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Australian wheat for the sponge and dough bread making process

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Abstract. This work investigates the suitability of Australian wheats for the sponge and dough bread market, and determines the wheat quality attributes most important for large loaf volume. A group of 30 genotypes was selected for quality testing and baking using a purpose-developed sponge and dough test baking method. Genotypes were grown at 2 sites in Queensland during winter of 2001 and 2002, and then grain from the field trials was tested in the laboratory. The traits measured included grain, flour, and dough quality, along with loaf volume as the main trait of interest. Glutenin alleles and *Wx-B1* allele status of the genotypes were also determined. Genetic correlations were calculated between loaf volume and all the quality traits. The quality trait with the strongest relationship to loaf volume was flour swelling volume. Glutenin alleles and *Wx-B1* alleles may also be important for sponge and dough bread quality but the data presented here were insufficient to draw strong conclusions. Consistent, large sponge and dough loaf volumes (>850 cm^3) were achieved by the Batavia/Pelsart double haploids QT8753, QT10793, and QT10778. The wheat varieties Hartog and Kennedy also performed well. The work demonstrated that Australia can produce wheat suitable for this market.

Additional keywords: wheat quality, loaf volume, gluten, starch, flour swelling volume.

Introduction

Sponge and dough bread is produced in north and south-east Asian countries to service their market for white, sliced bread. Surveys of bread production methods and flour quality in Asia have indicated that dough strength is an important quality attribute for this product. Currently, wheat for this market is supplied mainly by the USA and Canada, using Dark Northern Spring, Canadian Western Red Spring, and Canadian Western Extra Strong grades with protein over 13% and strong dough properties. This Asian market may be equally well supplied from Australia. To achieve this goal, the quality requirements for sponge and dough bread need to be understood and applied to Australian wheat-breeding programs.

The name sponge and dough is derived from its means of production. Unlike the rapid dough process common in Australia, sponge and dough bread manufacture involves fermenting a portion of the ingredients for several hours to form a light fluffy sponge. This is followed by remixing with the remainder of ingredients to form more conventional bread dough.

Research into the sponge and dough bread making system has been limited to studies in the USA, Canada, and Japan (Ikezoe and Tipples 1968; Kilborn *et al*. 1981; Kilborn and Preston 1982; Preston and Kilborn 1982; Shiiba *et al*. 1990; Yamada and Preston 1994). Collectively, research has focussed on examining the baking system, without detailing the relative importance of specific wheat quality traits for good sponge and dough bread. Indeed, there seems to be a dearth of investigations relating current wheat quality test methods and baking performance in the sponge and dough system.

Existing test methods can be divided into 3 groups: those that directly test grain quality; those that test flour or dough quality; and those that test end-product quality. Grain quality tests are easy to interpret as they focus on a single measure such as protein, moisture, or hardness. However, interpreting flour test results is more difficult since they broadly measure different physical responses of flour to interactions with water, heat, energy, and time. Unfortunately, the complex systems that physical dough tests are designed to measure are very different from that which occurs when processing flour into a consumable product such as noodles, biscuits, or bread. A study conducted in 1995 relating flour-water farinograph and extensograph measurements to those conducted on a bread formula system (Oliver and Allen 1992) concluded that the 2 systems did not relate well.

This study applies current tests of wheat quality in an effort to understand what is important in the sponge and dough baking system. For example, the extent of starch damage during milling could be important by affecting the amount of sugars available during dough fermentation (Simmonds

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1989). Also, starch gelatinisation during baking is mimicked by the flour swelling volume test, which involves heating flour in an excess of water. The measurement reflects the cumulative effect of starch quality, particularly the amylose-amylopectin ratio (AACC 2000). Amylose content is largely determined by the granule-bound starch synthase protein encoded for by 3 'Wx' alleles. A mutated form of the *Wx-B1* allele is associated with very low amylose content, good Japanese udon noodle quality, and a higher flour swelling volume (Zhao *et al*. 1998).

Protein is another factor known to play a key role in wheat quality. In bread baking systems, a gluten-starch matrix stabilises the gas cells important for good crumb structure and large loaf volume bread (Gan *et al*. 1990). In addition the importance of protein quality, especially glutenin to gliadin ratios, for the baking potential of flour has been well demonstrated by many fractionation and reconstitution studies (MacRitchie 1989). High molecular weight and low molecular weight subunits of glutenin have been successfully used as genetic markers for grain quality (Cornish *et al*. 2001). Measurement of glutenin alleles present in genotypes with a range of sponge and dough loaf volumes would be a judicious step to better understand the importance of protein quality in this product.

