

CSIRO Publishing

Australian  
Journal of  
Agricultural  
Research

VOLUME 52, 2001

© CSIRO 2001

A journal for the publication of original contributions  
towards the understanding of an agricultural system

**All enquiries and manuscripts should be directed to:**

*Australian Journal of Agricultural Research*  
CSIRO Publishing  
PO Box 1139 (150 Oxford St)  
Collingwood, Vic. 3066, Australia



**CSIRO**  
PUBLISHING

Telephone: +61 3 9662 7628  
Fax: +61 3 9662 7611  
Email: publishing.ajar@csiro.au

Published by CSIRO Publishing  
for CSIRO and the Australian Academy of Science

[www.publish.csiro.au/journals/ajar](http://www.publish.csiro.au/journals/ajar)

## Wheat Breeding in the new century—Preface

*DR Marshall<sup>A</sup>, P Langridge<sup>B</sup>, and R Appels<sup>BC</sup>*

<sup>A</sup>University of Sydney, Plant Breeding Institute Cobbitty, PMB 11 Camden, NSW 2570, Australia.

<sup>B</sup>Adelaide University, Waite Campus, Department of Plant Science, CRC for Molecular Plant Breeding, Adelaide, SA 5064, Australia.

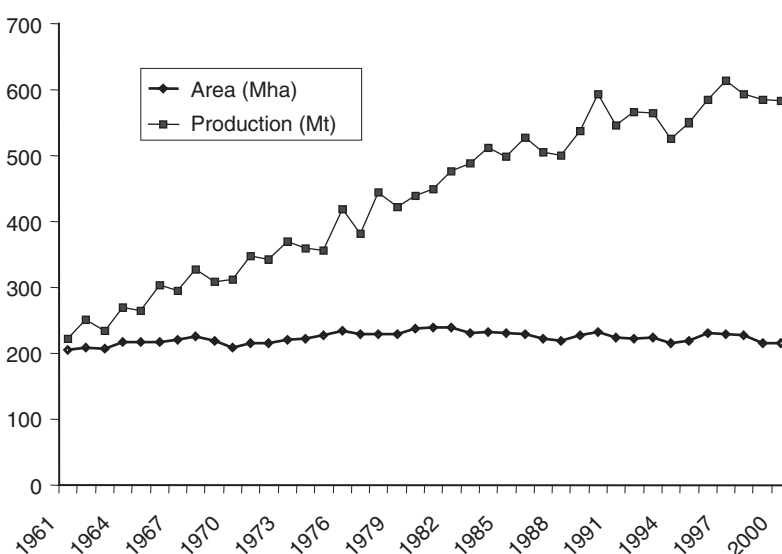
<sup>C</sup>Biological Sciences, Murdoch University, Murdoch, WA 6150; and Department of Agriculture, 3 Baron-Hay Court, South Perth, WA 6151, Australia.

Wheat is the world's most important crop species, grown on an area of over 200 million hectares and now yielding almost 600 million tonnes annually (FAO; <http://www.fao.org/>). Importantly, there has been a steady and highly significant increase in wheat yields, largely due to the release of new improved varieties. Since the early 1960s there has been little increase in the area sown to wheat, but over the same period, yields have increased almost 3-fold (Fig. 1). While much of this increase has been through improved agricultural practice, the breeding of new varieties has been crucial. The major challenge over the next few decades will be to maintain these rates of improvement, and the application of the remarkable advances made in molecular genetics and biotechnology over the last decade to wheat improvement is clearly a key strategy in achieving this.

Much of the media focus with respect to the application of molecular genetics and new biotechnologies to economically important plants and animals has been on

genetic transformation and the resultant genetically modified organisms, particularly those that enter the human food chain. The emphasis has been on the transfer of genes across previously unbridgeable species boundaries (e.g. those between bacteria, plants, and animals). However, genetic transformation is but one of the molecular genetic biotechnologies with the capacity to revolutionise traditional approaches to plant and animal improvement.

The use of DNA or molecular markers to improve the effectiveness and efficiency of gene manipulation within a species is highlighted in this special issue. The potential for the use of such markers in improving backcrossing efficiency, early selection/pyramiding of traits of interests, defining quantitative traits, selecting parents to use in a particular cross, and defining epistatic interactions affecting desirable traits has been widely recognised. As a result, such markers are seeing greater use in practical breeding programs.



