and methods

### Plant materials

The mapping population was RILs derived from a cross between an Australian hexaploid wheat and a spelt, Lang and CSCR6 (Ma et al., 2009). Lang is a high yielding cultivar extensively grown in Queensland and New South Wales, and CSCR6 belongs to the taxon *T. spelt*. Ninety-two RILs and the two parents were planted in Baoding and Zhangjiakou, Hebei province in 2010. The experiments were randomly arrayed with three replications, and four lines were planted for each RIL line with 2.5 m (40 seeds) in length and 25 cm spacing from each other.

### Determination of dough rheological properties

Dough rheological properties were measured using a farinograph (Brabender, Germany) according to AACC method 54–21 (American Association of Cereal Chemists, 1983). The parameters include water absorption (WA), development time (DT), stability time (ST), mixing tolerance

index (MTI), breaking time (BT), degree of softening (DS), band width (BW) and evaluation value (EV).

### QTL analysis

The means, standard errors, skewness, kurtosis and correlation coefficients for the dough rheological characters of the RIL population were calculated by using a software, SPSS Statistics 17.0. Genetic mapping was conducted using 967 polymorphic DArT and 54 SSR markers, of which, 776 markers were located on 18 out of 21 chromosomes in wheat. The linkage groups were 912.9 cM long in total with an averaged interval of 1.2 cM between markers (Ma et al., 2009). The QTL analysis was carried out via QTL Network-2.1, and *F* significance test via Henderson method III. One dimensional scan was served to detect major-effect QTL, and two dimensional scan to detect epistatic-effect QTL. The Permutation method was employed to test QTL significance and probability level for whole genome scan was  $P=0.05$ . The distribution of various QTL effects were determined by Bayesian method based on Gibbs sampling (Yang et al., 2005, 2008).

## Results and analysis

### Phenotypic variation of the RIL population

The differences existed among the dough rheological properties in the RIL population and their parents (Tables 1, and 2). Higher WA, DT, ST, BT and EV were found for Lang than those for the male parent, CSCR6. Dough rheological properties of CSCR6 were more stable in two environments, whereas those of Lang varied more, as the DT, ST, BT and EV were 9.6/6.9, 18.9/6.4, 30/14.5 and 80/69 at Baoding/Zhangjiakou locations, respectively. All the dough rheological parameters were normally distributed in the RIL

**Table 1** Dough rheological traits of RIL population at two locations

parameter		WA	DT	ST	MTI	BT	DS	BW	EV
L1	mean	65.42	8.56	13.87	13.90	21.71	28.68	69.42	74.23
	max	72.40	22.30	32.40	55.00	40.50	110.00	100.00	93.67
	min	57.80	4.60	4.00	0.00	9.00	0.00	47.33	58.00
	SD	2.57	2.79	6.09	11.50	6.41	21.21	9.05	7.56
	CSCR6	62.60	6.90	8.20	20.00	16.50	50.00	62.00	67.00
	Lang	66.00	6.90	6.40	29.00	14.50	35.00	70.00	69.00
L2	mean	61.43	9.33	16.49	8.37	24.67	19.80	77.96	75.22
	max	70.40	19.70	28.00	62.67	38.50	134.00	110.00	95.00
	min	54.20	3.47	4.00	0.00	8.80	0.00	49.00	54.00
	SD	3.11	3.74	5.88	11.14	6.23	20.07	13.34	8.92
	CSCR6	60.20	4.90	8.00	18.00	17.30	25.00	80.00	63.00
	Lang	64.00	9.60	18.90	5.00	30.00	0.00	70.00	80.00

Note: L1 represents Zhangjiakou location; L2 represents Baoding location.

**Table 2** Basic statistic parameters of eight dough rheological traits for RILs and their parents

trait	parent		RILs				
	Lang	CSCR6	average	rang	SD	skewness	kurtosis
WA/%	65.00	61.40	63.43	57.3–71.4	2.67	0.10	–0.05
DT/min	8.25	5.90	8.95	4.57–15.10	2.46	0.57	–0.54
ST/min	12.65	8.10	15.18	4.25–26.70	4.83	0.20	0.15
MTI/BU	17.00	19.00	11.14	0.00–41.33	8.75	0.98	1.00
BT/min	22.25	16.90	23.19	9.50–34.50	5.27	–0.16	0.18
DS/BU	17.50	37.50	24.24	0.00–82.00	16.01	0.98	1.00
BW/BU	70.00	71.00	73.69	53.67–100.00	9.57	0.07	–0.32
EV	75.50	65.00	74.72	58.67–92.17	6.82	0.09	–0.16

population, and high genetic variations were discovered between sites and RIL lines. The variation coefficients ranked as  $MTI > DS > ST > DT > BT > BW > EV > WA$ . Some dough rheological parameters showed a higher value than Chinese wheat cultivars, such as DT (8.95), ST (15.18), BT (23.19) and EV (74.72). It is valuable to the improvement of quality properties for Chinese common wheat. On all accounts, the tested RIL population and its parents contained abundant genetic variations and selection potentials in dough rheological properties.