Measures of dough rheology, such as that provided by the mixograph (Bekes *et al*. 2001), could also be useful. The mixograph band-width allows determination of the number of elongation–rupture–relax cycles required for peak dough development (Appels *et al*. 2001) rather than just the time taken for development as measured by the farinograph and resistograph. During the elongation–rupture–relax cycles, flour becomes hydrated and a protein, pentosan, lipid, starch complex is formed. Since it is the nature of this complex that is important during baking, relationships between mixograph trace characteristics and sponge and dough loaf volume warrant investigation.

Because bread-baking systems are so complex and dynamic, the most unequivocal way to test a wheat's potential is to mill a sample, bake it, and measure the final loaf volume (cm^3). Crumb qualities such as structure and texture are also considered. But because test baking is costly and time-consuming and requires impractical large amounts of flour, a smaller scale test of sponge and dough bread quality would be invaluable. This paper reports on relationships between 13 measures of wheat quality and sponge and dough loaf volume in 30 Australian wheat cultivars. It is hoped that an understanding of which quality traits are important for this product will allow targetted assessment in wheat breeding and production of varieties preferred by this expanding Asian market.

Materials and methods

Eight cultivars and 22 advanced breeding lines (Table 1) expected to provide a range of quality attributes, including strong dough properties, were chosen for field production. Trials were grown at Roma in south-western Queensland in 2001 and at Roma and Biloela in central Queensland in 2002.

Table 1. Pedigrees of 30 genotypes selected to explore characteristics required for sponge and dough bread

76ECN, 1976 Elite Crossing Nursery; MEC3, Sonora 64A//Tezanos Pintos Precos/Yaqui 54

Line name	Pedigree
Babbler	Janz/Lark
Banks	PWTH/Condor sib//2*Condor
Baxter	Inia F 66/Gamut/Cook//Jupeteco F 73/3/Lerma Rojo 64/Sonora 64A//Timgalen Sib
Chara	Beulah Sib//Pavon Sib/Condor
Hartog	Vicam 71//Ciano F 67/Siete Cerros T 66/ 3/Kalyanbluebird
Kennedy	Seri M 82/Hartog
Kukri	76ECN44/76ECN36/3/Madden//6*MEC3/2*Gabo
Lang	3AG3/4*Condor//Cook/Sunco
QT8974	Cunningham/Sunco
QT8620	Gatcher Selection 50A/3*Cunningham//Janz
QT8750	Batavia*2/Pelsart double haploid (EGA Hume)
QT8753	Batavia*2/Pelsart double haploid
QT9616	Gatcher Selection 50A/3*Cunningham//Janz
QT9274	Batavia/2*Hartog
QT9276	Batavia/2*Hartog
QT9293	F60374.76/Maioral//Ciano T 79/3/CMH73A.497/ *2Magpie Sib
QT9346	Aus 1408/3*Janz//Cunningham
QT9347	Aus 1408/3*Janz//Cunningham
QT9673	Aus 1408/3*Janz//Cunningham
QT9683	Inia F 66/Gamut/Cook//Jupeteco F 73/3/Lerma Rojo 64/Sonora 64A//Timaglen Sib
QT9900	Vulcan/2*Janz
QT9933	Vulcan/2*Janz
QT9913	Janz/2*Opata
QT9916	Janz/2*Opata
QT9919	Pelsart/2*Hartog/Pitic
QT10181	Miskle/Janz
QT10183	Miskle/Janz
QT10757	2*Batavia/PelsartDH
QT10778	2*Batavia/PelsartDH
QT10793	2*Batavia/PelsartDH

Experimental design

The wheat quality data in this trial were obtained from a multi-phase process. The first phase involved the field trial where genotypes were grown in plots. Grain was harvested from these plots and put through a milling process to produce flour. Flour was then tested in the laboratory to produce dough measurements and baking scores. The quality traits therefore contain variation from each of the field, milling, and laboratory processes (Smith *et al*. 2001). In addition, the field trials were grown across several environments (2001 Roma, 2002 Biloela, 2002 Roma) so genotype × environment interaction needed to be considered. Consequently, at each phase of the experimental process, replication was incorporated.

The 2001 trial was a 2-phase design. The experiment consisted of 30 genotypes grown at one location (Roma) in a replicated trial. The trial was planted as a Latinised rowcolumn design, in a 2-dimensional array defined by rows and columns in the field. Grain samples from each field plot were split into 2 duplicate samples and then processed in the mill and laboratory. Plots were allocated to positions within the milling process using an incomplete block design with blocks being test day. The same randomization and level of duplication was carried forwards from

milling to the laboratory procedures. Through this field and laboratory duplication, the set of 30 genotypes was expanded to include a total of 90 samples.

