

From Genome Structure to Breeding of Wheat and Barley

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Introduction

In a breeding program, the breeder is essentially seeking to exploit the variation in the target species to enhance a wide range of characters. For most crops the breeding objectives will cover quality and characters that affect yield and adaptation, including disease and pest resistance, and tolerance to abiotic stresses. Traditional breeding methods have been very successful in making major improvements in yield and quality. Indeed, breeding still represents the most efficient strategy for improved crop productivity and quality and for addressing changes in agricultural practice. For example, the shift to minimum tillage and direct drilling has become expedient in many parts of the world. However, these sowing methods have resulted in changes in the spectrum and severity of many diseases. Breeding, rather than the use of costly and often politically and environmentally undesirable agricultural chemicals, can most effectively generate varieties adapted to these conditions.

For annual crops such as wheat and barley, the time required to take a line through from the first cross to release of a new variety is long, usually over ten years for wheat and up to fifteen years for malting barley. This represents a major investment of time and resources by the breeding programs. In such a timeframe, it has often been difficult for breeders to experiment with new breeding strategies unless substantial additional resources are provided. In Australia, the Grains Research and Development Corporation has been providing support to accelerate the adoption of molecular technologies into wheat and barley improvement programs. The initial phases of these programs have been extremely encouraging. However, the technology and data on cereal genomes is expanding at such a rapid pace that it is now becoming necessary to ask if the current structures for cereal breeding in Australia will be adequate to ensure effective exploitation of new methodologies.

Testing molecular selection strategies

Given that plant breeding essentially involves the movement, manipulation and selection of genomic segments, an increased knowledge of genome organisation and behaviour can be expected to have a major impact on breeding methodologies. Although the methods for genome analysis are no longer new, their application to pragmatic plant breeding has not been extensively tested. Breeders will need to be convinced of the practicalities of the techniques of genome and gene analysis before they can be expected to wholeheartedly adopt the techniques. They will also need to have the necessary skills and tools to use the procedures. In Australia this has been achieved through the establishment of the National Wheat and Barley Molecular Marker Programs funded through the GRDC. The Marker Programs include a strong implementation component where support laboratories have been established at each of the main breeding sites. This strategy planned to involve the breeders in the development and application of markers and

provide support during the early stages of implementation. It was anticipated that, over time, a rationalisation would take place with labs specialising in specific types of marker analyses or with marker screening transferring to one or more central laboratories. However, changes in technologies and in the number and types of markers becoming available necessitates a re-evaluation of how markers should be used and the strategies that are adopted for their implementation. Table 1 summaries the traits in wheat and barley for which linked molecular markers have been identified. The list is impressive but in any given wheat or barley breeding program only a small proportion of these markers/traits are likely to be of interest. Nevertheless, if we take the South Australian barley improvement program as an example, markers are available for over ten traits of importance. While the availability of so many tagged loci is attractive the practicalities of selecting for so many loci is questionable at present.

When a large number of loci are to be combined from several sources, the probability of two or more loci being linked will rise. If linkage between desirable loci is in repulsion (the most probable situation in a backcrossing scenario involving multiple-linked loci) then a strategy needs to be devised to identify the progeny lines where a desired recombinational event has occurred between the target genes. In this situation monitoring the locus itself is less important than identifying recombinational breakpoints.

While it is clear that a selection strategy based on the identification of recombinational breakpoints has major advantages when dealing with linked loci, does this strategy also offer advantages when only a single locus is being transferred or when there is no linkage between the target loci? The answer depends largely upon the ease of marker screening, with respect to both markers for single loci and markers for genome-wide screening, and the distribution of the genome-wide markers. The importance of genome coverage becomes apparent if specific marker types are examined. Many markers, such as microsatellites in barley and RAPDs in both wheat and barley, show strong clustering around the centromeres. The use of such markers gives very poor genome coverage and can give a highly distorted view of genome composition. Indeed, even for markers such as RFLP and AFLPs, complete, unbiased genome coverage is a rarity and can change depending upon the cross. This becomes a particularly serious problem when the parents used in the cross are related; not an unusual occurrence in some breeding programs. Under such circumstances, some regions of the genome are essentially invisible to the markers screen.

