# Identification and Characterisation of a Novel Glutenin Subunit in Bread Wheat (*Triticum aestivum* L.)

A thesis submitted in fulfillment of the requirements for the degree of Doctor of Philosophy at the University of Adelaide

# By

### Xin Gao

**B** Agriculture (University of Northwest A&F)

School of Agriculture, Food and Wine
Faculty of Sciences
The University of Adelaide

### **List of Abbreviations**

AACC American Association of Cereal Chemists

AGT Australian Grain Technologies

A-PAGE Acid polyacrylamide gel electrophoresis

AWCC Australian Winter Cereals Collection

CSIRO Australian Commonwealth Scientific and Research Organisation

DNA Deoxyribonucleic acid

DTT Dithiothreitol

EBI European Bioinformatics Institute

EPP SDS-extractable polymeric protein

GRIS Genetic Resources Information System

HMW-GS High molecular weight glutenin subunit

HPLC High performance liquid chromatography

HRM High resolution melting

IPTG Isopropyl-β-*D*-thiogalactopyranoside

ISBP Insertion site-based polymorphism

LB Lysogeny broth

LC-MS Liquid chromatography-mass spectrometry

LMW-GS Low molecular weight glutenin subunit

LTR Long terminal repeat

MAR Matrix attachment region

MAS Molecular assisted selection

M<sub>r</sub> Molecular weight

NCBI National Center for Biotechnology Information

NIRS Near- infrared spectrophotometry

PCR Polymerase chain reaction

PEB Phosphate extraction buffer

PPK Putative protein kinase

PVDF Polyvinylidine difluoride

R<sub>max</sub> Extensograph maximum resistance

RP-HPLC Reverse-phase high performance liquid chromatography

SDS Sodium dodecyl sulphate

SDS-PAGE Sodium dodecyl sulphate polyacrylamide gel electrophoresis

SE-HPLC Size-exclusion high performance liquid chromatography

SNP Single nucleotide polymorphism

TCA Trichloroacetic acid

TFA Trifluoroacetic acid

TPP Total polymeric protein

UPP SDS-unextractable polymeric protein in total polymeric protein

UV Ultraviolet

4-VP 4-vinylpyridine

# **Table of Contents**

List of Abbreviations	i
Table of Contents	iii
List of Tables	ix
List of Figures	xi
List of Appendices	xix
Abstract	xxi
Declaration	xxiii
Acknowledgements	xxiv
Chapter 1 General Introduction	1
Chapter 2 Literature Review	4
2.1 Introduction	4
2.2 Endosperm Storage Proteins in Wheat Grain	5
2.2.1 Gliadins	5
2.2.2 Glutenins	6
2.3 Chromosomal Locations of Gluten Protein Genes	8
2.3.1 Gliadins	8
2.3.2 Low molecular weight glutenin subunits (LMW-GS)	9
2.3.3 High molecular weight glutenin subunits (HMW-GS)	9
2.4 Interactions of Gluten Subunits	10
2.5 Determination of Bread Making Quality Characteristics	15
2.5.1 Physical dough testing	15
2.5.2 Influence of dough rheology on bread making quality	16

2.5.3 Importance of glutenin size	16
2.5.4 Glutenin subunit composition	18
2.5.5 Genetic and environmental control of glutenin quality	18
2.6 Genetic Variation of HMW Glutenins	19
2.7 DNA Markers for HMW Glutenin Alleles	20
Chapter 3 A Second 'Overexpression' Allele at the Glu-B1 High-Molecule	ar-Weight
Glutenin Locus of Wheat: Sequence Characterisation and Functional Effects	23
Abstract	27
3.1 Introduction	28
3.2 Materials and Methods	30
3.2.1 Plant materials	30
3.2.2 Size-exclusion high-performance liquid chromatography (SE-HPLC)	30
3.2.3 SDS sedimentation test	31
3.2.4 SDS-PAGE analysis of glutenin and gliadin	32
3.2.5 Quantification of Bx7 expression	33
3.2.6 Molecular marker assays for puroindoline, serpin, storage protein act	ivator and
Glu-B1	34
3.2.7 Cloning and sequencing Bx genes from H45, VQ0437 and Glenlea	35
3.2.8 Restriction digest assay to detect a DNA polymorphism	36
3.3 Results	36
3.3.1 Comparison of the flour properties, protein composition and genotype	oes of H45
and VQ0437	36
3.3.2 Comparison of the protein composition of H45 and VQ0437	37