Correlation analysis indicated that the WA was significantly positively related to DT and EV, and negative to BW. There was a significantly positive relation between DT, ST, BT and EV each other, and they were remarkably negatively related to MTI and DS (Table 3). All the marked relations among the characters determined suggest that there exists the genetic linkage or one-gene-multiple effect.

### QTL analysis of dough rheological traits

The QTL analysis showed that nine QTLs were detected for the dough rheological traits, with additive effect and 5.81%–16.91% explanation of phenotypic variation (Table 4, Fig. 1). These QTLs were located on chromosome 1B, 2A, 2B, 4B and 5A, respectively, of which four on 1B with over 10.0% explanation of phenotypic variance. Two QTLs for ST located on 1B and 4B explained 16.91% and 6.74%

phenotypic variance and could make the dough stability time increased 2.255 min and 1.352 min, respectively, which come from Lang's alleles.

Two QTLs for WA located on 2A and 5A could give increased effects on flour water absorption via the alleles of Lang and CSCR6. The WPT-8832-WPT-1675 locus was simultaneously linked to four dough rheological traits, ST, BT, DS and EV, indicating the presence of one-gene-multiple effect. In addition, non-significant interaction effect was found for all the detected QTLs, suggesting that they are mainly controlled by additive loci, and more stable and easy for use.

Analysis of epistatic effect indicating that seven pairs of additive $\times$ additive effects of QTLs were identified for WA, BT, DS, MTI, BW, EV, involving chromosome 1B, 2A, 2B, 3A, 3B, 3D and 4A with 5.03%–11.70% explanation of phenotypic variance (Table 5). All the epistatic effects came from the interactions between non-linked loci, i.e. the interaction between different chromosomes. Moreover, no significant interaction was found between any epistatic effect and environment, showing the epistatic QTLs were impacted little by environment. A locus, WPT-6738-WPT-4153, appeared epistatic QTL with both WPT-0940-WPT-2559 and WPT-7614-WPT-5072.

It also can be seen that the nine additive QTLs (Table 4) and seven epistatic QTLs (Table 5) dealt with nine chromosomes. However, it seems that the additive QTL did not play a role in the epistatic.