The 2002 trial was a 3-phase design. The field phase involved growing the 30 genotypes at 2 locations, Roma and Biloela, each in a Latinised row–column design with 2 replicates. Once again, duplicate grain samples were taken from each field plot and allocated to the milling process using an incomplete block design for each site, with milling day forming the incomplete blocks. Whole grain measurements such as protein and falling number together with milling yield were measured at the second phase. Duplicate samples of flour were taken from these milled samples and allocated to the third phase of testing in the laboratory. Consequently, the set of 30 genotypes at 2 sites was expanded to include a total of 298 test samples.

Measurement of quality traits

Samples were cleaned through a Carter Dockage Tester (Carter Day International, Minneapolis, USA) over a 2-mm sieve to retain the main grain fraction. GAC 2100 Agri meter grain moisture, 1000-kernel weight, and NIR protein were performed on whole grain samples. Particle size index and falling number were performed on samples according to Approved Method 55-30 (AACC 2000) and ICC Method 107 (International Association for Cereal Science and Technology 1997), respectively. Samples were conditioned to 15% moisture before milling in a randomised order through a Buhler, MLU-202, pneumatic mill by Approved Method 26-21A (AACC 2000).

Water absorption (%) and dough development time (min) were determined using the 50-g Farinograph (Brabender Duisburg, Germany) as outlined in Method 06-02 (RACI 1995). Tests were repeated if the mean consistency at maximum development was not within 500 BU ±30 units.

Maximum extensibility (cm) and maximum resistance (BU) at 45 min were determined from 2 dough pieces of 150 g each from one mix as outlined in Method 06-01 (RACI 1995), using the farinograph-resistograph and extensograph (Brabender Duisburg, Germany). Results from the 2 dough pieces were accepted provided they agreed to within 15% of their mean value for each measure.

The 10-g mixograph was used for 2001 and 2002 harvest samples, according to Approved Method 54-40A (AACC 2000). The trace measurement, range of stability was used after a pilot study ($n = 90$) indicated that this measurement provided the only genetic correlation with sponge and dough loaf volume. Range of stability is defined as the distance between the 2 points where the line drawn through the curve peak parallel to the base cuts the edges of the curve (Harris 1943).

Sponge and dough test baking

A water-jacketed GRL-200 pin mixer (Muzeen and Blythe Ltd, Manitoba, Canada) was used for all mixing operations. The sponge component consisted of: flour 140 g, yeast 4 g, water 84 mL, bread improvers (calcium hydrogen orthophosphate 0.5 g, ammonium sulfate 0.06 g, malt flour 0.5 g) 1.62 g, mixed for 2 min at 60 rpm. Added water and waterbath temperatures were monitored and adjusted to achieve a finished sponge temperature of 26°C ± 0.5°C. The sponge was fermented in a sealed container at 28°C for 3 h and 55 min. The dough was formed with: flour 60 g, sugar 10 g, fat 6 g, salt 4 g, water variable, sponge total, mixed at 60 rpm until optimal dough development was observed by visual assessment (usually after 2–6 min mixing). Water temperatures were adjusted to achieve a finished dough temperature of 28°C ± 0.5°C. Water addition was calculated as:

$$\text{Total dough water mL} = (\text{Farinograph water absorption \%} - 6) \times 2 - 84\,\text{mL}$$

The mixed dough was rested for 20 min, divided into two 160-g dough pieces, moulded in a mono-universal moulder (D. Ayres, Jones and Co., Ltd, Swansea, Great Britain), rested for 10 min, moulded again, placed in an oiled 550-cm^3 loaf tin, then proofed at 39°C and 80% RH for 60 min. Loaves were baked for 15 min at 200°C, removed from the tin, cooled at room temperature, and the volume measured in a seed-displacement volumeter. Assessment and scoring for external appearance, oven spring and crumb texture, structure, and colour was completed between 18 and 24 h following baking. Test baking results reported are the average loaf volume of 2 dough pieces, from a single batch of dough divided before moulding.

A considerable amount of time was spent attempting to minimise sources of variation in the test baking method. Experiments with improver formulations, yeast storage and handling, mixing operations, moulder settings, cabinet temperatures, baking-tin dimensions, process timing, and general dough handling techniques were all examined carefully to eliminate possible sources of variation in the method. Air-bubble formation during moulding is an example of variation intrinsic to the method that is difficult to eliminate. A critical factor for repeatability of the method is timing. Each batch must be started at exactly equal intervals, so that time spent at each stage of the procedure is identical for each sample. Nonetheless, significant baking-day effects were found in the analysis and adjusted for in the statistical model. Randomisation and duplication of samples built into the statistical design meant that variation was measured using duplicated samples and not 'control' flour. Control flour was used for benchmark scoring of crumb qualites (baking score) but these scores are not reported in this work due to their qualitative nature and strong correlation with loaf volume.