3.3.3 Comparison of the genotypes of H45 and VQ0437	41
3.3.4 Sequences of Bx7 alleles	44
3.3.5 Variation among H45/VQ0437 F <sub>2</sub> progeny	46
3.4 Discussion	48
Chapter 4 Screening of Wheat Germplasm for Bx Overexpression Alleles a	t the Glu-B1
Locus	52
4.1 Introduction	52
4.2 Materials and Methods	53
4.2.1 Plant materials	53
4.2.2 Molecular marker assay and restriction digestion assay on a p	oanel of wheat
cultivars	54
4.2.3 SDS-PAGE analysis of HMW glutenins	54
4.2.4 Reversed phase high-performance liquid chromatography (RP-H	PLC)54
4.2.5 Size-exclusion high-performance liquid chromatography (SE-HP	'LC)55
4.3 Results	58
4.3.1 Molecular marker assay on a panel of wheat cultivars	58
4.3.2 HMW-GS composition analysis and SE-HPLC analysis on a p	oanel of wheat
lines	60
4.3.3 Restriction digestion assay on a panel of wheat lines that o	verexpress Bx
subunits	65
4.4 Discussion	66
4.4.1 Germplasm screening for <i>Glu-B1br</i> allele	66
4.4.2 Ancestral sources of Bx overexpression alleles	68

4	4.4.3 Possible sources that could be tested for the <i>Glu-B1br</i> allele72
2	4.4.4 Evolution of Bx overexpression alleles
4	4.4.5 Possible approaches to detect specific alleles for quality selection in wheat
ŀ	preeding77
Chapter	5 Efforts Made to Develop Alternative Markers for the <i>Glu-B1br</i> Allele78
5.1 In	ntroduction78
5.2 N	Naterials and Methods79
5	5.2.1 Plant materials79
5	5.2.2 Cloning and sequencing left and right junctions of a long terminal repeat (LTR)
r	retroelement at <i>Glu-B1</i> locus79
5	5.2.3 High resolution melting analysis for detection of DNA polymorphism in
i	ntrons of putative protein kinase gene at Glu-B1 locus and with ISBP markers in
ר	ГаВАС1215C0680
5	5.2.4 SSR genotyping analysis associated with UPP distribution84
5.3 R	Results84
5	5.3.1 Cloning and sequencing left and right junctions of a long terminal repeat (LTR)
r	retroelement at <i>Glu-B1</i> locus84
5	5.3.2 High resolution melting analysis for detection of DNA polymorphism in
i	ntrons of putative protein kinase gene at <i>Glu-B1</i> locus
5	5.3.3 High resolution melting analysis for detection of DNA polymorphism with
I	SBP markers in TaBAC1215C0687
5	5.3.4 SSR genotyping analysis and marker regression analysis93
5.4 D	Discussion95

5.4.1 DNA polymorphism targeted for marker design to distinguish the <i>Glu-E</i>	31 <i>b</i> r
allele	95
5.4.2 SSR genotyping analysis of association between SSR markers	and
unextractable polymeric protein	96
5.4.3 Possible approaches to detect DNA polymorphism associated with Glu-E	31 <i>br</i>
allele	96
Chapter 6 A Cysteine in the Repetitive Domain of a High-Molecular-Weight Glute	enin
Subunit Interferes with the Mixing Properties of Wheat Dough	98
Abstract	.102
6.1 Introduction	.103
6.2 Materials and Methods	.106
6.2.1 Site-directed mutagenesis	.106
6.2.2 Preparation of flour samples	.106
6.2.3 Analysis of mixing properties of plain flour samples	.107
6.2.4 Heterologous expression of high molecular weight glutenin subunit genes	.107
6.2.5 Isolation of heterologously expressed proteins	.108
6.2.6 Analysis of heterologously expressed proteins	.109
6.2.7 SDS sedimentation test	.109
6.2.8 Dough mixing test	.110
6.2.9 Size-exclusion high-performance liquid chromatography (SE-HPLC)	.111
6.3 Results	.111
6.3.1 Site-directed mutagenesis of <i>Bx7.1</i>	.111
6.3.2 Mixing and physiochemical properties of plain flour samples	.112