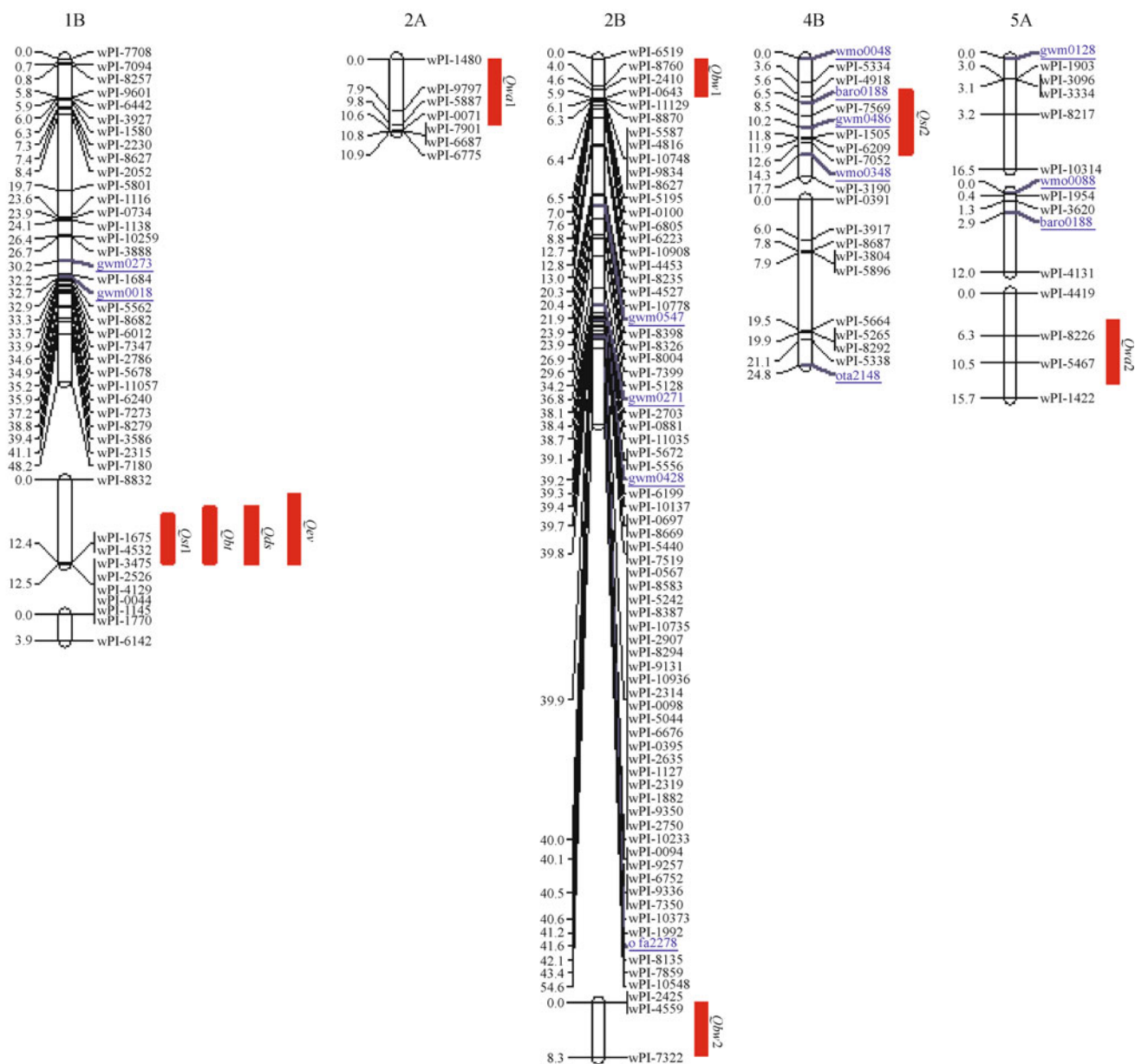
**Table 3** Correlation coefficients between dough rheological traits in the RIL population

trait	WA	DT	ST	MTI	BT	DS	BW
DT	0.366**	–	–	–	–	–	–
ST	0.042	0.603**	–	–	–	–	–
MTI	–0.119	–0.304**	–0.726**	–	–	–	–
BT	0.176	0.705**	0.916**	–0.708**	–	–	–
DS	0.054	–0.360**	–0.810**	0.783**	–0.824**	–	–
BW	–0.492**	–0.329**	0.004**	0.117	–0.115	–0.007	–
EV	0.340**	0.831**	0.754**	–0.547**	0.851**	–0.626**	–0.194

Note: \*\* represents significant difference at 0.01 probability level, the same as in the following tables.

**Table 4** Additive and additive×environment interaction effects of QTL for dough rheological traits

trait	QTL	marker-interval	position	range	A	R <sup>2</sup>	AE1	AE2
WA	Qwa-2A	WPT-1480-WPT-9797	3.0	0.0–9.8	-0.888**	8.03	-0.001	0.000
	Qwa-5A	WPT-8226-WPT-5467	8.3	4.0–13.5	1.302**	15.86	0.000	0.000
ST	Qst-4B	WPT-7569-GWM0495	9.5	4.6–14.3	1.352**	6.74	0.667	-0.669
	Qst-1B	WPT-8832-WPT-1675	12.0	5.0–12.5	2.255**	16.91	0.000	0.000
BT	Qbt-1B	WPT-8832-WPT-1675	10.0	4.0–12.5	2.192**	14.84	-0.459	0.460
DS	Qda-1B	WPT-8832-WPT-1675	10.0	4.0–12.5	-6.612**	12.23	0.000	0.000
BW	Qbw-2B	WPT-6519-WPT-8760	2.0	0.0–5.6	-1.795**	5.81	-1.082	1.090
	Qbw-2B	WPT-4559-WPT-7322	6.0	0.0–8.0	-3.391**	8.62	-0.255	0.260
EV	Qev-1B	WPT-8832-WPT-1675	10.0	2.0–12.5	2.798**	10.41	0.010	-0.010