The method was able to discriminate between flours of different quality used in Asian bread production (Fig. 1). With assistance from AWB, 3 grades of flour, Premium, Standard, and All-purpose, were obtained from FFM Berhard Mill in Malaysia and evaluated using the above baking method. Analytical data for these samples are listed in Appendix 1.

Statistical analysis

The extended mixed model approach of Smith *et al*. (2001) for multi-phase designs was used for analysis. Variance parameters were estimated using residual maximum likelihood (REML) (Patterson and Thompson 1971). The statistical model was fitted using samm (Butler *et al*. 2004), the S-Plus suite of functions for the statistical software program ASREML (Gilmour *et al*. 2001). Best linear unbiased predictors (BLUPs) for the random genotype effects were predicted for each quality trait. Biplots (Gabriel 1971) were constructed after performing

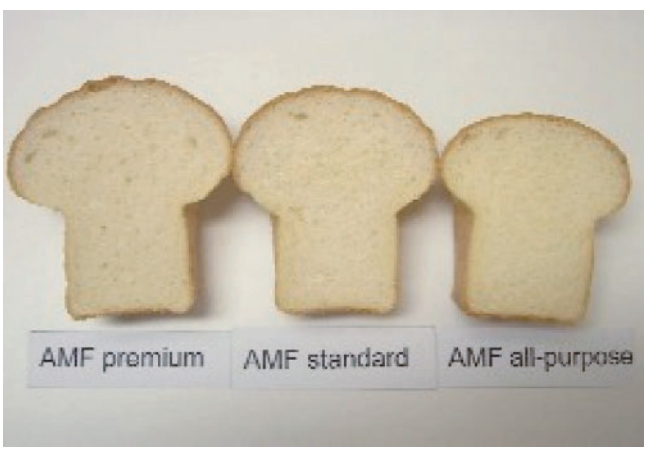

Fig. 1. Loaf volumes for Premium, Standard, and All-purpose grades of Asian milled flour (AMF) were 860 cm^3, 805 cm^3, and 680 cm^3, respectively.

principal component analysis on each of these sets of predictions. Genetic correlations were estimated between sites for each trait and the adequacy of a common correlation between sites or the need for separate correlations was tested. Where correlations between pairs of sites were high and similar, a common genotype effect for the trait was predicted across sites. A final biplot encompassing both 2001 and 2002 work was constructed after principal components analysis on the resulting combined and/or separate data. Genetic correlations were also calculated between loaf volume and all other traits for each site/year. The effect of glutenins and *Wx-B1* allele status on loaf volume was investigated by including each as a fixed effect factor in a linear mixed model analysis of loaf volume. Fixed effect means were estimated for loaf volume for each of the levels of the significant glutenin and *Wx-B1* allele factors.

Results

The genotypes provided a large range of quality test results for all the traits measured. The mean, standard deviation (s.d.), minimum, and maximum for each test are displayed in Table 2 for 2001 Roma harvest, in Table 3 for 2002 Roma harvest, and in Table 4 for 2002 Biloela harvest.

The samples from Roma (Table 3) and Biloela (Table 4) in 2002 differed in protein content. Samples from Roma had a protein content greater than 15% with the exception of one, which was slightly less at 14.8%, whereas the samples from Biloela were less than 15% with the exception of one at 16.1%. The samples from Roma also had relatively lower 1000-kernel weights (20.4–28.7 g), which suggested that the crop might have been stressed at this site compared to the previous year (Table 2) and also compared with the Biloela 2002 site (Table 4).

To broadly summarise test-baking results, the average loaf volume achieved by each of the 30 genotypes for both years and sites is displayed in Fig. 2.

Genetic correlations between the Biloela and Roma sites, 2002 harvest, were determined and are displayed in Table 5. Correlations between sites were greater than 0.6 for all traits except dough development time, NIR protein, and 1000-kernel weight. The remaining data were combined for all further analysis.

Table 2. Quality test result summary for 30 genotypes grown at Roma during 2001

Trait	Mean	s.d.	Min.	Max.
Loaf volume (cm^3)	807	51	683	920
NIR grain protein (%)	12	0.7	9.7	13.6
Falling number (s)	402	31	326	449
1000-kernel weight (g)	31	2.1	26.6	37.5
Particle size index	13	2	9	16
Milling yield (%)	77	1	75	79
Flour swelling volume (mL)	16	2	14	20
Max. extensograph				
Extensibility (cm)	22	2	16	27
Extens/protein (cm)	2	0	1	2
Resistance (BU)	501	72	246	680
Mixograph stability (min)	6	1	4	9
Farinograph				
Water absorption (%)	63	2	57	70
Dough development (min)	7	1	4	11