6.3.3 Heterologous expression of HMW-GS
6.3.4 Effects of incorporated proteins on SDS sedimentation volume116
6.3.5 Effects of incorporated proteins on mixing properties and unextractable
polymeric protein117
6.4 Discussion
6.4.1 Site-directed mutagenesis and heterologous expression of HMW-GS119
6.4.2 Effects of heterologously expressed glutenin subunits on SDS sedimentation
volume119
6.4.3 Conditions and base flour for polypeptide incorporation120
6.4.4 Effects of the incorporation of the heterologously expressed Bx7 <sup>OE</sup> and
Bx7 <sup>OE</sup> -like proteins in dough mixing tests122
6.4.5 Effect of Bx7 subunits on water absorption properties123
6.4.6 The extra cysteine residue and its effect on dough properties125
Chapter 7 General Discussion127
Chapter 8 Conclusions134
Chapter 9 Contributions to Knowledge136
Appendices138
Qafarancas 151

# **List of Tables**

<b>Table 3.1</b> Restriction fragments expected for an assay in which the restriction enzyme <i>Rsa</i> I
is used to digest a 2,391 bp fragment amplified from the first of two x-type
high-molecular-weight glutenin genes at the Glu-B1 locus of Glenlea, H45 and
VQ0437 wheat46
Table 4.1 Pedigrees of wheat lines.   56
Table 4.2 Quantities of individual alkylated high molecular weight glutenin subunits encoded
at the Glu-A1, Glu-B1 and Glu-D1 loci, expressed as percentages of the total amount
of high molecular weight glutenin as assessed by reverse-phase high-performance
liquid chromatography, and the percentage of unextractable polymeric protein (UPP)
as assessed by size-exclusion high-performance liquid chromatography, for 12 lines
of wheat64
<b>Table 5.1</b> Primers designed to amplify small intron regions of a putative protein kinase gene
based on the DNA sequence of TaBAC1215C06 (EU157184)82
Table 5.2 Insertion site-based polymorphism (ISBP) markers within TaBAC1215C06
designed by <i>IsbpFinder</i> program83
Table 5.3 Regression analysis between SSR markers and unextractable polymeric protein
among F <sub>2</sub> progeny of H45 and VQ043794
<b>Table 6.1</b> Protein and moisture contents, dough mixing properties assessed with a 10-g
mixograph, SDS sedimentation volume and SDS-unextractable polymeric protein

(UPP) of flour samples milled from four lines of wheat
Table 6.2 SDS sedimentation volumes of samples of base flour milled from Gabo wheat with
and without incorporation of heterologously expressed high-molecular weight
glutenin subunits116

# **List of Figures**

Fig. 2.1 The classification and nomenciature of wheat gluten proteins separated by
SDS-PAGE. The D-type LMW subunits are only minor components and are not
clearly resolved in the separation shown6
<b>Fig. 2.2</b> SDS-PAGE of HMW glutenin subunits encoded at the <i>Glu-1</i> loci
Fig. 2.3 Primary structure of gliadin and glutenin subunit types according to Wieser (2007).
Cysteine residues are marked as 'C'. Putative cysteines involved in inter-molecular
disulphide bonds are marked with '*'. Dashed lines represent intra-molecular
disulphide bonds14
Fig. 3.1 One-dimensional SDS-PAGE of glutenins extracted from flour of Chinese Spring
(CS), Gabo (Ga), H45, VQ0437 (VQ), Glenlea (Gl), Janz (Ja), Aroona (Ar) and
Wilgoyne (Wi) wheat. HMW-GS and LMW-GS high- and low-molecular-weight
glutenin subunits, respectively. 1 and 2* HMW-GS encoded by Glu-A1a and
Glu-A1b, respectively. 7 and 8 HMW-GS encoded by Glu-B1b. 17 and 18 HMW-GS
encoded by Glu-B1i. 7* and 9 HMW-GS encoded by Glu-B1c. 2 and 12 HMW-GS
encoded by Glu-D1a. 5 and 10 HMW-GS encoded by Glu-D1d38
Fig. 3.2 One-dimensional SDS-PAGE of gliadins extracted from flour of Chinese Spring (CS)
Gabo (Ga), H45, VQ0437 (VQ), Glenlea (Gl), Janz (Ja), Aroona (Ar) and Wilgoyne
(Wi) wheat
<b>Fig. 3.3</b> Experion <sup>TM</sup> automatic electropherograms of high-molecular-weight glutenin subunits
extracted from flour of Chinese Spring, Glenlea, H45 and VQ0437 wheat40