**Figure 1** Detected QTL for dough rheological traits

**Table 5** Epistatic and epistatic×environment interaction effects of QTL for dough rheological traits

trait	QTLi	Interval-i	position	QTLj	Interval-j	position	AA	R <sup>2</sup>	AAE1	AAE2
WA	Qwa-3B	WMC0754-WPT-8692	32.8	Qwa-4A	WPT-3363-WPT-2777	16.3	-0.834**	7.87	-0.000	0.000
BT	Qbt-3B	WPT-0940-wpt-2559	30.9	Qbt-3D	WPT-6738-WPT-4153	7.3	1.625**	5.77	1.167	-1.225
DS	Qds-3B	WPT-7614-WPT-5072	30.7	Qds-3D	WPT-6738-WPT-4153	7.3	-4.949**	5.56	3.223	-3.356
MTI	Qmti-3B	WPT-5072-WPT-0940	30.8	Qmti-3D	WPT-8185-WPT-4237	4.6	-3.466**	9.11	-1.753	1.792
BW	Qbw-3B	WPT-11419-STM0538	28.5	Qbw-3A	WPT-9422-WPT-3697	32.4	2.193**	5.03	1.720	-1.710
	Qbw-2B	WPT-2703-WPT-0981	38.1	Qbw-2A	WPT-0071-WPT-7901	10.6	3.268**	9.12	1.266	-1.237
EV	Qev-3B	WPT-8959-WPT-1884	24.7	Qev-1B	WPT-1770-WPT-6142	3.0	2.983**	11.70	0.533	-0.546

### Prediction superior line genotype

Based on the additive and epistatic effects, the genetic effects of all QTLs genotypic combinations were estimated for each trait. The combination with the maximum genetic effects was regarded as the superior line genotype. The general superior lines (GSL) of traits were predicted based on the genetic effects of QTLs estimated in the present study (Table 6). As all detected QTLs were seldom affected by environments, the genetic effects of superior lines from each environment were the same as those of GSL. The genetic effects of GSL for WA, ST, BT, and EV were the same as those of female parent, indicating P<sub>1</sub> is a superior line for improvement of these traits. Similarly, P<sub>2</sub> was a superior line for BW to be meliorated. However, the genetic effects of GSL for MTI and DS were obviously higher than those of parents, suggesting an over-parent dominant effect existing.

The QTL genotype (QG) of GSL for each trait was also predicted (Table 7), with the *QQ* expression of the alleles in a locus from P<sub>1</sub>, whereas *qq* from P<sub>2</sub>. The QG of GSL for the QTL controlling ST, BT and EV were the same as those of P<sub>1</sub>. It can be seen that the QG of GSL for the same trait QTL on chromosomes were different from each other.

### Discussion

Several dough rheological traits of RILs from two Australian wheats, Lang and CSCR6, were evaluated in two different environments and the QTLs controlling these traits were detected based on a genetic linkage map using DArT and SSR markers in the current study. Some previous studies demonstrated that DArT markers showed characteristic of a single locus and tended to distributing in gene-rich regions of chromosomes compared to AFLP, RFLP and SSR markers in hexaploid wheat (Jaccoud et al., 2001; Semagn et al., 2006; Peleg et al., 2008; Hong et al., 2009). Genetic mapping and QTLs detection were conducted using DArT markers by researchers (Semagn et al., 2006; Li et al., 2008; Mantovani et al., 2008; Peleg et al., 2008) as well as our present study, by which and some SSR markers, we constructed a map and identified four major QTL of dough rheological traits locating in the interval of WPT-8832-WPT-1675 on chromosome 1B. This as the same that QTL related to bread baking quality was detected in other populations (Kuchel et al., 2006; Elangovan et al., 2008), indicating 1B could be the enrichment region controlling the gluten intensity. QTLs detected in this study provided fresh instance for DArT application and source of

**Table 6** Prediction of genetic effects for P<sub>1</sub>, P<sub>2</sub> and GSL for dough rheological traits

trait	entry	G	trait	entry	G	trait	entry	G	trait	entry	G
WA	P <sub>1</sub>	4.514	BT	P <sub>1</sub>	3.817	BW	P <sub>1</sub>	0.275	EV	P <sub>1</sub>	5.781
	P <sub>2</sub>	-2.699		P <sub>2</sub>	0.567		P <sub>2</sub>	10.647		P <sub>2</sub>	0.185
	GSL	4.514		GSL	3.817		GSL	10.647		GSL	5.781
ST	P <sub>1</sub>	4.514	MTI	P <sub>1</sub>	-3.466	DS	P <sub>1</sub>	-11.561	-	-	-
	P <sub>2</sub>	-2.699		P <sub>2</sub>	-3.466		P <sub>2</sub>	1.663	-	-	-
	GSL	4.514		GSL	3.466		GSL	11.561	-	-	-