Table 3. Quality test result summary for 30 genotypes grown at Roma during 2002

Trait	Mean	s.d.	Min.	Max.
Loaf volume (cm^3)	833	59	635	950
NIR grain protein (%)	17	1	15	19
Falling number (s)	503	68	377	643
1000-kernel weight (g)	22.5	2.0	19	27
Particle size index	20	1	17	23
Milling yield (%)	73	1	70	76
Flour swelling volume (mL)	15	1	12	17
Max. extensograph				
Extensibility (cm)	23	3	18	27
Extens/protein (cm)	1	0	1	2
Resistance (BU)	662	84	473	865
Mixograph stability (min)	5	1	3	8
Farinograph				
Water absorption (%)	68	2	64	80
Dough development (min)	9	1	7	12

Table 4. Quality test result summary for 30 genotypes grown at Biloela during 2002

Trait	Mean	s.d.	Min.	Max.
Loaf volume (cm^3)	810	47	703	938
NIR grain protein (%)	13.4	1.0	11	16
Falling number (s)	448	43	347	558
1000-kernel weight (g)	23	2	20	28.7
Particle size index	14	1	11	17
Milling yield (%)	73	1	70	82
Flour swelling volume (mL)	15	1	13	19
Max. extensograph				
Extensibility (cm)	20	2	16	27
Extens/protein (cm)	1	0	1	2
Resistance (BU)	630	62	457	764
Mixograph stability (min)	7	2	4	14
Farinograph				
Water absorption (%)	64	2	58	74
Dough development (min)	8	1	6	13

Relationships between test results from the 2 harvest years, 2001 and 2002, were also examined. The analyses showed that a common correlation among the 3 sites for sponge and dough loaf volume was not suitable and separate predictions were required for 2001 and 2002 (Table 6). The analyses also showed that dough development time, 1000-kernel weight, and falling number had low common correlation among the 3 sites and so also required separate predictions. For all other traits, an overall genotype effect was predicted, on the basis of a moderate to high (>0.6) genetic correlation common to all pairs of sites.

Principal components analysis and bi-plot

Best linear unbiased predictors (BLUPs) from the individual trait analyses were used as input to a principal components analysis. This principal components analysis resulted in the

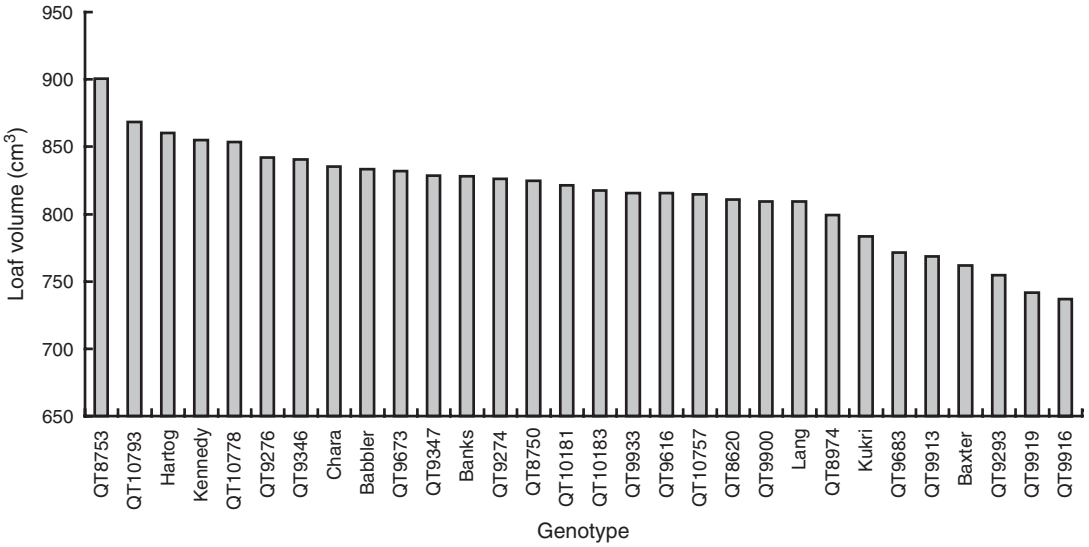

Fig. 2. Average sponge and dough loaf volumes for 30 genotypes produced at Roma during 2001 and at Roma and Biloela during 2002.