These features would support a selection model based on the use of markers to identify recombinational breakpoints rather than simply to monitor for presence or absence of particular loci, based on linked markers, and random genome screening. Telomeric regions would be transferred by identifying proximal recombination events and interstitial regions or loci would be selected based on identification of progeny lines carrying a proximal or distal breakpoint. At each selection stage two objectives will be followed; identification of recombinational breakpoints flanking the target locus or region and fixation of the recurrent parent chromosomes, or chromosome regions unlinked to the targeted region or regions.

Table 1. Traits in wheat and barley for which linked molecular markers have been published.

	Wheat	Barley
Agronomic And Stress Tolerance	Boron tolerance	Boron tolerance
	Cold tolerance	Manganese efficiency
	Aluminium tolerance	Zn uptake
	Sprouting tolerance	Salt tolerance
	Na/K discrimination	Drought tolerance
		Osmotic adjustment
Quality		Malting
	Grain hardness	Extract
	Waxy	Diastatic power
	Milling yield	Milling yield
	Flour colour	Enzymes, α -amylase, β -amylase, limit dextrinase, glucanase
	Polyphenol oxidase	Water absorption
	Grain protein (durum)	GA responsiveness
	Cadmium content	Protein
		β -glucan
		Feed
		Metabolisable energy
		Starch digestibility
		Dry matter digestibility
		Particle size
	Fibre digestibility	
Plant Type	Vernalisation	Vernalisation
	Photoperiod	Photoperiod
	Plant height	Plant height
	Dwarfing	Dwarfing
	Seed dormancy	Hulless
	Awns	2 row/6 row
	Red coleoptyl	Grain size and shape
	Shoot differentiation rate	Lodging
Disease	33 loci	35 loci
	Leaf, stripe and stem rust	Rust
	Powdery mildew	Powdery mildew
	Cereal cyst nematode	Scald
	Hessian fly	Net blotch
	Virus, WSMV	Virus, BYDV & BYMV
	Eyespot	Cereal cyst nematode
	Russian wheat aphid	Russian wheat aphid
	Tan spot	
	Loose Smut	
Common bunt		

Where clear information is available about the location of the target loci, the populations sizes needed to have a good chance of obtaining the desired recombinants can be calculated. Since

wheat and barley chromosomes are in the order 200cM in length, in 100 meiotic products, the probability of finding an individual progeny line with a recombinational breakpoint within about 5cM of a target locus, is high (greater than 95%). If two meioses are involved, as in production of progeny from a selfing, then the population size can be further reduced. The screening of such lines is also simple. Once the target region has been defined, markers can be sought that flank the region. Recombination events between the markers are identified as non-parental combinations of alleles. Any conventional marker type can be used. Assuming several recombinant lines are identified, further screening with markers within the target region, can be used to more closely define the breakpoints and identify the optimal line. Only in exceptional circumstances, for instances if two target loci are very closely linked in repulsion, will a recombinational event closer than about 10cM be required. In such cases the populations of fewer than 50 lines are likely to be needed. This contrasts to the very slow gain achieved at each round of a conventional backcrossing program where unrecombined blocks of 50cM will still remain, after even three backcrosses.

The points made above are aimed at demonstrating that, as a result of the effort into marker development, the large number of tagged loci now identified for both wheat and barley, and our ability to scan and analyse the genome configuration of individual lines, alternative selection strategies may offer major advantages. The trend over the next few years will be to increase the number of traits being monitored and selected and an increase in our ability to conduct genome wide screening. This will see an emphasis on strategies that minimise population size while maximising the number of traits under analysis. Selection for recombinational breakpoints rather than individual traits may be the most effective way of fully utilising the new marker technologies.