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Effect of high-molecular-weight glutenin allele, *Glu-B1d*, from synthetic hexaploid wheat on wheat quality parameters and dry, white Chinese noodle-making quality

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Abstract. Synthetic hexaploid wheat (SHW) represents a valuable source of new resistances to a range of biotic and abiotic stresses. Exploitation of these resistances in bread wheat breeding programs, however, is not necessarily straightforward and requires an assessment of potential negative effects on quality particularly from the genomes contributed by the durum parents used in the development of SHW. In particular, high-molecular-weight glutenin subunits (HMW-GS) 6+8 that are common in durum and SHW but, in bread wheat, are present at only a very low frequency in Chinese wheat cultivars and landraces and as a result there is only limited data on the effects of HMW-GS 6+8 on wheat processing quality and especially on dry, white Chinese noodles (DWCN). In this study, 131 recombinant inbred lines (RIL) were developed from a cross between a CIMMYT SHW 'Syn-CD780' and an elite Sichuan common wheat cultivar 'ChuanYu12'.The aim of this study was to investigate the effect of the HMW glutenin allele, *Glu-B1d* (6+8), from SHW on quality-related characteristics and DWCN making quality compared with the alternate allele *Glu-B1u* (7*+8). The RIL and parents were grown in three environments and analysed for 21 quality and noodle test parameters. Results showed the effect of *Glu-B1d* depended on both the parameters tested and glutenin subunit background contributed by alleles at the *Glu-A1* and *Glu-D1* loci. RIL with the *Glu-B1d* allele *v.* those with the *Glu-B1u* had significantly higher Zeleny sedimentation volume and falling number in the subunit backgrounds *Glu-A1c/Glu-D1a* and *Glu-A1c/Glu-D1ah*, significantly higher *L** of dry flour in the background *Glu-A1a/Glu-D1a*; significantly higher dough development time, dough stability time, breakdown time and lower softness in both backgrounds *Glu-A1c/Glu-D1a* and *Glu-A1c/Glu-D1ah*; significantly higher values of most rapid visco analysis parameters, especially pronounced in the background *Glu-A1c/Glu-D1a*. The RIL with the *Glu-B1d* allele also showed significantly higher ($P < 0.05$) noodle total score (NTS) in the *Glu-A1a/Glu-D1a* background and significantly higher ($P < 0.01$) NTS and most components of sensory assessment in the *Glu-A1c/Glu-D1a* background. Overall, the results indicate that the allele *Glu-B1d*, 6+8, from synthetic hexaploids could, in general, have a positive influence on most bread wheat quality parameters and DWCN noodle-making, particularly when combined with particular glutenin subunits at *Glu-A1* and *Glu-D1*.

Additional keywords: high-molecular-weight glutenin subunit, recombinant inbred line, synthetic hexaploid wheat.

Introduction

Wheat gluten proteins account for ~80% of total flour protein and consist of polymeric glutenins and monomeric gliadins. The polymeric glutenins are assembled from high-molecular-weight glutenin (HMW-GS) and low-molecular-weight glutenin (LMW-GS) subunits. The HMW-GS are recognised as the primary determinant of wheat dough rheological and bread-making quality although they account for only 5–10% of total flour protein. The genes encoding HMW-GS are located at three complex loci, *Glu-A1*, *Glu-B1* and *Glu-D1* on the long arms of chromosomes 1A, 1B and 1D, respectively (Rogers *et al*. 1989). Previous studies have demonstrated that bread-making quality correlates with the presence or absence of specific allelic variants of HMW-GS (Payne 1987; Barro *et al*. 1997; Wieser and Zimmermann 2000). Several systems for evaluating the importance of different encoding loci and allelic variants at same loci on affecting bread-making quality have been proposed (Payne and Lawrence 1983; Payne 1987; Fu 1993; Zhao *et al*. 1994; Eagles *et al*. 2002; Song *et al*. 2003).

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Noodles are one of the most important consumptive styles for wheat throughout Asia. However, limited research has been done on the effect of the HMW-GS on noodle-making quality. Relationships between allelic variation at the *Glu-1* loci and the quality of different noodles have been studied but with contradictory results (Park *et al*. 2003; Liu *et al*. 2004; Zhao *et al*. 2005; Kang *et al*. 2006; Yanaka *et al*. 2007).

Synthetic hexaploid wheat (SHW), artificially created by intercrossing tetraploid durum wheat with present-day derivatives of goat grass (*Triticum tauschii*), represents an important genetic resource, containing superior new resistances to diseases and pests, tolerance to environmental stresses, and potentially improved end-product quality (Pena *et al*. 1995; reviewed by van Ginkel and Ogbonnaya 2007). However, possible negative effects on bread-baking quality associated with SHW are a concern for wheat breeders (reviewed by van Ginkel and Ogbonnaya 2007). Large numbers of SHW have been introduced to China from CIMMYT (Zhang *et al*. 2001; Chen and Li 2005) and several new wheat varieties such as 'Chuanmai 42' with high-yield potential have been developed (reviewed by van Ginkel and Ogbonnaya 2007; Tang *et al*. 2007). Synthetic hexaploids contain several traits derived from the durum parent that may not be particularly useful in bread wheat. In this cross, the SHW contained *Glu-B1d* (6+8), at *Glu-B1*, generally regarded as a 'poor subunit', compared with *Glu-B1u* (7*+8), which has been associated with good quality (Payne 1987). The frequency of HMW-GS 6+8 encoded by *Glu-B1d* in Chinese wheat cultivars and landraces is extremely low but very high in SHW from CIMMYT (Zhang *et al*. 2001, 2002; Song *et al*. 2003; Liu *et al*. 2004; Zhao *et al*. 2005; Kang *et al*. 2006).

A set of recombinant inbred lines (RIL) was developed by crossing a CIMMYT SHW, 'Syn-CD780', with 'ChuanYu12' (CY12), a high-quality Chinese noodle wheat in order to evaluate the potential influence on grain yield, resistance to diseases and end-use quality of introgressing genes into local elite cultivar.

The aim of this research was to compare the effects of *Glu-B1d* from SHW Syn-CD780 with *Glu-B1u* from CY12 on the quality in general and of dry, white Chinese noodles (DWCN) in particular. This information would be useful in determining whether *Glu-B1d* should be retained or discarded during early generation selection in breeding programs.

Materials and methods

Plant materials

The SHW Syn-CD780 (originally coded DW68-510) was introduced from CIMMIT and has proved to be highly resistant to yellow rust and to have high tillering ability (Pena *et al*. 1995). CY12, developed and released in Sichuan province, is one of the best varieties for DWCN in China that is cultivated widely in south-western regions due, in part, to its early maturity and good yield. CY12 has two protein composition biotypes, 1, 7*+8, 5+10 and 1, 7*+8, 2+12. The latter, (1, 7*+8, 2+12) was used as one parent to cross with Syn-CD780 for construction of the RIL. Both parents are soft grain types. The *Glu-B1x* subunit of CY12 had a slightly greater mobility in sodium dodecyl sulfate–polyacrylamide gel electrophoresis (SDS-PAGE) than *Glu-B1x* from Chinese Spring (data not shown) and is numbered 7* according to earlier reports by Ng *et al*. (1989), Pogna *et al*. (1989) and Zhen and Mares (1992). Similarly, the *Glu-B1* allele of CY12 is denoted as *Glu-B1u*.