Fig. 3.	4 PCR products amplified with primers for the puroindoline genes Pina-D1 and
	Pinb-D1 from genomic DNA of H45, VQ0437 (VQ), Glenlea (Gl), Currawong (Cu;
	Pina-D1b / Pinb-D1a) and Stiletto (St; Pina-D1a / Pinb-D1b) wheat. M: 100 bp
	ladder42
Fig. 3.5	S PCR products amplified with primers for the serpin gene <i>Srp5B</i> from genomic DNA
	of H45, VQ0437 (VQ), Glenlea (Gl; Srp5Bb) and Glover (St; Srp5Ba) wheat and
	products amplified with primers for the storage protein activator gene Spa-B from
	Chinese Spring (CS), Glenlea (Gl), H45 and VQ0437 (VQ) wheat. M: 100 bp
	ladder
F: 2	
Fig. 3.0	6 PCR products amplified with BxFp and MAR primers for the Bx glutenin genes
	from genomic DNA of Janz (Ja, Bx7*), Chinese Spring (CS, Bx7), Glenlea (Gl,
	Bx7 <sup>OE</sup> ), H45 and VQ0437 (VQ) wheat. M: 100 bp ladder43
Fig. 3.7	7 PCR products amplified from genomic DNA of H45, VQ0437 (VQ), Glenlea (Gl;
	Bx7 <sup>OE</sup> ), Janz (Ja; Bx7*) and Chinese Spring (CS; Bx7) wheat using primers
	designed at the left and right junctions of a retroelement between duplicate copies of
	the Bx gene in the <i>Glu-B1al</i> allele of Glenlea. M: 100 bp ladder43
Fig. 3.8	3 Amino acid sequences translated from the nucleotide sequence of a duplicated gene
	at the $Glu$ - $B1$ locus that encodes the high-molecular-weight glutenin subunit $Bx7^{OE}$
	in Glenlea wheat (EU157184), aligned with the amino acid sequences translated
	from each copy of the corresponding gene from the wheat variety H45 (JF938070,
	JF938071) and the wheat breeding line VQ0437 (JF938072, JF938073). The
	positions of cysteine residues are shown by arrows45

Fig. 3.9	Frequency distribution of percentage SDS-unextractable polymeric protein in flour
	samples of $F_3$ grains harvested from $F_2$ plants from a cross between H45 and
	VQ0437
Fig. 3.1	<b>0</b> Restriction fragments from <i>Rsa</i> I digestion of PCR products of first of two x-type
	high-molecular weight glutenin genes at the Glu-B1 locus of H45, VQ0437 (VQ)
	and sets of 20 H45/VQ0437 $F_2$ plants with low and high SDS-unextractable
	polymeric protein
Fig. 4.1	PCR products amplified from genomic DNA of a panel of wheat cultivars using
	primers designed at the left (447 bp) and right (884 bp) junctions of a retroelement
	between duplicate copies of the Bx gene in the Glu-B1al allele of Glenlea. Positive
	control Glenlea $(Bx7^{OE})$ and negative controls Chinese Spring $(Bx7)$ , Janz $(Bx7*)$
	were included. M: 100 bp ladder
Fig. 4.2	One-dimensional SDS-PAGE of HMW glutenins extracted from flour of Chinese
	Spring, Janz, Glenlea, H45, VQ0437, Kukri, Chara, AGT Katana, Magenta, Mace,
	LongReach Lincoln, and Wyalkatchem wheat. 1 and 2* HMW-GS encoded by
	$Glu$ - $A1a$ and $Glu$ - $A1b$ , respectively. 7 and 8 HMW-GS encoded by $Glu$ - $B1b$ . $7^{OE}$ and
	8* HMW-GS encoded by Glu-B1al. 7* and 8 HMW-GS encoded by Glu-B1u. 2 and
	12 HMW-GS encoded by <i>Glu-D1a</i> . 5 and 10 HMW-GS encoded by <i>Glu-D1d</i> 61
Fig. 4.3	RP-HPLC chromatograms of various wheat lines
Fig. 4.4	4 Restriction fragments from Rsa I digestion of PCR products of first Bx
	high-molecular weight glutenin gene of a panel of wheat cultivars, with Glenlea,