**Fig. 1.** Wheat production worldwide compared with the area sown to wheat from 1961 to 2000.

The development of molecular markers in wheat, and their application in breeding and related research programs, pose several significant challenges compared with some other crop plants. These are, in part, biological—related to the large genome size and allopolyploid nature of wheat—and in part economic—reflecting the fact that wheat breeding has traditionally been in the public domain and has not received the same level of private investment in crop-specific genome research as hybrid crops like maize and sorghum. As a consequence, the Grains Research and Development Corporation of Australia (GRDC) provided core funding to establish the National Wheat Molecular Marker Program (NWMMP) in 1996. The factors driving the investment by the GRDC in wheat molecular marker researcher were:

- (i) recognition of the need for the wheat industry stakeholders to invest in molecular marker research if wheat, which is Australia's most important crop, is to stay competitive with other crops internationally; and
- (ii) recognition that the specialised nature of the Australian environment, and the wheat germplasm adapted to it, required a specific program of research, complimentary to that done elsewhere to establish molecular markers suitable for use in regional Australian Wheat Breeding Programs strongly supported by the GRDC.

The quality attributes important to maintaining a competitive wheat export position, namely, protein percentage, milling yield, starch qualities, dough extensibility, and flour colour were recognised as priority targets for the utilisation of markers. The NWMMP established and analyzed doubled haploid populations from 4 crosses: Cranbrook × Halberd, CD87 × Katepwa, Sunco × Tasman, and Egret × Sunstar.

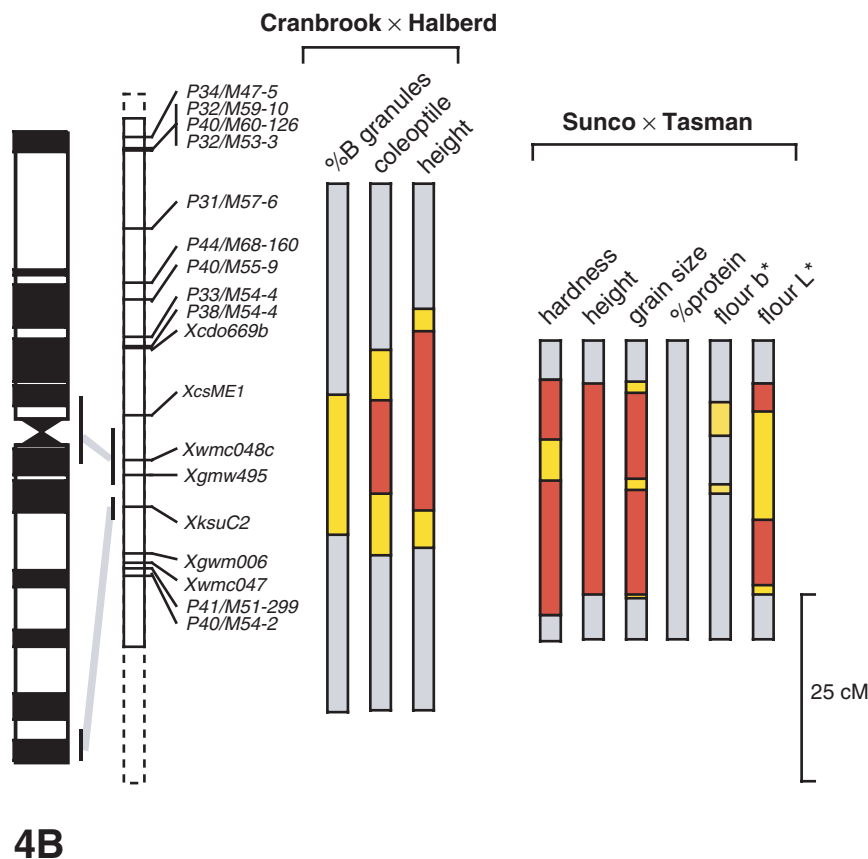
The manuscripts in this special issue document some of the outcomes from this national program and they fall into 3 broad categories:

- The results on the molecular genetic mapping in the populations derived from 3 crosses, Cranbrook × Halberd, CD87 × Katepwa, and Sunco × Tasman, provide the basis for linking variation in traits such as grain texture or flour colour to particular regions of chromosomes. These chromosomal regions define the locations of quantitative trait loci (QTLs) controlling the expression of the traits. The establishment of the maps included the assessment of new marker technologies to complement the well-established restriction fragment length polymorphism (RFLP) and the incorporation of a particularly useful class of marker, microsatellites into the linkage maps. Candidate genes, such as seed storage proteins (analysed using electrophoretic techniques), for particular traits were also incorporated into the maps. Potential candidate genes for a range of grain properties were derived from gene sequences expressed in developing endosperm and were assayed using single nucleotide polymorphisms in order to assign chromosomal locations.