These genotypes were hybridised (Syn-CD780 × CY12) and random F_2 to F_8 lines were developed by RIL methods at Chengdu, Sichuan Province, People's Republic of China. One-hundred and thirty-one RIL, were assayed as single seeds for HMW-GS using SDS-PAGE after William *et al*. (1993) and AS-PCR after Lu *et al*. (2005), Biotechnology Research Institute of CAS, Chengdu, and the Capital Normal University, Beijing. The protein subunit bands were numbered (Table 1) according to the system developed by Payne and Lawrence (1983). In the population of 131 RIL, 2 were heterozygous at one or more HMW glutenin loci and were not used for quality analysis. The HMW-GS 1.5+10 was first identified in SHW by William *et al*. (1993) and the corresponding allele name, *Glu-D1ah* assigned.

Field experiments

Field experiments were conducted at Jinhua Village, Lianshan Township of Guanhan City located in the Chengdu plain in 2006 and 2007 (E1 and E2) and at Datong Village, Jiyi

Table 1. High-molecular-weight (HMW) glutenin alleles and sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) band designations with frequencies of homozygous genotypes observed among recombinant inbred lines (RIL) from the F_8 Syn-CD780 × CY12

HMW glutenin allele			SDS-PAGE band			Genotype code	Number of RIL[A]
Glu-A1	*Glu-B1*	*Glu-D1*	*Glu-A1*	*Glu-B1*	*Glu-D1*		
a	u	a	1	7*+8	2+12	111[C]	13
a	u	ah	1	7*+8	1.5+10	112	9
a	d	a	1	6+8	2+12	121	21
a	d	ah	1	6+8	1.5+10	122	14
c	u	a	n[B]	7*+8	2+12	211	15
c	u	ah	n	7*+8	1.5+10	212	13
c	d	a	n	6+8	2+12	221	23
c	d	ah	n	6+8	1.5+10	222[D]	21

[A]In the population of 131 RIL, two were heterozygous at one or more HMW glutenin loci and not used for quality analysis.
[B]n, null; no band expressed.
[C]Parent CY12 band type.
[D]Parent Syn-CD780 band type.

Table 2. Quality traits measured in recombinant inbred lines and its parents in experimental environments

Abbr.	Traits (units)	Method of measurement	Environment[A]	Reference
GH	Grain hardness (–)	Near infrared reflectance (NIR), Perten SKCS4100	E1, E2, E3	–
GPC	Grain protein content (%)	NIR, Perten DAT200, AACC	E1, E2, E3	–
WGC	Wet gluten content (%)	Perten 2200, according to GB/T14608-93	E1, E2, E3	–
SED	Zeleny sedimentation volume (mL)	According to AACC approved method 56-63	E2, E3	Liu *et al*. (2004)
FN	Falling number (s)	Perten 1800 (Sweden Falling Number Co.), AACC, 56-81B	E1, E2, E3	–
FWH	Flour whiteness (–)	Intelligent whiteness meter WSB-IV (Hangzhou Dacheng Photoelectricity Instrument Co., Ltd)	E2, E3	–
AC	Ash content (%)	GB/T 5505-1985	E2	–
Minolta chromameter parameters				
*L**	CIELAB *L** (flour)	Tristimulus colourimeter CR-400 (Japan Minolta Co., Ltd)	E2, E3	Yun *et al*. (1997)
*b**	CIELAB *b** (flour)	Tristimulus colourimeter CR-400 (Japan Minolta Co., Ltd)	E2, E3	–
Farinograph parameters				Liu *et al*. (2002)
FWA	Flour water absorption (%)	BRABENDER, AACC54-21	E1, E2, E3	–
DDT	Dough development time (min)	As above	E1, E2, E3	–
DST	Dough stability time (min)	As above	E1, E2, E3	–
SOF	Farinograph softening (B.U.)	As above	E2, E3	–
BRT	Breakdown time (min)	As above	E2, E3	–
Rapid visco analysis (RVA) parameters				Yun *et al*. (1997)
PV	Peak viscosity (RVU[B])	Rapid Visco-Analyser Super3 (Newport Scientific Ltd, Australia) (GB/T 14490-93)	E2, E3	–
HT	Hold through (RVU)	As above	E2, E3	–
BD	Breakdown (RVU)	As above	E2, E3	–
FV	Final viscosity (RVU)	As above	E2, E3	–
SB	Setback (RVU)	As above	E2, E3	–
PET	Peak time (min)	As above	E2, E3	–
PAT	Pasting time (°C)	As above	E2, E3	–
Sensory assessment of dry, white Chinese noodles				Liu *et al*. (2004)
COL	Colour (–)	LS/T 320-1993	E2, E3	–
APP	Appearance (–)	LS/T 320-1993	E2, E3	–
PAL	Palate (–)	LS/T 320-1993	E2, E3	–
VEL	Viscoelasticity (–)	LS/T 320-1993	E2, E3	–
STI	Stickiness (–)	LS/T 320-1993	E2, E3	–
SMO	Smoothness (–)	LS/T 320-1993	E2, E3	–
TAS	Taste (–)	LS/T 320-1993	E2, E3	–
NTS	Noodle total score (–)	LS/T 320-1993	E2, E3	–

[A]Abbreviation of experimental environment: E1 – Guanghan 2006, E2 – Guanghan 2007, E3 – Jingyan 2007.
[B]Rapid visco analyser unit.

Table 3. Mean squares and coefficients of variation from the ANOVA for high-molecular-weight glutenin subunits (HMW-GS) combinations in two or three experimental environments[A]

See Table 2 for abbreviations of the traits and their units

Source	GH	GPC	WGC	SED	FN	FWH	*L**	*b**	FWA	DDT	DST	SOF	BRT	PV
G[B]	544**	2.7**	28*	324**	12 126**	3.9	0.55**	1.39*	32.9**	9.8**	42**	2630**	15.7**	6947**
E[C]	827**	152**	1828**	2660**	42 580**	12.6*	7.01**	7.68**	30.2**	231**	172**	4893**	19.6*	4459
G × E	21.4	0.59	4.77	23.29	1462	0.67	0.07	0.07	3.47	1.56	2.85	140	1.46	664
Error	146.8	0.80	12.59	43.31	2807	1.96	0.19	0.57	5.45	1.65	6.25	501	3.35	1299
Source	HT	BD	FV	SB	PET	PAT	COL	APP	PAL	VEL	STI	SMO	TAS	NTS
G	5529**	402**	10 985**	1002**	0.42**	6.2*	1.76**	0.52	3.46**	4.15*	1.73	0.42	0.31*	38.2**
E	16 022**	3577**	31 205**	2507**	3.36**	143.6**	0.26	16.90**	27.2**	355**	358**	12.9**	3.42**	2717**
G × E	439	38.76	984	125	0.04	1.45	0.58	0.83*	2.59*	2.52	0.74	0.43	0.15	21.78
Error	1060	89.56	2083	207	0.09	3.03	0.57	0.40	1.28	1.69	1.25	0.33	0.12	13.20

[A]Ash content not included due to data collection at only one environment.
[B]G represents means for 8 combinations of HMW-GS (Table 1).
[C]E represents environments, where GH, GPC, WGC, FN, FWA, DDT and DST were measured at three environments and other parameters at two environments.