H45 and wheat line V	Q0437 as controls. M: 1	pUC19 DNA/MspI	(HpaII) ladder65

- Fig. 4.5 One-dimensional SDS-PAGE of HMW glutenins extracted from flour of single seed of Mace, LongReach Lincoln, three lines of Wyalkatchem from a mixed stock from AWCC. 1 and 2\* HMW-GS encoded by *Glu-A1a* and *Glu-A1b*, respectively. 7<sup>OE</sup> and 8\* HMW-GS encoded by *Glu-B1al*.13 and 16 HMW-GS encoded by *Glu-B1f*. 2 and 12 HMW-GS encoded by *Glu-D1a*.
- **Fig. 4.6** RP-HPLC chromatogram of flour milled from 10 Wyalkatchem grains from AWCC.

  1 HMW-GS encoded by *Glu-A1a*. 7<sup>OE</sup> and 8\* HMW-GS encoded by *Glu-B1al*. 13 and 16 HMW-GS encoded by *Glu-B1f*. 2 and 12 HMW-GS encoded by *Glu-D1a*...68
- **Fig. 4.7** Pedigree of Glenlea. The accessions with detailed pedigrees could be tracked back to the possible accessions carrying the original Bx overexpression allele. Detailed pedigrees not shown for other accessions that unlikely inherited the Bx overexpression allele based on the information provided by GRIS. G+ Positive result tested with LTR markers (Ragupathy et al. 2008) in this research, R+/R-Positive/negative result tested with LTR markers (Ragupathy et al. 2008)......70

Fig. 4.9	Pedigree of H45: Kalyansona/Bluebird//Anza*3/WW80/3/Olympic*2/Ciano 67. The
	accessions with detailed pedigree information could be tracked back to the possible
	accessions carrying the original Bx overexpression allele. Detailed pedigrees not
	shown for other accessions that unlikely inherited the Bx overexpression allele based
	on the information provided by GRIS. $^{\mathrm{G+/G-}}$ Positive/negative result tested with LTR
	markers (Ragupathy et al. 2008) in this research, R+/R- Positive/negative result tested
	with LTR markers (Ragupathy et al. 2008)74

- **Fig. 5.2** DNA polymorphism analysis in intron regions of putative protein kinase gene at *Glu-B1* locus. A. PCR products amplified with PPK primers from genomic DNA of Glenlea, H45, VQ0437 and a progeny of H45 and VQ0437 F<sub>2</sub>-3, with Chinese

Spring and its nullisomic-tetrasomic lines N1AT1B, N1AT1D, N1BT1A, N1BT1D, N1DT1A, and N1DT1B and water as controls. B. High-resolution melting curves for these PCR products, with Glenlea and VQ0437 marked in blue, H45 and F<sub>2</sub>-3 marked in red and Chinese Spring and its nullisomic-tetrasomic lines marked in green.

