Characterisation and mapping of chromosome regions associated with improved growth and grain yield of barley on sandy soils of low fertility

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By

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Abstract

Sandy soils of low fertility constitute approximately 30% of the total area (958,600ha) sown to barley in South Australia (SA). With such a significant proportion of the barley sown on sandy soils, the development of specifically adapted cultivars for this soil type is a very important barley breeding objective in the SA Barley Improvement Program (SABIP).

It is generally recognised that barley displays better adaptation on these soil types than wheat, triticale and oats, but is inferior to cereal rye. Even so, the inherently poor properties of sandy soils make the production of barley unreliable. A large part of the lower grain yield potential of crops grown on these soils is associated with the poor establishment and growth typically observed in these environments. This compares with the superior yield potential of crops grown on heavier soil types and in more favourable environments. Furthermore, the efficiency and progress in breeding and selecting varieties with superior adaptation on sand is impeded by the low heritability of traits important to adaptation to this environment. The low heritability is related to low genetic variance, partly related to the germplasm available, and the high error variance of yield trials conducted on sandy sites. In addition, genetic gain for sand adaptation has been limited by traditional selection methods that tend to discriminate against low yield potential environments.

Despite these limitations, some genetic gain for adaptation has been achieved. Yagan, an introduction of unknown pedigree from the International Maize and Wheat Improvement Center (CIMMYT), was released by the Western Australian (WA) Department of Agriculture barley breeding program in 1988 because of improved yield and superior agronomic features on sandy soils in low rainfall environments. In 1996 Mundah, a selection developed from a simple cross between Yagan and O’Connor (WA bred variety of feed quality), was commercially released by WA. Since being introduced into SA Research and Development Institute (SARDI) field evaluation trials Mundah has consistently shown superior grain yield potential over Yagan and SA bred varieties on sand but has ranked lower than SA selections.
in high yield potential environments. Such genotype × environment interaction for adaptation response provides evidence of genotypic variability for sand adaptation. While potential genetic variation for sand adaptation has been observed, there has been no concerted effort to identify the physiological, morphological or biochemical characteristics of Mundah and Yagan that contribute to their superior performance on sand. Neither has there been efforts directed at understanding the genetic control of these characteristics.

The objective of this study was to re-address this deficiency in our knowledge of sand adaptation and use molecular marker technology to characterise the genetic basis of adaptation.

A comprehensive review of the literature on the inherent properties of sandy soils and the mechanisms likely to be associated with improved growth and grain yield on these soils led to the definition of a putative barley 'idiotype' (i.e. ideal plant type) for sand adaptation.

Field and controlled environment experiments were designed to characterise the traits associated with genotypic differentiation for adaptation on sandy soils, and to test the validity of the putative idiotype previously defined. In these experiments, the superior performance and grain yield of Mundah on sandy soils was found to be associated with improved establishment, early vigour (both in terms of dry matter production and leaf area development), phosphorus utilisation efficiency, and a deep root system.

A study of the impact of seed size on growth and productivity on sandy soils led to the conclusion that establishment, early vigour and grain yield could be improved by selecting the large seed size fraction for sowing. Large seed size was also associated with longer coleoptile length and higher seed nutrient content. The control of seeding depth on sandy soils is difficult and consequently longer coleoptiles set the potential for improved establishment and early vigour, which can ultimately lead to improved productivity.

Varieties with superior adaptation on sandy soils exhibited an erect growth habit and an earlier flowering phenology, while poorly adapted varieties had a more prostrate growth habit. It is likely that an erect growth habit balanced the necessity for moisture conservation and
improved water use efficiency, and crop photosynthesis. The leaf architecture provides sufficient ground cover to reduce evaporative loss from the soil surface, while minimizing transpiration loss (i.e. improved transpiration efficiency). In addition, such a leaf structure may also provide an effective leaf area for efficient light capture following full canopy closure to maintain adequate crop photosynthesis. The reallocation of carbohydrates from the stem to the developing grain post-anthesis was also found to be a mechanism associated with superior adaptation on these soils. Invariably, adaptation is a complex inter-relationship or combination of traits, and it seems unlikely that a variety will be developed that possesses the optimum level of expression for any one trait. Rather a balanced portfolio of traits associated with adaptation appears to be the key to improved growth and grain yield on sandy soils.

While the studies presented here identified a suite of important traits, the unreliable phenotypic expression of traits in low yield potential environments has necessitated the development of an effective and efficient system of selecting germplasm possessing a superior combination of these traits. In this regard, marker assisted selection (MAS) is an attractive option because selection of superior breeding lines with improved adaptation is based solely on the presence of alleles for molecular markers cosegregating with key quantitative trait loci (QTL) (i.e. genotypic expression), and not on the phenotypic expression of a trait, which is strongly influenced by environmental pressures. The development of a mapping population, from a cross between Mundah (very good adaptation) and Keel (moderately poor adaptation), for this study has allowed statistically significant marker-trait associations to be identified, and QTL conferring adaptation to be mapped (Chapter 5).

Research aimed at understanding the genetic basis for adaptation response to sand was confounded by the prevailing environmental conditions, particularly moisture stress. This illustrated the likely importance of traits for superior grain yield under moisture stress conditions, and the interaction between these traits and those important for sand adaptation. The high level of trait by environment interaction in these environments provides further support for the use of marker-assisted selection (MAS) as a valid selection tool. Problems
and limitations encountered with this mapping population, due to limited marker availability, low polymorphism and an incomplete map, were also discussed. Significant QTL for traits associated with adaptation on sandy soils were identified and our understanding of the genetic and physiological mechanisms for sand tolerance has improved. However, the implementation of MAS for sand adaptation is not, at this stage, feasible. Recommendations for further studies aimed at achieving this goal are made.

Both the wild progenitor of cultivated barley and landrace germplasm can provide a rich resource of novel genes for adaptation with the potential contribution to genetic gain for abiotic stress tolerance both speculated and clearly demonstrated. Accordingly, a preliminary evaluation of germplasm from the International Centre for Agricultural Research in Dry Areas (ICARDA) was conducted and described in Chapter 6. Although the ICARDA material was found to offer no immediate commercial value, two breeders lines have been found to provide significant potential as parents. A strategy to identify superior genetic variation for sand adaptation is presented and discussed.