**Table 7** QTL Genotypes of the predicted GSL for dough rheological traits

trait	QTL	GSL	trait	QTL	GSL	trait	QTL	GSL	trait	QTL	GSL	
WA	Qwa-2A	<i>qq</i>	BW	Qbw-2B	<i>qq</i>	BT	Qbt-1B	<i>QQ</i>	MTI	Qmti-3B	<i>qq</i>	
	Qwa-5A	<i>QQ</i>		Qbw-2B	<i>qq</i>		Qbt-3B	<i>QQ</i>		Qmti-3D	<i>QQ</i>	
	Qwa-3B	<i>qq</i>		Qbw-3B	<i>QQ</i>		Qbt-3D	<i>QQ</i>		EV	Qev-1B	<i>QQ</i>
	Qwa-4A	<i>QQ</i>		Qbw-3A	<i>QQ</i>		DS	Qds-1B		<i>qq</i>	Qev-3B	<i>QQ</i>
ST	Qst-4B	<i>QQ</i>	Qbw-2B	<i>QQ</i>	Qds-3B	<i>qq</i>		Qev-1B	<i>QQ</i>			
	Qst-1B	<i>QQ</i>	Qbw-2A	<i>QQ</i>	Qds-3D	<i>QQ</i>		-	-	-		

selection for future wheat genetic improvement.

Most researchers considered that QTL detection was impacted by genetic populations and molecular markers that were used. Whether a QTL was able to be used for marker-aided selection or not, the most conservative way was to judge it could or not repeatedly appeared among populations and environments, and it was or not negatively correlated with the other important traits (Suprayogi et al., 2009). Actually, QTL with higher contribution ratio and large number of total QTL were more normally to be detected in a single environment than in multiple environments. Therefore it was suggested that QTL analysis should be carried out based on multiple environment test (Blanco et al., 2002). The QTL detected base on multiple environment tests were normally with higher LOD value and therefore were more truly inherited (Ma et al., 2007). The current study identified some QTLs related to dough DT, ST and BT at two locations, and they did not significantly interact with environment. This provides references for marker-assisted selection in quality breeding of wheat.

Dough rheological traits belong to the important processing properties in wheat. It was found that Australian wheats had longer dough DT and ST than those of Chinese varieties. So the dough viscosity deteriorated the quality of steamed bread making (Zhu et al., 2001). The results of this study showed that the RIL lines from two Australian wheats were markedly superior to those of Chinese commercial varieties in dough rheological properties. There was a high genetic variation for dough stability, mixing tolerance index and breaking time in the RIL population. Determination of dough rheological characters usually uses many a seeds, which makes a difficulty for their selection in early generations. This can be overcome via an indirect selection through a linked character to the dough rheological characters, such as using the sedimentation value that has a higher heritability and is closely linked to dough rheological characters (Li et al., 1990; Zhang et al., 2003; Yang et al., 2006).

As a whole, the detection of loci affecting the investigated traits in the RILs from Australian wheats may provide fresh opportunities for the application of marker-assisted selection to improve yield and quality.

