Journal of Cereal Science 64 (2015) 147–152

Contents lists available at ScienceDirect

Journal of Cereal Science

journal homepage: www.elsevier.com/locate/jcs

Genetic control of grain protein, dough rheology traits and loaf traits in a bread wheat population grown in three environments

Lancelot Maphosa [a], Peter Langridge [a], Helen Taylor [b], Livinus C. Emebiri [c], Diane E. Mather [a, *]

[a] Australian Centre for Plant Functional Genomics and School of Agriculture, Food and Wine, Waite Research Institute, The University of Adelaide, PMB 1, Glen Osmond, SA 5064, Australia
[b] NSW Department of Primary Industries, Wagga Wagga, NSW 2650, Australia
[c] Graham Centre for Agricultural Innovation, NSW Department of Primary Industries, Wagga Wagga Agricultural Institute, Wagga, NSW 2650, Australia

ARTICLE INFO

Article history:
Received 29 November 2014
Received in revised form
22 April 2015
Accepted 26 May 2015
Available online 27 May 2015

Keywords:
Baking
Dough
Heat
QTLs

ABSTRACT

The processing and baking quality of bread wheat can be affected by both genetic and environmental factors and by interactions between them. Here we report on the genetic control of grain protein content, flour water absorption, dough and bread making quality in wheat grown in three experiments under differing environmental conditions. The research used a recombinant inbred line mapping population derived from a cross between two Australian cultivars, Drysdale and Gladius. Three field experiments were conducted, including one that was sown late in order to expose the lines to high temperatures during grain filling and one in a year in which conditions were unusually cool and wet. Genomic regions containing photoperiod sensitivity loci affected grain protein content while the *Ha* (puroindoline) locus on chromosome 5D was associated with loaf quality traits. Other QTLs (on chromosomes 2B, 3B and 5A) were novel and not associated with any known quality or phenology genes.

1. Introduction

Bread wheat (*Triticum aestivum* L.) is a major cereal crop worldwide and is mainly consumed in the form of baked products. Dough properties and baking quality vary among wheat cultivars and can be influenced by abiotic stresses such as high temperature, especially during grain filling.

Endosperm proteins that have been found to be associated with flour and dough quality include puroindolines, serpins, glutenins and gliadins, all of which are encoded by well-characterised genes. Puroindolines, though primarily associated with grain texture (Morris, 2002), can influence flour extraction, water absorption and the properties of baked products (Maphosa et al., 2013). Serpins, which function as defence proteins, also affect flour extraction (Cane et al., 2008). Gluten proteins (glutenins and gliadins) largely determine the viscoelasticity of wheat dough. Viscoelasticity allows the trapping of carbon dioxide during fermentation and the production of leavened bread. Scoring systems and statistical models have been devised to predict dough quality based on combinations of some or all of the genes that encode these proteins (Békés et al., 2006; Eagles et al., 2002, 2004; Payne et al., 1987). Measured and/or predicted dough properties are in turn often used as predictors of baking quality. No specific genes have been identified as being directly associated with properties of baked products, but some quantitative trait loci (QTLs) have been mapped for these traits (Groos et al., 2004; Mann et al., 2009; Maphosa et al., 2013).

Environmental conditions such as high temperature can affect wheat quality. The impact of high temperature on quality partly depends on the developmental stage in which the stress occurs. High temperatures during grain filling have been reported to decrease dough strength (Randall and Moss, 1990) and percentage unextractable polymeric protein (% UPP), a trait related to dough strength (Cavanagh et al., 2010; Irmak et al., 2008; Naeem and MacRitchie, 2005). The aim of the research reported here was to investigate the genetic control of grain protein content, dough properties and loaf properties through mapping of QTLs associated

Abbreviations: AACC, American Association of Cereal Chemists; BLUEs, best linear unbiased estimates; DArT, Diversity Arrays Technology; NIR, Near-infrared reflectance; QTL, quantitative trait locus; RACI-CCD, Royal Australian Chemical Institute – Cereal Chemistry Division; RIL, recombinant inbred line; SSR, simple sequence repeat.

* Corresponding author.
E-mail address: diane.mather@adelaide.edu.au (D.E. Mather).

http://dx.doi.org/10.1016/j.jcs.2015.05.010
0733-5210/

with these quality traits in a wheat population grown in three contrasting sets of conditions.

2. Material and methods

2.1. Plant material

The materials used for this research were the wheat cultivars Drysdale and Gladius and a set of 155 Drysdale/Gladius recombinant inbred lines (RILs). The parental cultivars were chosen on the basis of their contrasting physiological and agronomic performance under drought and heat stress conditions, with Gladius being the drought and heat tolerant parent and Drysdale more water use efficient, producing more biomass per unit area per unit of water (Fleury et al., 2010). As shown in Table 1, these cultivars differ for major phenology genes (Eagles et al., 2009), yet they head or reach anthesis within five days of each other (Maphosa et al., 2014a, 2014b). In environments in which they head at different times, Drysdale heads before Gladius. Drysdale and Gladius also differ for several quality-related genes (Eagles et al., 2009) (Table 1): the glutenin loci *Glu-B1*, *Glu-A3* and *Glu-D3*, but not *Glu-A1*, *Glu-D1* or *Glu-B3*. Both are classified as Australian Hard wheat in Southern New South Wales where the experiments were conducted. Australia Hard wheat has good dough strength and is suitable for sponge-and-dough baking. As reported by Maphosa et al. (2014a), the 155 Drysdale/Gladius lines used for this research were selected from a larger set of 205 lines based on similarity of maturity.