Table 4. Minimum, maximum and mean for recombinant inbred lines (RIL) and parents in each experimental environment with standard errors (s.e.) for environment means
See Table 2 for abbreviations of the traits and their units

Character	RIL									Mean	s.e. for all	6+8	7*+8	CY12				Syn-CD780				Difference
	E1			E2			E3			of RIL	genotypes	group	group	E1	E2	E3	Mean	E1	E2	E3	Mean	between parents[A]
	Min.	Max.	Mean	Min.	Max.	Mean	Min.	Max.	Mean													
GH	–2.8	73.2	26.6	–1.7	75.6	26.2	–14.4	67.2	22.1	25.0	11.8	24.2	25.8*[B]	22.7	21.9	21.4	22.0	37.7	32.3	32.1	34.0	**
GPC	11.9	17.0	14.3	10.3	15.9	13.1	10.6	13.9	12.1	13.2	0.8	13.2	13.1n.s.	14.3	12.3	11.5	12.7	16.6	15.4	14.3	15.4	**
WGC	16.5	44.4	29.2	18.8	42.4	30.3	14.8	34.7	23.0	27.5	3.2	27.3	27.7n.s.	29.8	28.6	20.6	26.4	32.3	36.6	28.8	32.5	**
SED	n.d.[C]	n.d.	n.d.	12.0	51.8	31.7	11.9	39.8	25.0	28.4	6.4	30.4	25.5**	n.d.	35.1	24.8	30.0	n.d.	41.8	39.7	40.8	**
FN	224	489	377	146	479	350	244	521	387	371	48.3	380	358**	387	357	373	372	328	258	285	290	**
FWH	n.d.	n.d.	n.d.	76.6	84.3	81.2	76.3	83.4	80.7	80.9	1.3	81.0	80.8n.s.	n.d.	83.7	81.9	82.8	n.d.	79.4	77.6	78.5	*
*L**	n.d.	n.d.	n.d.	90.0	92.8	91.8	89.5	92.4	91.5	91.7	0.4	91.7	91.5n.s.	n.d.	92.5	91.9	92.2	n.d.	91.6	90.6	91.1	n.s.
*b**	n.d.	n.d.	n.d.	5.5	9.4	7.1	5.4	9.6	6.8	7.0	0.7	7.0	6.9n.s.	n.d.	6.2	6.0	6.1	n.d.	7.9	8.0	8.0	*
AC	n.d.	n.d.	n.d.	0.43	0.71	0.56	n.d.	n.d.	n.d.	0.56	0.05	0.57	0.56n.s.	n.d.	0.47	n.d.	0.47	n.d.	0.61	n.d.	0.61	*
FWA	52.5	67.5	59.3	52.7	65.0	58.2	51.5	64.3	58.5	58.7	2.1	58.6	58.7n.s.	56.5	56.2	57.3	56.7	65.1	62.1	59.9	62.4	*
DDT	1.4	11.3	5.1	0.5	6.0	3.3	0.9	6.2	2.3	3.6	1.0	3.8	3.2*	2.0	5.8	1.7	3.2	7.8	4.7	4.7	5.7	*
DST	1.0	20.3	6.2	1.3	13.2	4.2	1.1	11.6	4.1	4.8	2.1	5.4	4.0**	13.1	9.7	7.0	9.9	7.3	5.2	5.1	5.9	**
SOF	n.d.	n.d.	n.d.	5.2	164.0	71.3	16.0	123.0	62.2	66.8	20.9	61.6	74.2*	n.d.	31	24	28	n.d.	62	71	67	**
BRT	n.d.	n.d.	n.d.	0.4	13.0	5.4	1.4	10.8	4.8	5.1	1.6	5.5	4.5*	n.d.	10.8	7.7	9.3	n.d.	7.3	6.9	7.1	*
PV	n.d.	n.d.	n.d.	43	241	166	88	242	174	170	35.1	180	155**	n.d.	184	186	185	n.d.	86	105	95	**
HT	n.d.	n.d.	n.d.	–1.4	171	99	27	171	115	107	31.9	116	93**	n.d.	111	103	107	n.d.	32	50	41	**
BD	n.d.	n.d.	n.d.	45	98	67	36	94	59	63	8.8	65	62n.s.	n.d.	73	83	78	n.d.	54	55	54	**
FV	n.d.	n.d.	n.d.	7.3	278	179	73	276	201	190	44.3	203	171**	n.d.	197	191	194	n.d.	76	108	92	**
SB	n.d.	n.d.	n.d.	8.8	117	80	45	113	86	83	13.5	87	78n.s.	n.d.	86	88	87	n.d.	44	58	51	*
PET	n.d.	n.d.	n.d.	4.2	6.5	6.0	5.3	6.7	6.2	6.1	0.3	6.2	6.0n.s.	n.d.	6.1	6.1	6.1	n.d.	5.3	5.7	5.5	n.s.
PAT	n.d.	n.d.	n.d.	60.9	70.3	66.8	62.0	74.3	68.3	67.5	1.6	67.7	67.2n.s.	n.d.	69.3	69.4	69.3	n.d.	65.2	66.1	65.6	*
COL	n.d.	n.d.	n.d.	4	9	7.1	5	9	7.2	7.1	0.6	7.2	6.9n.s.	n.d.	8.0	7.0	7.5	n.d.	8.0	7.0	7.5	n.s.
APP	n.d.	n.d.	n.d.	6	8	7.6	3	8	7.1	7.3	0.4	7.4	7.3n.s.	n.d.	8.0	7.0	7.5	n.d.	8.0	7.0	7.5	n.s.
PAL	n.d.	n.d.	n.d.	12	18	16.1	12	17	15.5	15.8	0.9	16.0	15.5*	n.d.	17.0	18.0	17.5	n.d.	15.0	16.0	16.7	n.s.
VEL	n.d.	n.d.	n.d.	14	20	17.8	12	20	15.5	16.7	1.0	16.9	16.4*	n.d.	18.0	19.0	18.5	n.d.	16.0	17.0	16.5	*
STI	n.d.	n.d.	n.d.	16	21	18.5	13	19	16.1	17.3	0.7	17.4	17.1n.s.	n.d.	17.5	18.0	17.7	n.d.	16.0	17.0	16.5	n.s.
SMO	n.d.	n.d.	n.d.	3	5	3.9	2	5	3.5	3.7	0.4	3.7	3.7n.s.	n.d.	4.5	5.0	4.7	n.d.	3.0	3.0	3.0	*
TAS	n.d.	n.d.	n.d.	3	5	4.3	4	5	4.0	4.1	0.3	4.1	4.2n.s.	n.d.	4.0	4.0	4.0	n.d.	4.0	4.0	4.0	n.s.
NTS	n.d.	n.d.	n.d.	63	83	75.3	54	78	68.9	72.1	2.6	72.7	71.2n.s.	n.d.	77.0	78.0	77.5	n.d.	70.0	71.0	70.5	**

[A]Difference between parents; *$P < 0.05$; **$P < 0.01$; n.s., not significant.
[B]Difference between 6+8 and 7*+8 groups; *$P < 0.05$; **$P < 0.01$; n.s., not significant.
[C]n.d., No data.