## References

- American Association of Cereal Chemists (1983). Approved methods of the AACC. MN, USA: The American Association of Cereals Chemists
- Blanco A, Pasqualone A, Troccoli A, DiFonzo N, Simeone R (2002). Detection of grain protein content QTLs across environments in tetraploid wheats. *Plant Mol Biol*, 48(5/6): 615–623
- Elangovan M, Rai R, Dholakia B B, Lagu M D, Tiwari R, Gupta R K, Rao V S, Röder M S, Gupta V S (2008). Molecular genetic mapping of quantitative trait loci associated with loaf volume in hexaploid wheat (*Triticum aestivum*). *J Cereal Sci*, 47(3): 587–598
- Groos C, Bervasb E, Charmet G (2004). Genetic analysis of grain protein content, grain hardness and dough rheology in a hard×hard bread wheat progeny. *J Cereal Sci*, 40(2): 93–100
- Hong Y H, Xiao N, Zhang C, Su Y, Chen J M (2009). Principle of diversity arrays technology (DArT) and its applications in genetic research of plants. *Hereditas*, 31(4): 359–364
- Jaccoud D, Peng K, Feinstein D, Kilian A (2001). Diversity arrays: a solid state technology for sequence information independent genotyping. *Nucleic Acids Res*, 29(4): 2–7
- Kuchel H, Langridge P, Mosionek L, Williams K, Jefferies S P (2006). The genetic control of milling yield, dough rheology and baking quality of wheat. *Theor Appl Genet*, 112(8): 1487–1495
- Li H B, Vaillancourt R, Mendham N, Zhou M X (2008). Comparative mapping of quantitative trait loci associated with waterlogging tolerance in barley (*Hordeum vulgare* L.). *BMC Genomics*, 9(1): 401
- Li Z Z, Sun F T, Zhang C Y, Jin Y C (1990). Quality traits of different varieties and correlations among them in wheat. *Scientia Agricultura Sinica*, 23(6): 35–40
- Ma J, Li H B, Zhang C Y, Yang X M, Liu Y X, Yan G J, Liu C J (2009). Identification and validation of a major QTL conferring crown rot resistance in hexaploid wheat. *Theor Appl Genet*, 120(6): 1119–1128
- Ma W J, Sutherland M W, Kammholz S, Banks P, Brennan P, Bovill W, Daggard G (2007). Wheat flour protein content and water absorption analysis in a doubled haploid population. *J Cereal Sci*, 45(3): 302–308
- Ma W, Appels R, Bekes F, Larroque Q, Morell M K, Gale K R (2005). Genetic characterization of dough rheological properties in a wheat doubled haploid population: additive genetic effects and epistatic interactions. *Theor Appl Genet*, 111(3): 410–422
- Mantovani P, Maccaferri M, Sanguineti M C, Tuberosa R, Catizone I, Wenzl P, Thomson B, Carling J, Huttner E, DeAmbrogio E, Kilian A (2008). An integrated DArT-SSR linkage map of durum wheat. *Mol Breed*, 22(4): 629–648
- McCartney C A, Somers D J, Lukow O, Ames N, Noll J, Cloutier S, Humphreys D G, McCallum B D (2006). QTL analysis of quality traits in the spring wheat cross RL4452×‘AC Domain’. *Plant Breed*, 125(6): 565–575
- Peleg Z, Saranga Y S, Suprunova T, Ronin Y, Röder M S, Kilian A, Korol A B, Fahima T (2008). High-density genetic map of durum wheat × wild emmer wheat based on SSR and DArT markers. *Theor Appl Genet*, 117(1): 103–115
- Semagn K, Bjørnstad Å, Skinnes H, Marøy A G, Taregne Y, William M (2006). Distribution of DArT, AFLP, and SSR markers in a genetic linkage map of a doubled-haploid hexaploid wheat population. *Genome*, 49(5): 545–555
- Suprayogi Y, Pozniak, Curtis Jerry, Clarke F R, Clarke J M, Knox R E, Singh A K (2009). Identification and validation of quantitative trait loci for grain protein concentration in adapted Canadian durum wheat populations. *Theor Appl Genet*, 119: 437–448
- Yang H, Shang H Y, Li W, Wei Y M, Zhang Y L (2006). Analysis of agronomic and quality characters of new wheat varieties and lines in Sichuan. *Southwest China J Agric Sci*, 19(2): 170–177
- Yang J, Hu C C, Ye X Z, Zhu Z H, Zhu Z X, Zhu J (2005). QTL Network-2.1 User Manual. Hangzhou: Zhejiang University, China
- Yang J, Hu C, Hu H, Yu R, Xia Z, Ye X, Zhu J (2008). QTL Network: mapping and visualizing genetic architecture of complex traits in experimental populations. *Applications Note*, 24(5): 721–723.

- 
- Zanetti S, Winzeler M, Feuillet C, Keller B, Messmer M (2001). Genetic analysis of bread-making quality in wheat and spelt. *Plant Breed*, 120 (1): 13–19
- Zhang X P, Wang S Z, Wang C L, Gao H T, Wu S H, Duan G H, Lu S Z (2003). Analysis of the major qualities and characteristics of new winter wheat breeds and its inspiration for breeding. *J Henan Vocation-Technical Teachers College*, 31(2): 5–7
- Zhu J, Huang S, Khan K, Brien L O (2001). Relationship of protein quantity, quality and dough properties with Chinese steamed bread quality. *J Cereal Sci*, 33(2): 205–212