Table 5. Genetic correlations between 2002 harvest sites, Biloela and Roma

Trait	Genetic correlation
Loaf volume (cm^3)	0.921
NIR grain protein (%)	0.559
Falling number (s)	0.706
1000-kernel weight (g)	0.164
Particle size index	0.754
Milling yield (%)	0.658
Flour swelling volume (mL)	0.947
Extensograph extensibility (cm)	0.639
Extensograph extens/protein (cm)	0.714
Extensograph resistance (BU)	0.885
Mixograph stability (min)	0.703
Farinograph water absorption (%)	0.969
Farinograph DDT (min)	0.399

bi-plot displayed in Fig. 3. The bi-plot shows the relationship between the quality traits and sponge and dough loaf volumes. It also superimposes the genotype scores on each of the axes. Low genetic correlations between sites and seasons (Table 6) meant that some data could not be pooled and so are displayed separately on the bi-plot.

Relationships between quality traits and loaf volume

Genetic correlations are adjusted for sources of variation in the work such as site, genotype, field trial, milling process, and laboratory variation. Genetic correlations of all the test results with sponge and dough loaf volume are displayed in Table 7.

Glutenin alleles and granule-bound starch synthase (GBSS)

Determination of the glutenin alleles present and status of the *Wx-B1* loci important for encoding the GBSS proteins was completed for all the genotypes in the trial as shown in Table 8.

A limitation of the glutenin data is that there are 18 different glutenin patterns present among the 30 genotypes in the trial, indicating an insufficient number of individuals to fully explore the glutenin effects. Individual glutenin effects were tested, however, and are displayed in Table 9. They must be interpreted with caution.

Discussion

The genotypes selected for this work exhibited a large range of quality characteristics and sponge and dough loaf volumes (Tables 2, 3, and 4; Fig. 2). The exception was particle size index but a small range was expected since only hard wheats are used for bread making and no soft wheats were included in this trial.

The best performing genotypes for sponge and dough loaf volume were the Batavia/Pelsart double haploids QT8753, QT10793, and QT10778. Hartog and Kennedy also performed well. Some of these entries, in particular QT8753 have shown excellent yellow alkaline noodle sheet colour in other studies. Perhaps Australia could produce a dual-purpose wheat, combining good sponge and dough bread and excellent yellow alkaline noodle sheet colour.

In general, genotype × environment interaction was low for most quality traits. Both sites in 2002 provided supporting information on the quality of the genotypes except for the

Table 6. Genetic correlations of traits, between 2001 and 2002, indicate that data for loaf volume, dough development time, and falling number cannot be pooled for analysis

Trait	Site correlations	Biloela 02 Roma 01	Biloela 02 Roma 02	Roma 01 Roma 02
Loaf volume (cm^3)	–	0.559	0.904	0.505
NIR grain protein (%)	0.857			
Falling number (s)	0.070[A]			
1000-kernel weight (g)	0.565[A]			
Particle size index	0.637			
Milling yield (%)	0.628			
Flour swelling volume (mL)	_[B]			
Extensograph extensibility (cm)	0.768			
Extensograph resistance (BU)	0.832			
Mixograph stability (min)	0.808			
Farinograph water absorption (%)	0.959			
Farinograph DDT (min)	0.505[A]			

[A]Predictions for each of the 3 sites, whereas all other traits have one average prediction over the 3 sites.
[B]Genotype × environment interaction component very small.

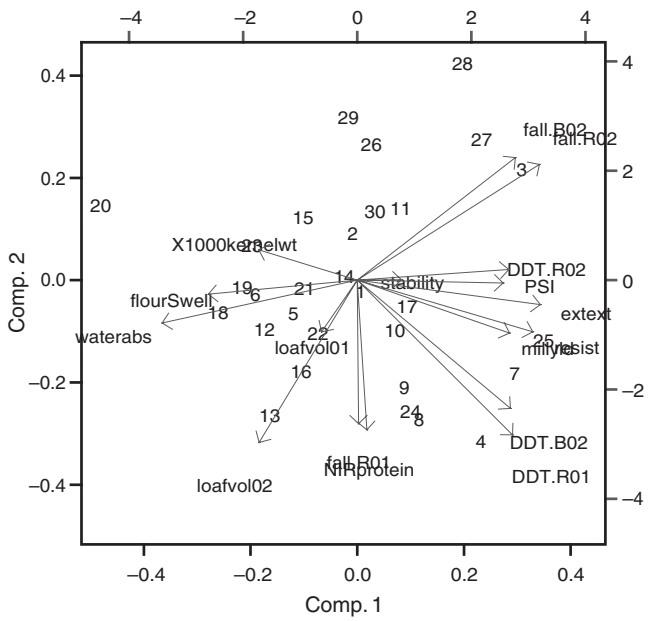

Fig. 3. A bi-plot of 30 genotypes (labelled 1–30), from Roma in 2001 and Roma and Biloela in 2002, arranged spatially according to their loaf volumes and scores in the quality tests: 1 Babbler, 2 Banks, 3 Baxter, 4 Chara, 5 Hartog, 6 Kennedy, 7 Kukri, 8 Lang, 9 QT10181, 10 QT10183, 11 QT10757, 12 QT10778, 13 QT10793, 14 QT8620, 15 QT8750, 16 QT8753, 17 QT8974, 18 QT9274, 19 QT9276, 20 QT9293, 21 QT9346, 22 QT9347, 23 QT9616, 24 QT9673, 25 QT9683, 26 QT9900, 27 QT9913, 28 QT9916, 29 QT9919, 30 QT9933.