Township of Jingyan County located in the shallow hills at the centre of the Sichuan Basin in 2007 (E3). The soil at Jinhua Village was clay and previously cultivated with rice. The experiment was a random block design with 3 replicates and 6 replicates of the parents. Each plot, 1.2 × 1.8 m, was sown as 6 rows with 20-cm row spacing on 27 October. After emergence, the number of seedling was thinned to 180/m^2. Fertiliser, nitrogen, phosphate and potassium, was applied at 150, 60 and 40 kg/hm^2, respectively. Sixty percent of urea, all the lime superphosphate and KCl were applied before sowing while the remainder of the urea was applied at shooting stage. The soil at Datong Village was clay loam and previously cultivated with maize. The experiment was again a random block design and replicated as described above. Each plot, 1.5 × 1.0 m, was sown as 4 rows on October 30. After emergence, the number of seedling was thinned to 200/m^2. Fertiliser application was the same as at Jinhua.

Plastic nets fixed by bamboo were used to prevent lodging. A plastic film-shelter, 2.5 m at the peak and 1.8 m at the side was erected at the beginning of milk ripeness to avoid the effects of rainfall. Yellow rust, mildew and aphids were controlled with one spray application. All plots were used for quality assays and statistical analysis. Samples were stored for 3 months at low temperature (5°C) with pesticide treatment before quality analysis.

Quality assay

The physic and chemical quality traits were assayed by the Laboratory of Wheat Quality at Shandong Agricultural University in Taian City, Shandong Province. Noodles were made and scored according to the standard method LS/T320-1993 used by the Laboratory of Crop Quality Analysis at the Institute of Crop Sciences, CAAS in Beijing. Twenty-one quality parameters were measured, including 9 grain and flour parameters, 5 Farinograph parameters, 7 rapid visco analysis (RVA) parameters and 8 noodle quality components. Grain hardness (GH) was measured on 300-kernel samples with a Perten SKCS 4100 (Perten Instruments, Springfield, IL, USA). Grain protein content (GPC, %) was measured by a near infrared reflectance analyser (Perten DAT200, AACC 2000). Wet gluten content of flour (WGC, %) was determined according to GB/T 14608-1993. Zeleny sedimentation volume (SED, ml) was determined according to the AACC approved method 56-63 (AACC 1995). Falling number (FN, s) used for determining

Table 5. Effect of variation at *Glu-B1* on grain and flour quality parameters between lines grouped according to genotype at *Glu-A1* and *Glu-D1* in different environments

See Table 2 for abbreviations of the traits and their units. *$P < 0.05$, **$P < 0.01$, n.s., not significant

Parameter	Environment	*Glu-A1a/Glu-D1a*			*Glu-A1a/Glu-D1ah*			*Glu-A1c/Glu-D1a*			*Glu-A1c/Glu-D1ah*		
		6+8	7*+8	*P*	6+8	7*+8	*P*	6+8	7*+8	*P*	6+8	7*+8	*P*
GH	E1	26.2	31.0	n.s.	29.9	24.0	n.s.	24.0	22.0	n.s.	25.4	31.9	n.s.
	E2	24.5	32.1	n.s.	29.7	23.0	n.s.	22.6	22.7	n.s.	26.8	30.0	n.s.
	E3	22.0	27.0	n.s.	24.5	15.0	*	19.6	20.4	n.s.	21.1	26.7	n.s.
	Mean	24.2	30.0	n.s.	28.0	20.7	n.s.	22.1	21.7	n.s.	24.4	29.5	n.s.
GPC	E1	14.1	14.8	*	14.6	14.6	n.s.	14.2	14.0	n.s.	14.3	14.6	n.s.
	E2	13.2	13.4	n.s.	13.5	12.8	**	12.9	12.4	n.s.	13.3	13.4	n.s.
	E3	12.0	12.4	n.s.	12.2	12.1	n.s.	12.2	11.9	n.s.	12.3	12.1	n.s.
	Mean	13.1	13.5	n.s.	13.5	13.2	n.s.	13.1	12.8	n.s.	13.3	13.3	n.s.
WGC	E1	28.3	30.8	n.s.	30.7	26.7	*	29.0	29.3	n.s.	28.8	29.4	n.s.
	E2	29.7	31.5	*	31.9	29.9	n.s.	29.5	29.6	n.s.	30.4	31.5	n.s.
	E3	22.5	24.1	n.s.	22.9	22.3	n.s.	22.8	23.2	n.s.	23.0	23.7	n.s.
	Mean	26.8	28.8	*	28.3	26.3	*	27.1	27.3	n.s.	27.4	28.2	n.s.
FN	E1	398.1	380.0	n.s.	358.1	394.8	n.s.	390.8	355.7	n.s.	379.0	341.9	n.s.
	E2	367.4	355.4	n.s.	347.9	352.6	n.s.	361.2	318.4	*	361.3	323.8	*
	E3	395.5	376.8	n.s.	403.2	392.6	n.s.	386.8	358.1	*	397.8	372.2	n.s.
	Mean	387	371	n.s.	370	380	n.s.	380	344	*	379	346	*
SED	E2	35.3	31.9	n.s.	36.1	30.7	n.s.	33.6	24.8	**	31.5	27.9	n.s.
	E3	26.2	26.5	n.s.	28.0	22.1	*	26.8	20.2	**	26.6	21.5	*
	Mean	29.4	29.2	n.s.	30.8	26.4	n.s.	30.2	22.5	**	29.0	24.7	*
FWH	E2	81.6	80.9	n.s.	81.8	81.8	n.s.	81.0	81.0	n.s.	80.7	80.7	n.s.
	E3	81.0	80.4	n.s.	81.0	81.0	n.s.	80.3	80.7	n.s.	80.6	80.7	n.s.
	Mean	81.3	80.6	n.s.	81.4	81.4	n.s.	80.7	80.8	n.s.	80.7	80.7	n.s.
*L**	E2	92.0	91.6	*	91.9	92.0	n.s.	91.9	91.8	n.s.	91.8	91.5	n.s.
	E3	91.6	91.3	*	91.5	91.4	n.s.	91.6	91.5	n.s.	91.5	91.4	n.s.
	Mean	91.8	91.4	*	91.7	91.7	n.s.	91.7	91.6	n.s.	91.7	91.4	n.s.
*b**	E2	6.9	7.1	n.s.	6.9	6.8	n.s.	7.4	7.2	n.s.	7.4	7.0	n.s.
	E3	6.7	6.7	n.s.	6.5	6.5	n.s.	7.0	6.9	n.s.	6.9	6.7	n.s.
	Mean	6.8	6.9	n.s.	6.7	6.7	n.s.	7.2	7.1	n.s.	7.1	6.9	n.s.
AC	E2	0.57	0.55	n.s.	0.54	0.54	n.s.	0.58	0.56	n.s.	0.57	0.56	n.s.