Fig. 5.3 DNA polymorphism analysis with insertion site-based polymorphism markers designed based on sequence of TaBAC1215C06 (EU157184). A. PCR products amplified from genomic DNA of Glenlea, H45, VQ0437 and a progeny of H45 and VQ0437 F<sub>2</sub>-3, with Chinese Spring and its nullisomic-tetrasomic lines N1AT1B, N1AT1D, N1BT1A, N1BT1D, N1DT1A, and N1DT1B and water as controls. 1. PCR products amplified with ISBP-2339. 2. PCR products amplified with ISBP-11765. 4. PCR products amplified with ISBP-11868. 5. PCR products amplified with ISBP-18254. B. High-resolution melting curves for these PCR products, with Glenlea and VQ0437 marked in blue, H45 and F<sub>2</sub>-3 marked in red and Chinese Spring and its nullisomic-tetrasomic lines marked in green.

Fig. 5.4 DNA polymorphism analysis with insertion site-based polymorphism markers designed based on sequence of TaBAC1215C06 (EU157184). A. PCR products amplified from genomic DNA of Glenlea, H45, VQ0437 and a progeny of H45 and VQ0437 F<sub>2</sub>-3, with Chinese Spring and its nullisomic-tetrasomic lines N1AT1B, N1AT1D, N1BT1A, N1BT1D, N1DT1A, and N1DT1B and water as controls. 1. PCR products amplified with ISBP-3565. 2. PCR products amplified with ISBP-14667. 3. PCR products amplified with ISBP-24694. 4. PCR products

amplified with ISBP-35718. B. High-resolution melting curves for these	PCR
products, with Glenlea and VQ0437 marked in blue, H45 and F <sub>2</sub> -3 marked in re	d and
Chinese Spring and its nullisomic-tetrasomic lines marked in green	90

- Fig. 5.5 DNA polymorphism analysis with insertion site-based polymorphism markers designed based on sequence of TaBAC1215C06 (EU157184). A. PCR products amplified from genomic DNA of Glenlea, H45, VQ0437 and a progeny of H45 and VQ0437 F<sub>2</sub>-3, with Chinese Spring and its nullisomic-tetrasomic lines N1AT1B, N1AT1D, N1BT1A, N1BT1D, N1DT1A, and N1DT1B and water as controls. 1. PCR products amplified with ISBP-5194. 2. PCR products amplified with ISBP-38013. 3. PCR products amplified with ISBP-42211. B. High-resolution melting curves for these PCR products, with Glenlea and VQ0437 marked in blue, H45 and F<sub>2</sub>-3 marked in red and Chinese Spring and its nullisomic-tetrasomic lines marked in green.
- **Fig. 5.6** Linkage groups of H45/VQ0437 population with eight SSR markers on Chromosome 1B, with genetic distances shown in cM. .....94
- **Fig. 6.1** SDS–PAGE profiles of purified and heterologously expressed HMW-GS. Lanes 1-3, HMW components extracted from Glenlea, H45 and VQ0437 flour; lanes 4-10, purified proteins of Bx7<sup>OE</sup> copy1, Bx7<sup>OE</sup> copy2, Bx7.1, Bx7.2, Bx7.3, Bx7<sup>OE</sup> from VQ0437 and MutBx7.1; lane 11, pET-24a in BL21 (DE3)-plysS cells induced by isopropyl-β-*D*-thiogalactopyranoside; lane 12, pET-24a-Bx7 in BL21 (DE3)-plysS cells not induced by isopropyl-β-*D*-thiogalactopyranoside; lanes 13-19, pET-24a-Bx7<sup>OE</sup> copy1, pET-24a-Bx7<sup>OE</sup> copy2, pET-24a-Bx7.1, pET-24a-Bx7.2,

	pET-24a-Bx7.3, pET-24a-Bx7 <sup>OE</sup> -VQ0437 and pET-24a-MutBx7.1 in BL21
	(DE3)-plysS cells induced by isopropyl-β- <i>D</i> -thiogalactopyranoside115
Fig. 6.2	Percentage changes in dough mixing properties and unextractable polymeric protein
	with heterologously expressed glutenin subunits incorporated at two levels (20 mg
	and 40 mg) into 4 g of Gabo base flour, relative to those of the base flour118
Fig. 6.3	3 Schematic representations of (A) the Bx7 <sup>OE</sup> glutenin polypeptide showing the
	positions of its four cysteine residues and an expected intramolecular disulphide
	bond (dashed line), with two terminal-domain cysteines remaining available to
	participate in intermolecular linkages; (B) the Bx7.1 glutenin subunit showing the
	positions of its five cysteine residues and the same intramolecular disulphide bond
	that is expected in Bx7 <sup>OE</sup> , leaving two terminal-domain cysteines and one
	repetitive-domain cysteine available to participate in intermolecular linkages; (C)
	and (D) the Bx7.1 glutenin subunit showing two hypothetical combinations of
	intrachain disulphide bonds, each leaving one terminal-domain cysteine available to