traits of grain protein, 1000-kernel weight, and farinograph dough development time. Similarly, most traits, except loaf volume, dough development time and falling number, were pooled for analysis across 2001 and 2002.

While there was little genotype × environment interaction for most of the measured traits, the inter-trait relationships, particularly those with loaf volume, did vary across environments. Some of this variation could be due to the very high grain protein achieved by samples produced at Roma during 2002. Speculating on environment interactions with grain quality is probably beyond the scope of this work. However, to be useful in wheat breeding, associations of tests with loaf volume need to be robust enough to be expressed from season to season.

Table 7. Genetic correlations of quality traits with loaf volume for 2001 and 2002 harvests, Roma and Biloela

Trait	Roma 2001	Roma 2002	Biloela 2002
NIR grain protein (%)	–	−0.176	0
Falling number (s)	–	–	–
1000-kernel weight (g)	–	0.618	−0.292
Particle size index	–	–	–
Milling yield (%)	−0.307	−0.20	0.48
Flour swelling volume (mL)	0.493	0.595	0.637
Extensograph extensibility (cm)	−0.026	−0.229	0.188
Extensograph resistance (BU)	0.381	−0.357	−0.075
Mixograph stability (min)	0.517	−0.297	−0.140
Farinograph water absorption (%)	−0.095	0.332	0.280
Farinograph DDT (min)	−0.208	−0.149	−0.141

Flour swelling volume was the only trait exhibiting a significant correlation with sponge and dough loaf volume. This positive correlation is evident across sites in both years, indicating some stability of the effect across environments. In this study the relationship was observed across a range of grain protein, indicating that this test could be a useful indicator of sponge and dough loaf volume.

Analysis of relationships among glutenin alleles needs to be interpreted with caution, because some glutenin patterns are represented by only 1 or 2 genotypes. Further work with a greater number of genotypes representing selected glutenin

Table 8. Glutenin alleles, null 4A status, and predicted (BLUP) loaf volumes of genotypes, ranked overall and sorted into groups of glutenin patterns

Genotype	Loaf vol. 2001	Loaf vol. 2002	Rank 2001 2002	Glu-A1	Glu-B1	Glu-D1	Glu-A3	Glu-B3	Glu-D3	Wx-B1
QT8753	876	893	1	a	u	a	b	b	c	b
QT10793	853	871	2	a	u	a	c	b	c	b
QT10778	847	856	3	a	u	a	c	b	c	b
QT8750	806	820	11	a	u	a	c	b	c	b
QT10757	814	779	15	a	u	a	c	b	c	a
Hartog	850	847	4	a	i	d	b	h	b	b
Kennedy	822	848	5	a	i	d	b	h	b	b
Babbler	833	827	5	a	i,u	a	b	b	c	a
QT9274	833	820	6	a	i	ad	c	h	b	b
QT9347	819	827	7	a	u	a	e	b	c	a
Chara	799	855	8	b	al	a	b	b	b	ab
QT9276	795	866	8	a	i	a	c	h	b	b
Banks	829	818	8	b	u	a	b	b	c	a
QT10181	822	817	11	b	u	a	b	b	c	a
QT9346	786	861	10	a	f	a	c	b	c	a
QT10183	826	805	10	a	u	a	b	b	b	a
QT8620	751	833	15	a	u	a	b	b	b	a
QT9933	810	817	12	a	u	a	b	b	b	a
QT9900	794	817	16	a	u	a	b	b	b	a
QT9673	803	846	9	a	u	a	c	b	b	a
QT9616	795	824	13	a	u	a	c	b	b	a
QT8974	798	799	17	a	u	a	c	b	b	a
Lang	787	821	14	a	u	a	bc	b	b	a
Baxter	830	758	13	a	f	a	b	h	a	a
QT9683	758	804	20	a	f	a	b	h	a	a
QT9919	808	733	18	a	i	a	b	h	b	a
Kukri	786	783	19	a	al	d	d	h	b	a
QT9913	822	756	15	b	f	a	b	d	a	a
QT9916	770	737	21	b	f	a	b	d	a	a
QT9293	750	774	21	a	c	a	b	j	c	b

Table 9. *Wx-B1* status had a significant effect on loaf volume in 2002

The effect of glutenin alleles on loaf volume was different for 2001 and 2002

Trait	Probability 2001	Probability 2002
Glu-A1	n.s.	n.s.
Glu-B1	0.01**	n.s.
Glu-D1	n.s.	n.s.
Glu-A3	n.s.	n.s.
Glu-B3	n.s.	0.0189*
Glu-D3	0.055	0.0267*
Wx-B1 status	0.09	0.0347*

n.s., Not significant.
*$P < 0.05$; **$P < 0.01$.

patterns is required to understand the importance of glutenin alleles for sponge and dough bread quality.