sprouting damage and α-amylase activity was measured using a Falling Number apparatus (Perten 1500, GB10361-89). Flour whiteness (FWH) was measured using intelligent whiteness meter WSB-IV following the manufacturer's (Hangzhou Dacheng Photoelectricity Instrument Co., Ltd, China) instruction. Ash content (AC, %) was measured by the 550℃ cauterant method (GB/T 5505-1985). Colour reflectance parameters of dry flour (*L**, *b**) were determined with a Tristimulus colourimeter CR-400 (Minolta Co., Japan). Farinograph parameters, including flour water absorption (FWA, %), dough development time (DDT, min), dough stability time (DST, min), farinograph softening (SOF, B.U.) and breakdown time (BRT, min), were measured with a Brabender Farinograph (AACC54-21). RVA parameters including peak viscosity (PV, RVU), hold through (HT, RVU), breakdown (BD, RVU), final viscosity (FV, RVU), setback (SB, RVU), peak time (PET, min) and pasting time (PAT, ℃) were obtained with a Rapid Visco-Analyser Super3 (Newport Scientific Ltd, Australia) according to Konik *et al*. (1994) (GB/T 14490-93). The AC was measured at only one experimental environment (E2). Two environments (E2, E3) were assessed for SED, FWH, *L**, *b**, SOF, BRT, all RVA parameters and sensory assessment components, whereas three environments (E1, E2, E3) were analysed for the remaining traits.

Preparation and sensory assessment of DWCN was conducted according to LS/T320-1993 (Liu *et al*. 2004) and assessment components included colour (COL, 10), appearance (APP, 10), palate (PAL, 20), viscoelasticity (VE, 25), stickiness (STI, 25), smoothness (SMO, 5), taste (TAS, 5), and noodle total score (NTS, 100).

All the quality traits, acronyms, measurement units and the reference for the method used are listed in Table 2.

Statistical analysis

Experimental data were processed using EXCEL software, and statistical analysis was conducted using the software package Addinssoft (XLSTAR version 2009).

Results

Environment effects and distribution of parameters among RIL

Highly significant differences were observed for most characteristics between the combinations of HMW-GS and experimental environments (Table 3). There was no evidence of genotype × environment interaction, except for APP and PAL. The parents, CY12 and Syn-CD780, differed greatly for most of the traits tested except for *L**, PET and five of the noodle sensory assessment components (COL, APP, PAL, STI, TAS). Syn-CD780 had significantly higher GH, GPC, WGC, SED, *b**, AC, FWA, DDT and SOF whereas CY12 showed significantly higher FN, FWH, DST, BRT, all RVA parameters but PET, and some components (VEL, SMO) and total score of noodle sensory assessment (Table 4). The mean values of the RIL were, on average, intermediate to the parents for most characteristics except for SED, DST, BRT, and four sensory assessment components. Among the RIL, significant differences were observed for some quality characteristics especially for those reflecting quantity and quality of wheat gluten. Compared to the other two experimental environments, E3 had substantially lower GPC, WGC, SED, DDT, DST and BRT. When the locus effects of *Glu-A1* and *Glu-D1* were not considered, allelic variation at *Glu-B1* had obvious influence on some quality parameters of wheat. The RIL with HMW-GS 6+8 had significantly higher values of SED, FN, DDT, DST,

Table 6. Effect of variation at *Glu-B1* on Farinograph parameters between lines grouped according to genotype at *Glu-A1* and *Glu-D1* in different environments

See Table 2 for abbreviations of the traits and their units. *$P < 0.05$, **$P < 0.01$, n.s., not significant

Parameter	Environment	*Glu-A1a/Glu-D1a*			*Glu-A1a/Glu-D1ah*			*Glu-A1c/Glu-D1a*			*Glu-A1c/Glu-D1ah*		
		6+8	7*+8	*P*	6+8	7*+8	*P*	6+8	7*+8	*P*	6+8	7*+8	*P*
FWA	E1	59.3	60.3	n.s.	60.5	58.0	**	58.8	57.6	n.s.	59.6	59.9	n.s.
	E2	57.6	59.1	n.s.	59.6	58.3	n.s.	57.0	57.0	n.s.	58.7	59.1	n.s.
	E3	58.5	59.5	n.s.	59.3	57.5	*	58.0	58.2	n.s.	58.4	59.6	n.s.
	Mean	58.5	59.5	n.s.	59.8	57.8	**	57.9	57.6	n.s.	58.9	59.5	n.s.
DDT	E1	6.0	5.6	n.s.	5.2	5.1	n.s.	5.4	3.7	**	5.0	4.2	n.s.
	E2	3.7	3.4	n.s.	3.9	3.0	n.s.	5.4	3.7	*	5.0	4.2	*
	E3	2.4	2.5	n.s.	2.7	1.8	n.s.	2.7	1.9	n.s.	2.2	2.0	n.s.
	Mean	4.0	3.8	n.s.	3.9	3.3	n.s.	3.8	2.8	**	3.5	3.0	n.s.
DST	E1	8.1	5.7	n.s.	5.9	6.7	n.s.	7.1	4.1	*	6.3	5.0	*
	E2	5.3	3.8	n.s.	4.5	4.2	n.s.	5.0	2.8	**	4.0	3.0	n.s.
	E3	4.8	4.6	n.s.	4.4	3.5	n.s.	4.7	2.8	**	4.1	3.1	n.s.
	Mean	6.0	4.7	n.s.	4.9	4.8	n.s.	5.6	3.2	**	4.7	3.7	n.s.
SOF	E2	61.5	72.6	n.s.	64.0	65.3	n.s.	63.6	88.1	**	74.9	85.7	n.s.
	E3	54.3	58.1	n.s.	60.4	60.9	n.s.	56.9	76.7	**	60.3	75.3	*
	Mean	57.9	65.3	n.s.	62.2	63.1	n.s.	60.3	82.4	**	67.6	80.5	*
BRT	E2	6.4	5.3	n.s.	5.9	5.2	n.s.	6.0	4.2	**	5.3	4.4	n.s.
	E3	5.1	5.5	n.s.	5.2	4.3	n.s.	5.4	3.6	**	4.8	4.0	n.s.
	Mean	5.8	5.4	n.s.	5.6	4.8	n.s.	5.7	3.9	**	5.1	4.2	*

Table 7. Effect of variation at *Glu-B1* on rapid visco analysis parameters between lines grouped according to genotype at *Glu-A1* and *Glu-D1* in different environments

See Table 2 for abbreviations of the traits and their units. *$P < 0.05$, **$P < 0.01$, n.s., not significant