2.2. Field experiments

The grain samples used in this research were produced in field experiments conducted at Yanco, Southern New South Wales, Australia in 2009 (experiments NSW09L and NSW09) and 2010 (experiment NSW10). Each experiment included two replicates of each of Drysdale, Gladius and 155 Drysdale/Gladius RILs. The experiments and the environmental conditions under which they were conducted have been described in detail by Maphosa et al. (2014a). They can be characterised as having hot (NSW09L), warm (NSW09) and cool (NSW10) temperatures during grain filling. The NSW09L experiment was sown very late (August) in order to expose the plants to high temperatures during grain filling. The NSW09 and NSW10 experiments were both sown at the conventional time (June), but the 2010 growing season was unusually cool and wet.

Table 1
Alleles carried by Drysdale and Gladius at high molecular weight glutenin, low molecular weight glutenin, puroindoline, serpin and phenology loci.

		Parent	
Locus type	Locus	Drysdale	Gladius
High molecular weight glutenin	*Glu-A1*	*a* *(Ax1)*	*a* *(Ax1)*
	Glu-B1	*i* *(Bx17 + By18)*	*b* *(Bx7 + By8)*
	Glu-D1	*d* *(Dx5 + Dy10)*	*d* *(Dx5 + Dy10)*
Low molecular weight glutenin	*Glu-A3*	*b*	*c*
	Glu-B3	*b*	*b*
	Glu-D3	*g*	*a*
Puroindoline	*Pina-D1*	*b*	*a*
	Pinb-D1	*a*	*b*
Serpin	*Srp*	*a*	*a*
Phenology	*Ppd-B1*	*b*	*a*
	Ppd-D1	*a*	*b*
	Vrn-A1	*v*	*a*
	Vrn-D1	*a*	*v*

2.3. Grain protein content

Grain protein content was estimated by near-infrared reflectance (NIR) (RACI-CCD, 2010) using a Foss 6500 NIR instrument (FOSS NIR Systems, Inc., Laurel, MD). The NIR prediction was based on calibration to Leco protein determination (RACI-CCD, 2010), and reported on an 'as is' basis (AACC, 1999).

2.4. Dough properties

Grain samples were milled using a Bühler MLU-202 laboratory test mill (Bühler AG, Uzwil, Switzerland) as described by Maphosa et al. (2014a). Dough properties were assessed using the Perten-Newport Scientific DoughLAB (Newport Scientific Pty Ltd., NSW, Australia), which is an electronic alternative for the Brabender farinograph. The baseline was set by mixing flour only, for one minute before water was added. Dough stability (seconds), development time (seconds), softening (FU units) and percentage water absorption (RACI-CCD, 2010) were calculated.

2.5. Baking quality

The long fermentation baking test method (RACI-CCD, 2010), which is based on AACC approved methods 10:09 and 10:10b (AACC, 1999), was used. Bake mixing time was taken as time to full dough development. The baking ingredients were flour, water, sugar, α-amylase, ammonium chloride, sodium chloride, fat, and ascorbic acid. Baked products were evaluated for loaf volume (cc units) using the rapeseed displacement method (AACC, 1999). To permit evaluation of crumb texture (feel) and crumb structure (appearance), loaves were cut diagonally from corner to corner to allow maximum view. For loaf texture, a scale of 1–10 was used with 1 being "very tight under thumb pressure, crumb tears, rough to the feel" and 10 being "very soft feel under the thumb, very smooth, recovers with no indentation". For loaf structure a score of 1–10 was also used with 1 being "round cells with thick cell walls, crumpet like appearance" and 10 being "very fine cell walls, elongated cells around the edges of the loaf".

2.6. Statistical and genetic analysis

A two-stage statistical and genetic analysis was done with GenStat14 (http://www.vsni.co.uk/software/genstat). In the first stage, spatial analysis (Gilmour et al., 1997) was conducted and best linear unbiased estimates (BLUEs) were generated, taking into account experimental design factors. In the second stage, a multi-environment QTL analysis using a genome-wide significance threshold ($p = 0.05$) was done using composite interval mapping and a linkage map consisting of 720 DArT, SSR and gene-based markers distributed over 28 linkage groups as described by Maphosa et al. (2014a). The BLUEs were also used to generate a phenotypic correlation matrix with GenStat among the multi-environment means for traits measured. Map diagrams were drawn using MapChart software (Voorrips, 2002).

3. Results

3.1. Phenotypic variation and trait heritability

Samples from the experiment that was sown late (NSW09L) and experienced high temperatures during grain filling generally had higher grain protein content, longer dough development time, greater dough stability, longer bake mixing time, less dough softening and larger loaf volume than those from the other experiments (Table 2). For grain protein content, broad sense heritability