### **List of Appendices**

Appendix 1. Size-exclusion HPLC separations of extractable and unextractable protein from
a control sample of bakers' flour and from flour milled from H45 and VQ0437 wheat
The areas to the left of the vertical dashed lines indicate polymeric protein138

- Appendix 2. The nucleotide sequence of a duplicated gene at the *Glu-B1* locus that encodes the high-molecular-weight glutenin subunit Bx7 in Glenlea wheat (EU157184), aligned with the sequences of corresponding genes from the wheat variety H45 (JF938070, JF938071) and the wheat breeding line VQ0437 (JF938072 JF938073). In the H45 and VQ0437 sequences, nucleotides that differ from the corresponding nucleotide in the Glenlea sequence are shown in white on a black background.......139
- Appendix 4. Alignment of amino acid sequences of high-molecular weight glutenin subunits encoded by the  $Bx7^{OE}$  genes of the Glu-B1al allele of Glenlea), the Bx7.1 and Bx7.2 genes of the Glu-B1br allele of H45, and the Bx7.3 and  $Bx7^{OE}$  genes of the Glu-B1bs allele of VQ0437 wheat and by a mutant gene (MutBx7.1) derived from Bx7.1 by site-directed mutagenesis. The regions of the protein shown are those that contain cysteine residues and/or in which there are sequence differences among the proteins. Conserved cysteine residues are boxed, and an extra cysteine residue is indicated by

an arrow. Amino acid differences are highlighted in grey.	.149
<b>Appendix 5.</b> 10-g mixograph mixing curves of Gabo, Glenlea, H45 and VQ0437	.150

#### **Abstract**

Bread is one of the major constituents of the human diet and wheat (*Triticum aestivum* L.) is the most important cereal for bread making. The gluten proteins (glutenins and gliadins) are recognised as important components affecting the processing quality of wheat flour. *Glu-B1al* is an allele that includes a duplication of a gene encoding an x-type high-molecular-weight glutenin subunit, and is thought to increase dough strength through overexpression of that subunit. In this research, a particular glutenin subunit in an Australian cultivar, H45, was investigated. H45 seemed to carry *Glu-B1al*, but it has relatively low unextractable polymeric protein (UPP, an indicator of weak dough). Two Bx genes from H45 were cloned and sequenced. Their sequences differ from each other, and each differ by four single nucleotide polymorphisms (SNPs) from the sequence of the Bx genes of *Glu-B1al* in the Canadian wheat cultivar Glenlea. One of the SNPs leads to an extra cysteine residue in one of the subunits. The *Glu-B1* allele of H45 was designated *Glu-B1br*.

With a restriction digest assay designed to distinguish the *Glu-B1br* allele from other overexpression alleles, it was demonstrated that *Glu-B1br* is co-inherited with low UPP. Among accessions present in the pedigree of H45 and accessions carrying overexpression alleles, *Glu-B1br* was detected only in H45.

Efforts were made to develop alternative markers for *Glu-B1br*. Potential polymorphic regions within or close to *Glu-B1* locus were investigated, but no closely linked polymorphisms were found that could be targeted for marker design.

Individual glutenin subunits encoded by overexpression alleles and a mutant gene (MutBx7.1)

derived from the first gene (*Bx7.1*) of *Glu-B1br* were obtained by heterologous expression. Flour incorporation tests showed that the glutenin subunit with the extra cysteine residue (Bx7.1) affects flour and dough mixing properties differently from MutBx7.1 and from the Bx subunits encoded by other overexpression alleles. Given that Bx7.1 and MutBx7.1 differ only with respect to the additional cysteine in Bx7.1, the effects of Bx7.1 on the dough properties of H45 can be attributed directly to that cysteine, which may act by impeding polymerisation.