Parameter	Environment	*Glu-A1a/Glu-D1a*			*Glu-A1a/Glu-D1ah*			*Glu-A1c/Glu-D1a*			*Glu-A1c/Glu-D1ah*		
		6+8	7*+8	*P*	6+8	7*+8	*P*	6+8	7*+8	*P*	6+8	7*+8	*P*
PV	E2	180.9	155.1	n.s.	166.0	167.5	n.s.	185.7	141.8	**	170.9	142.5	*
	E3	185.6	153.0	**	189.5	172.6	n.s.	185.0	155.3	**	176.2	162.8	n.s.
	Mean	183.2	154.0	*	177.7	170.0	n.s.	185.4	148.5	**	173.6	152.7	*
HT	E2	112.2	89.3	n.s.	99.1	103.8	n.s.	111.1	75.7	**	105.9	77.9	*
	E3	126.6	95.1	**	126.4	116.9	n.s.	120.3	95.4	**	121.3	104.9	n.s.
	Mean	119.4	92.2	*	112.7	110.4	n.s.	115.7	85.6	***	113.6	91.4	*
BD	E2	68.7	65.8	n.s.	66.9	63.6	n.s.	74.6	66.1	*	65.0	64.6	n.s.
	E3	58.9	57.9	n.s.	63.1	55.7	n.s.	64.7	63.0	n.s.	54.9	57.9	n.s.
	Mean	63.8	61.9	n.s.	65.0	59.7	n.s.	69.7	63.0	*	60.0	61.2	n.s.
FV	E2	199.3	165.9	n.s.	175.7	183.9	n.s.	197.6	145.5	**	189.3	148.2	*
	E3	218.6	175.0	**	214.1	199.6	n.s.	210.5	174.8	**	208.1	188.7	n.s.
	Mean	208.9	170.4	*	194.9	191.8	n.s.	204.0	160.1	**	198.7	168.4	*
SB	E2	87.2	76.6	n.s.	76.7	80.1	n.s.	86.5	69.8	**	83.4	70.3	*
	E3	91.9	79.9	**	87.7	82.8	n.s.	90.2	79.4	**	86.9	83.8	n.s.
	Mean	89.6	78.2	*	82.2	81.4	n.s.	88.3	74.6	**	85.1	77.0	*
PET	E2	6.1	5.9	n.s.	6.0	6.0	n.s.	6.1	5.8	**	6.1	5.8	*
	E3	6.3	6.0	**	6.3	6.3	n.s.	6.2	6.0	*	6.3	6.2	n.s.
	Mean	6.2	6.0	*	6.2	6.2	n.s.	6.2	5.9	**	6.2	6.0	*
PAT	E2	67.3	66.7	n.s.	66.9	66.8	n.s.	66.8	66.2	n.s.	66.8	66.3	n.s.
	E3	68.8	68.1	n.s.	68.6	69.1	n.s.	67.9	67.4	n.s.	68.9	67.8	n.s.
	Mean	68.0	67.4	n.s.	67.8	68.0	n.s.	67.4	66.8	n.s.	67.8	67.0	n.s.

Table 8. Effect of variation at *Glu-B1* on sensory assessment of dry, white Chinese noodles between lines grouped according to genotype at *Glu-A1* and *Glu-D1* in different environments

See Table 2 for abbreviations of the traits and their units. *$P < 0.05$, **$P < 0.01$, n.s., not significant

Parameter	Environment	*Glu-A1a/Glu-D1a*			*Glu-A1a/Glu-D1ah*			*Glu-A1c/Glu-D1a*			*Glu-A1c/Glu-D1ah*		
		6+8	7*+8	*P*	6+8	7*+8	*P*	6+8	7*+8	*P*	6+8	7*+8	*P*
COL	E2	7.5	6.8	**	6.9	7.1	n.s.	7.4	7.0	n.s.	7.1	6.5	*
	E3	7.4	6.8	*	7.0	6.9	n.s.	7.2	7.1	n.s.	7.2	7.2	n.s.
	Mean	7.5	6.8	**	7.0	7.0	n.s.	7.3	7.1	n.s.	7.1	6.8	n.s.
APP	E2	7.5	7.5	n.s.	7.1	7.3	**	7.6	7.6	n.s.	7.7	7.7	n.s.
	E3	7.2	7.2	n.s.	7.1	6.8	n.s.	7.3	6.8	*	7.2	6.8	n.s.
	Mean	7.4	7.4	n.s.	7.1	7.3	n.s.	7.5	7.2	*	7.5	7.2	n.s.
PAL	E2	16.1	16.1	n.s.	16.1	16.9	n.s.	16.3	16.2	n.s.	15.7	16.1	n.s.
	E3	15.7	14.6	*	16.1	15.3	n.s.	16.1	14.8	**	15.6	14.9	n.s.
	Mean	15.9	15.3	n.s.	16.1	15.6	n.s.	16.2	15.5	*	15.6	15.5	n.s.
VEL	E2	18.0	18.0	n.s.	18.1	18.3	n.s.	18.0	17.5	n.s.	17.6	17.7	n.s.
	E3	15.9	15.1	n.s.	15.8	15.1	n.s.	16.4	15.1	*	15.5	14.6	n.s.
	Mean	16.9	16.5	n.s.	17.0	16.7	n.s.	17.2	16.3	*	16.5	16.2	n.s.
STI	E2	18.7	18.1	n.s.	18.7	18.7	n.s.	18.6	18.3	n.s.	18.3	18.5	n.s.
	E3	16.3	16.0	n.s.	16.5	15.7	n.s.	16.3	15.5	*	16.1	15.8	n.s.
	Mean	17.5	17.0	**	17.6	17.2	n.s.	17.4	16.9	*	17.2	17.2	n.s.
SMO	E2	3.8	4.0	n.s.	3.9	4.1	n.s.	4.0	4.1	n.s.	3.6	4.0	*
	E3	3.6	3.3	n.s.	3.6	3.4	n.s.	3.7	3.5	n.s.	3.5	3.3	n.s.
	Mean	3.7	3.7	n.s.	3.8	3.8	n.s.	3.9	3.8	n.s.	3.5	3.7	n.s.
TAS	E2	4.3	4.3	n.s.	4.1	4.3	n.s.	4.2	4.3	n.s.	4.1	4.6	**
	E3	4.0	4.0	n.s.	4.1	4.0	n.s.	4.0	4.0	n.s.	4.0	4.2	n.s.
	Mean	4.1	4.2	n.s.	4.1	4.2	n.s.	4.1	4.1	n.s.	4.0	4.4	**
NTS	E2	75.9	74.8	n.s.	75.1	76.3	n.s.	76.1	75.0	n.s.	74.0	75.1	n.s.
	E3	70.0	67.1	*	70.1	67.2	n.s.	71.0	66.8	**	69.0	66.7	n.s.
	Mean	73.0	70.9	*	72.6	71.8	n.s.	73.5	70.9	**	71.5	70.9	n.s.

BRT, PV, HT, FV and two sensory assessment components, PAL, VEL, than that with HMW-GS 7*+8 (Table 4).