Overall, for this dataset, which comprises cultivars of prime hard type, the results indicated that no single quality trait could encompass what is important to achieve high loaf volume in sponge and dough bread. This supports the perceived need for new technologies that allow more accurate assessment of wheat flour quality (Appels *et al*. 2001). Traditional tests of physical dough properties are designed to capture the process of flour mixing and hydration. In addition, traditional quality tests of grain tend to measure flour components separately. Both approaches are complicated by seasonal influence and component interactions. Yet, the traditional tests used in this work have previously allowed development of the many quality wheat varieties present today.

Considering the characteristics of the sponge and dough baking system should assist in selecting a measure that will define a wheat's suitability for this process. It is recognised that gluten and starch play an important role in forming the strong gaseous matrix essential for good bread (Gan *et al*. 1990). Perhaps their role becomes even more important in the sponge and dough process where fermentation increases the volume of gas, lowers pH and increases dough elasticity.

Because many glutenin patterns in this work were represented by only 1 or 2 genotypes, the importance of their role in this baking system is still not clear. However, based on the limited information reported here, breeders could select varieties with the glutenin pattern from Table 8

associated with the 3 highest ranking loaf volumes from the duration of the trial and those with the null *Wx-B1* allele. The best performing variety, QT8753, could prove to be a useful reference variety.

The implied importance of the *Wx-B1* allele for sponge and dough bread is supported by the correlation of flour swelling volume discussed above. The null allele results in absence of the gene product, granule-bound starch synthase, and has been reported to be associated with higher flour swelling volume (Zhao *et al*. 1998). It would be useful to further investigate associations of glutenins and forms of the *Wx-B1* allele with sponge and dough loaf volume in a purpose-selected population.

In addition, new techniques could be investigated and developed to replace the traditional tests of wheat quality used here. Novel tests used recently in the USA and Canada have shown very strong correlations with sponge and dough loaf volume. In the USA, Wang and Sun (2002) demonstrated that creep recovery of flour–water doughs had a correlation of 0.939 with bread volume. The authors proposed that the elasticity measured by recovery strain assessment was an important factor for this result. If the predictive power continues beyond the 11 commercial flour samples used, the test could prove practical for end-product selection in wheat breeding, as it only requires 0.5 g of dough at constant water absorption.

Similarly, in Canada, a derivative of the sedimentation test (Zeleny *et al*. 1960), the sodium dodecyl sulfate (SDS) protein gel test, has recently been modified to reduce sample size to <1 g and used to predict bread loaf volume, achieving R^2s of 0.89 and 0.95 for flour and ground wheat, respectively (Sapirstein and Suchy 1999). Again the test could have excellent potential in wheat-quality screening if reproducibility extends beyond the 7 Canadian commercial wheat flours used in the study.

Early selection in breeding programs may also be achieved with near infrared techniques. Calibrations to detect the key constituents for baking performance could be developed based on flour or ground grain from wheats with a range of sponge and dough quality. The technology is fast and only requires small amounts of grain but success is dependent on attaining suitable samples for the calibration. Recent work has demonstrated that by using native substrates such as gliadin and glutenin in wheat (Wesley *et al*. 1999, 2001) and hordein in barley (Fox *et al*. 2002), important information on spectra associations with protein fractions can be attained.

Although the need for more decisive wheat quality tests is indisputable, this work has confirmed that Australia can produce wheat's suitable for the sponge and dough bread making process.

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Appendix 1. Analytical data for Premium, Standard, and All-purpose grades of Asian milled flour
Data were supplied by the manufacturer from the analysis of a larger flour sample from which these subsamples were obtained

	Premium bread flour	Standard bread flour	All-purpose flour
Protein (%)	13.8	13.1	11.7
Ash (%)	0.53	0.54	0.51
Farinograph			
Water absorption (%)	65.4	64.2	61.2
Development time (min)	10.2	6.7	4.5
Departure time (min)	18.0	13.2	11.0
Extensograph			
Max. extensibility (cm)	20.7	17.5	17.5
Max. resistance (BU)	480	505	495
Area (cm^2)	137	126	124