### **Declaration**

I certify that this work contains no material which has been accepted for the award of any other degree or diploma in any university or other tertiary institution and, to the best of my knowledge and belief, contains no material previously published or written by another person, except where due reference has been made in the text. In addition, I certify that no part of this work will, in the future, be used in a submission for any other degree or diploma in any university or other tertiary institution without the prior approval of the University of Adelaide and where applicable, any partner institution responsible for the joint-award of this degree.

I give consent to this copy of my thesis when deposited in the University Library, being made available for loan and photocopying, subject to the provisions of the Copyright Act 1968.

The author acknowledges that copyright of published works contained within this thesis resides with the copyright holder(s) of those works.

I also give permission for the digital version of my thesis to be made available on the web, via the University's digital research repository, the Library catalogue and also through web search engines, unless permission has been granted by the University to restrict access for a period of time.

### Acknowledgements

I gratefully acknowledge my principal supervisor Professor Diane Mather, co-supervisor Associate Professor Kenneth Chalmers and external supervisor Associate Professor Daryl Mares, who have always supervised, supported and encouraged me during my research project. Professor Diane Mather kindly offered me this opportunity to study in the University of Adelaide as an international student and provided me much help initially from my application for my scholarship. She always gave me valuable advice and comments on research design and implementation and especially on my thesis and manuscript writing. She respected and supported my own ideas and took the initiative to cooperate with other research institutes, which improved the research. I also appreciated her patience to even teach me English grammar and language rules when I wrote up this thesis, which is quite critical to me as a second language speaker.

I would like to sincerely thank the University of Adelaide, China Scholarship Council and Shandong University for awarding me the scholarship. Professor Richard Russell, Ms Sandy McConachy and Ms Iris Liu at the University of Adelaide gave me much instruction and encouragement during my candidature. Professor Guangmin Xia, who was my supervisor at Shandong University, gave me much support and trust throughout study.

I would like to thank Dr Marie Appelbee and Dr Genet Mekuria, who initiated this research project and passed it to me with great help and advice.

I thank the South Australian Research and Development Institute, Australian Research Council Centre of Excellence in Plant Cell Walls, Australian Centre for Plant Functional Genomics and CSIRO Division of Plant Industry for providing laboratory equipment and facilities, and the School of Agriculture, Food and Wine for research funding.

I would like to express my deep appreciation to the following people,

Dr Haydn Kuchel for drawing our attention to the properties of H45;

Dr Howard Eagles for valuable advice, including the suggestion of VQ0437 as a useful control and for providing seeds of several accessions and information on pedigrees;

Dr Russell Eastwood for providing seed of VQ0437;

Dr Karen Cane for providing protocols for assaying puroindoline, serpin and Spa-B alleles;

Dr Robert Dickinson for assistance with preparation of some of the figures;

Dr Qisen Zhang for assistance and advice on heterologous expression;

Dr Marcus Newberry and Mr Ibrahim Kutty for assistance in the operation of the z-arm mixer and 10-g mixograph system and data analysis;

Associate Professor Peter Hoffmann and Mr James Eddes for discussions on possible uses of mass spectrometry to investigate disulphide linkages between glutenin subunits;

Ms Elise Tucker for kind advice and help in the skills of molecular biotechnology;

Mr Greg Lott for assistance in mapping data analysis;

Dr Vidya Nagasandra for assistance in the operation of SE-HPLC analysis;

Post-graduate coordinators Dr Elton Li and the late Professor Otto Schmidt for support and

encouragement;

Dr Margaret Cargill and lecturers of the Integrated Bridging Program for helping me to develop academic writing skills;

Dr Ming Li for assistance in proofreading this thesis; and

all members of the University of Adelaide Molecular Marker Lab for laboratory guidance and encouragement, and especially for their friendship.

Last but not least, I would like to thank my parents and my husband Younian Li for their selfless love, solicitude and support.