- The papers that follow these mapping studies provide detailed analyses of a number of traits and provide the locations of the corresponding genetic loci (QTLs). The statistical techniques used to analyse the data were important in revealing significant loci. Table 1 provides a summary of the QTLs that were mapped in the papers in this special issue, and Fig. 2 provides an example of the QTLs on chromosome 4B and indicates that the same

**Table 1. Overview of the QTLs analyses in the NWMMP**

Chromosome	Traits mapped as QTLs
1AS	M-extensibility
1AL	—
1BS	M-extensibility
1BL	Mixing time, Yr29
1DS	M-extensibility
1DL	Mixing time
2AS	—
2AL	Sprouting tolerance
2BS	Seed weight, flag leaf length/width, height at stem elongation, tiller number, time to anthesis
2BL	Ear compactness
2DS	Flour colour (b*), flag leaf length/width, height at stem elongation, leaf 1 length (field), leaf 2 length (field), Yr29, time to anthesis, ear compactness
2DL	Sprouting tolerance, PPO, YAN colour, % protein
3AS	Flour colour (b*)
3AL	—
3BS	Pbc, late maturing alpha-amylase (LMA)
3BL	Internode length, flour colour (b*), xanthophyll
4AS	—
4AL	Starch viscosity, flour swelling, preharvest sprouting
4BS	Plant height, leaf 1 length (+GA), internode length, coleoptile length, flour colour (b*, L*), grain size, hardness, % B granules
4BL	Coleoptile tiller, coleoptile length
4DS	Plant height
4DL	—
5AS	—
5AL	Leaf 1 length (field)
5BS	—
5BL	Milling yield, % protein, flour colour (b*)
5DS	Grain texture (hardness, Smax)
5DL	Sr30
6AS	Pbc
6AL	—
6BS	Grain texture (Smax)
6BL	—
6DS	—
6DL	—
7AS	—
7AL	Flour colour (b*), xanthophyll, starch gelatinisation
7BS	—
7BL	Flour colour (b*), late maturing alpha-amylase (LMA)
7DS	Yr18
7DL	—



**Fig. 2.** A compilation of the agronomic and quality traits mapped as QTLs on chromosome 4B in the manuscripts featured in this special issue of AJAR. The view of chromosome 4B on the far left is from the standard C-banded karyotype of wheat and next to this is the genetic map for this chromosome reported in this special issue. The grey lines joining the karyotype and the genetic map indicate the approximate relationships between these two views of chromosome 4B. The information displayed to the right of the genetic map indicates the locations of significant (yellow,  $P \leq 0.05$ ) and highly significant (red,  $P \leq 0.001$ ) associations between the respective trait (identified for the crosses analysed) and the markers in the particular region of the genetic map. The scale on the far right is in centiMorgans (cM).

chromosome regions can often affect many different traits. For example, the short arm of chromosome 4B, defined by *XcsME1* (the *Rht1* gene, see Ellis *et al.* 2002) and *Xwmc048* (a microsatellite), has multiple influences on plant growth traits and quality attributes. As this knowledge database develops, detailed selection strategies can be established to ensure that, for example, selection for certain features of coleoptile length does not have adverse effects on quality attributes such as flour L\* values and grain texture (hardness).

- The third broad group of manuscripts deals with validation and implementation issues for markers associated with selected traits. A key outcome of a DNA marker program is the improved efficiency of breeding programs. In order to achieve this, markers that are found to be closely linked to, for example, flour colour or a particular disease resistance locus, need to be tested in a breed-

ing program. The manuscripts in this special issue provide a detailed examination of the application of markers for starch quality, flour colour, and disease resistance genes in breeding programs and document how specific problems were solved as laboratories associated with breeding programs applied the DNA markers. A central aspect of marker application to breeding programs is the requirement of high throughput technologies and several papers in this special issue provide novel solutions to marker application.

The papers in this special issue provide a glimpse of the impact that new biotechnological procedures will have on a major crop such as wheat. The databases underpinning the manuscripts set the stage for integrating new knowledge from model systems such as rice and *Arabidopsis* where candidate genes for certain biological processes can be assessed for their significance in wheat. It is evident that the

polyploid genetic structure of wheat increases the significance of epistatic interactions that may be much more significant in controlling agronomic and quality phenotypes relative to model diploid organisms. A key achievement of the NWMMP has been the establishment of linkages between molecular laboratories, cereal chemistry groups, and wheat breeding programs, to provide the means for capturing new knowledge from model systems and to move

this forward into analysing the unique genetic and biological environment found in wheat.

#### **Reference**

- Ellis M, Spielmeier W, Rebetzke GJ, Richards RA (2001) 'Perfect' markers for the *Rht-B1b* and *Rht-D1b* dwarfing genes in wheat. *Theoretical and Applied Genetics* (in press)