Effect of Glu-B1d alleles on grain and flour quality characteristics

The RIL were divided into four groups according to the alleles at the *Glu-A1* and *Glu-D1* loci and within each group the differences in quality characteristics associated with the *Glu-B1* alleles, subunit 6+8 and 7*+8, were compared (Table 1, Tables 5–8). Differences between subunit 6+8 and 7*+8 varied both for the characteristics tested and subunit background at *Glu-A1* and *Glu-D1* (Table 5). No significant differences in GH were found between 6+8 and 7*+8 except for the subunit background of *Glu-A1a*/*Glu-D1ah* in E3. For FWT, *b**, AC, there were no significant differences between 6+8 and 7*+8 in any subunit background. RIL with 6+8 had significantly higher *L** than those with 7*+8 in E2, E3, and on average over environments for the subunit background *Glu-A1a*/*Glu-D1a*. There was a trend towards higher GPC and WGC in the 6+8 group in the background *Glu-A1a*/*Glu-D1ah* but the reverse situation occurred in *Glu-A1a*/*Glu-D1a*. No significant differences between 6+8 and 7*+8 were observed for the other two subunit backgrounds. SED, one of most important predictive characteristics for dough strength, differed significantly between 6+8 and 7*+8 within three subunit backgrounds (Table 5). The effect of HMW-GS 6+8 was most pronounced in the background of *Glu-A1c*/*Glu-D1a*. For example, the SED values of the 6+8 group were higher by 35.5, 32.7 and 34.2% than that of the 7*+8 group in E2, E3, and mean over these two environments, respectively. Overall, RIL with 6+8 had higher FN particularly in the subunit backgrounds *Glu-A1c*/*Glu-D1a* and *Glu-A1c*/*Glu-D1ah*.

Effect of Glu-B1d alleles on Farinograph parameters

The RIL containing subunit 6+8 had significantly higher FWA than those with 7*+8 in the background *Glu-A1a*/*Glu-D1ah*, but no significant differences between 6+8 and 7*+8 were observed in other backgrounds (Table 6). For DDT, DST and BRT, there was a similar trend where means for RIL with 6+8 at *Glu-B1* tended to be higher than those with 7*+8 in backgrounds *Glu-A1c/Glu-D1a* and *Glu-A1c/Glu-D1ah*. For these three parameters, the RIL with 6+8 also had slightly higher values in the other two backgrounds although the differences between two groups were not statistically significant. Contrarily, the values of SOF for the 6+8 group were consistently lower than for the 7*+8 group, particularly pronounced in the backgrounds *Glu-A1c/Glu-D1a* and *Glu-A1c/Glu-D1ah*.

Effect of Glu-B1d alleles on RVA parameters

The RIL with 6+8 in combination with *Glu-A1c/Glu-D1a*, had significantly higher values for PV, HT, BD, FV, SB and PET compared with those with subunit 7*+8, the only exception being BD in E3 (Table 7). This trend also applied to the background *Glu-A1c/Glu-D1ah* although differences were not statistically significant in E3. Significant differences for these parameters in the *Glu-A1a/Glu-D1a* background, 6+8 > 7*+8, were observed for E3 and the mean of environments, but not for E2. There were no significant differences for PAT or within the subunit background *Glu-A1a/Glu-D1ah*.

Effect of Glu-B1d on sensory assessment of DWCN

Significant differences between 6+8 and 7*+8 groups for total DWCN score were observed in two subunit backgrounds, *Glu-A1c/Glu-D1a* and *Glu-A1a/Glu-D1a* (Table 8). In both backgrounds, 6+8 group had significant higher NTS than the

Table 9. Phenotypic correlations between quality parameters and noodle assessment components
See Table 2 for abbreviations of the traits and their units. *$P < 0.05$, **$P < 0.01$, n.s., not significant

Traits	COL	APP	PAL	VEL	STI	SMO	TAS	NTS
GH	–0.06n.s.	–0.09n.s.	–0.06n.s.	0.03n.s.	0.02n.s.	–0.05n.s.	0.10n.s.	–0.02n.s.
GPC	–0.12n.s.	0.31**	0.00n.s.	0.27**	0.32**	–0.15*	0.01n.s.	0.21**
WGC	–0.13*	0.31**	0.04n.s.	0.40**	0.49**	0.02n.s.	0.12*	0.35**
SED	0.04n.s.	0.25**	0.21**	0.42**	0.35**	–0.01n.s.	0.03n.s.	0.36**
FN	0.34**	–0.07n.s.	0.03n.s.	–0.15*	–0.18**	0.03n.s.	–0.10n.s.	–0.06n.s.
FWH	0.19**	0.04n.s.	0.12*	0.13*	0.17**	0.13*	0.07n.s.	0.19**
*L**	0.42**	0.15*	0.31**	0.33**	0.38**	0.33**	0.10n.s.	0.45**
*b**	0.05n.s.	0.08n.s.	0.08n.s.	0.16**	0.17**	0.13*	0.06n.s.	0.17**
AC	–0.20**	0.02n.s.	–0.20**	–0.20**	–0.23**	–0.19**	–0.07n.s.	–0.25**
FWA	–0.18**	–0.15*	–0.18**	–0.14*	–0.18**	–0.24**	–0.06n.s.	–0.24**
DDT	0.00n.s.	0.25**	0.14*	0.35**	0.35**	0.01n.s.	0.05n.s.	0.32**
DST	0.12n.s.	0.08n.s.	0.23**	0.24**	0.12n.s.	–0.04n.s.	–0.02n.s.	0.20**
SOF	–0.21**	0.02n.s.	–0.23**	–0.12n.s.	0.05n.s.	0.02n.s.	0.13*	–0.10n.s.
BRT	0.09n.s.	0.11n.s.	0.21**	0.27**	0.18**	–0.04n.s.	–0.01n.s.	0.23**
PV	0.38**	–0.04n.s.	0.13*	0.02n.s.	0.01n.s.	0.19**	0.02n.s.	0.12*
TV	0.39**	–0.07n.s.	0.05n.s.	–0.08n.s.	–0.10n.s.	0.10n.s.	–0.07n.s.	0.01n.s.
BD	0.08n.s.	0.10n.s.	0.24**	0.32**	0.35**	0.37**	0.29**	0.39**
FV	0.40**	–0.06n.s.	0.08n.s.	–0.06n.s.	–0.09n.s.	0.11n.s.	–0.06n.s.	0.03n.s.
SB	0.37**	–0.01n.s.	0.10n.s.	–0.03n.s.	–0.08n.s.	0.13*	–0.03n.s.	0.06n.s.
PET	0.35**	–0.09n.s.	0.02n.s.	–0.17**	–0.21**	0.01n.s.	–0.09n.s.	–0.09n.s.
PAT	0.04n.s.	0.37**	0.23**	0.60**	0.68**	0.30**	0.27**	0.61**

7*+8 group in E3 and on average over two environments. Total score and components of sensory assessment of 6+8 group were similar to those of 7*+8 group in the subunit background *Glu-A1a/Glu-D1ah* with one exception, APP in E2. In the other subunit background, *Glu-A1c/Glu-D1ah*, the 6+8 group was significantly higher than 7*+8 group for GOL and SMO in E2 but the reverse was true for TAS in E2. As a result, there was little difference in total score. Within the background *Glu-A1a/Glu-D1a*, the 6+8 group had significantly higher COL in both environments, PAL in E3, and STI on average over two environments compared with the 7*+8 group.

For NTS, a wide range of variation and transgressive segregation was observed within both 6+8 and 7*+8 groups (Fig. 1). However, the 6+8 group contained a relatively higher percentage of lines with high NTS than the 7*+8 group in both E2 and E3. Eight lines containing subunit 6+8 exceeded a score 80, (three, three, one, one, respectively, for subunit combinations 'n, 6+8, 2+12', '1, 6+8, 2+12', 'n, 6+8, 1.5+10', and '1, 6+8, 1.5 +10' in E2), whereas only two lines with subunit combination '1, 7*+8, 1.5+10' achieved this score.

Relationship between quality characteristics and noodle sensory assessment components

Correlations between the quality characteristics and sensory assessment components of DWCN were calculated (Table 9). Of 168 phenotypic correlations, 88 were statistically significant at $P < 0.05$ or $P < 0.01$. GH was not correlated with any of the sensory assessment components. AC and FWA correlated significantly and negatively with most of sensory assessment components and total score. TV and FV were significantly correlated ($P < 0.01$) with COL but not with other sensory assessment components or total score. There were stronger relationships between quality and instrumental parameters including GPC, WGC, SED, FWH, *L**, DDT, PV, BD, PAT and sensory assessment components. In particular, the stronger correlations involving SED, *L**, BD, PAT may be useful for improving noodle quality though breeding.

Discussion

The results of this study suggest that there are no substantial adverse effects of HMW-GS 6+8, a subunit that occurs frequently in durum and synthetic hexaploid germplasm, on quality parameters and DWCN quality compared with HMW-GS 7*+8, a subunit commonly associated with good quality in bread wheat. Indeed, several lines containing HMW-GS 6+8 were ranked at the top of the list when progeny were sorted according to noodle quality. While these observations require further confirmation, it seems clear that there is no need to select against the subunit 6+8 derived from the durum genome present in synthetic hexaploid germplasm at least for DWCN. Eight of the top ten RIL in E2 and nine of the top ten RIL in E3 in NTS contained subunit 6+8 at *Glu-B1*. These results indicate that elite lines with improved wheat quality in south-western China can be identified during exploitation of elite genes in SHW for increasing yield and resistance to diseases and adverse conditions.

Further, the results provide evidence of variation dependent on combination or interaction of *Glu-B1* subunits with the HMW-GS at the *Glu-A1* and *Glu-D1* loci indicating that selection based on full glutenin composition would be advantageous. For example, Farinograph parameters DDT, DST and BRT for the 6+8 group were significantly higher than the 7*+8 group in both *Glu-A1c/Glu-D1a* and *Glu-A1c/Glu-D1ah* subunit backgrounds and while not statistically significant, this trend also applied to the other two subunit backgrounds (Tables 5, 6). This indicates that *Glu-B1d* may have the potential to improve the quality of gluten and dough strength of wheat grown in south-western China with weak gluten. Strong interactions between HMW-GS, LMW-GS and gliadins reported by Carrillo *et al*. (1990), Flæte and Uhlen (2003) and Liu *et al*. (2004) suggest that the genetic effect from LMW-GS and gliadin should also be considered in future studies.

Studies of the effect of HMW-GS 6+8 on bread quality have been limited by the low frequency in hexaploid germplasm and generally HMW-GS 6+8 has been regarded as 'poor subunit' (Payne 1987; Fu 1993; Zhao *et al*. 1994; Song *et al*. 2003). Studies on durum wheat by Ram (2003) and Ammar (2000) indicated that dough strength and/or bread-baking quality of 6 +8 was better than that of 20 or 7+8 and 20, respectively. Another study reported that lines with 6+8 had higher flour protein content, alveograph P : L ratio, and number of vitreous kernels but poor alveograph extensibility and strength

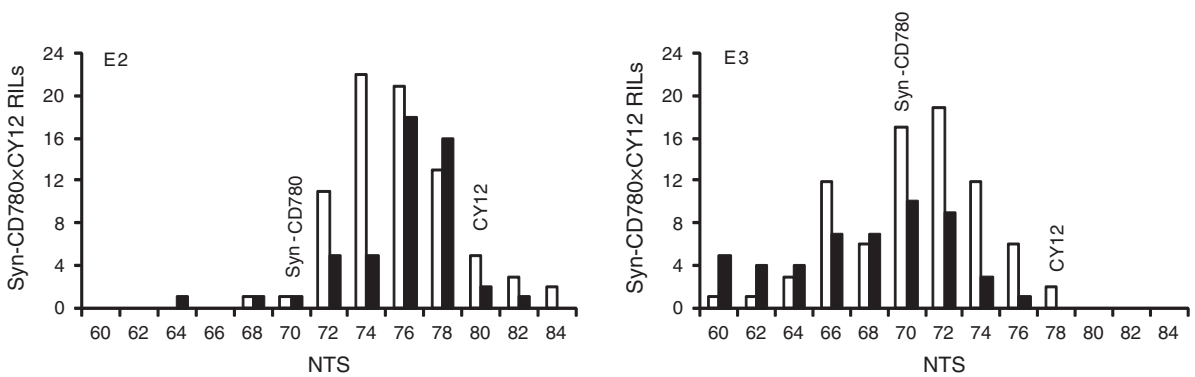

Fig. 1. Distribution of noodle total scores of dry, white Chinese noodles measured from Syn-CD780 × CY12 recombinant inbred lines, grouped according to high-molecular-weight glutenin subunits 6+8 (open bars) and 7*+8 (solid bars). E2, E3 indicate Guanghan site 2007 and Jingyan site 2007, respectively.

(Labuschagne and van Deventer 1995). No significant difference between 6+8 and 7+8 on extensibility of dough was found by Færgestad *et al*. (2004).

The locally adapted parent CY12 is regarded as a high-quality noodle-making cultivar by farmers and consumers in China. Its total noodle score in this study, however, was not as high (<80) as expected despite being significantly higher ($P < 0.01$) than the synthetic hexaploid parent, Syn-CD780. The mean total score for the population was 72.1 and only six lines exceeded 80 in E2. This may have been due to the ecoclimatic conditions or possibly the scoring system DWCN (SB/T10137-93) used in the present study. This scoring system was more suitable for wheat grain grown in northern China and a modified version was developed by Zhang *et al*. (2005) and Liu *et al*. (2002) in which more weight was given to noodle COL and SMO. The total scores of CY12 and/or its derivatives could increase in this modified scoring system because CY12 has higher FWH, lower AC, and higher SMO than other cultivars including the high-quality Australian wheat cultivar 'Sunco' (Storlie *et al*. 2006).

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