The genetic improvement of wheat and barley for reproductive frost tolerance

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Abstract

The aim of the research reported in this thesis was to identify genetic variation for Reproductive Frost Tolerance (RFT) in barley, characterise the genetic basis of the observed tolerance and devise and execute a strategy to incorporate the tolerance into germplasm adapted to Australian production environments. Effects of wheat chromosome regions syntenous to the barley RFT loci were also investigated.

A field based screening nursery was developed to characterise barley germplasm for RFT. A diverse collection of international barley germplasm was screened for RFT to identify barley genotypes exhibiting better levels of RFT than what was available in Australian cultivated germplasm. Three lines were identified as having an increased level of RFT and populations derived from these three lines were used to QTL map RFT traits. One QTL was common between the three populations and a second QTL was common between 2 of the populations. These two loci were found to control a reduction in Frost Induced Sterility (FIS) and frost induced grain damage.

One of the barley QTL spanned the vernalisation response gene and vegetative frost tolerance locus *vrn*-H1/*Fr*-H1. The syntenous genomic regions in hexaploid wheat were investigated to determine if they had an effect on RFT. Two sets of wheat germplasm containing variation for winter/spring alleles of *vrn*-A1, *vrn*-B1 and *vrn*-D1 loci revealed that no measurable differences in RFT were associated with these loci in wheat.

Targeted populations were developed from selected tolerant and intolerant genotypes. The location of the RFT locus on chromosome 5HL in barley was refined further by developing molecular markers within the QTL region. A population phenotyped for RFT using a frost

simulation chamber revealed that the RFT locus on chromosome 5HL was distal to the major phenology gene *vrn*-H1 segregating in the population.

A breeding strategy was devised to rapidly incorporate the two RFT loci into Australian adapted barley that utilised specific germplasm, newly developed FIS phenotyping methods, molecular markers and doubled haploid technology. A recurrent parent was selected based on adaptation to regions that experience frequent damaging frost events. Germplasm derived from this breeding strategy was screened with diversity array technology markers to determine the effect of donor introgression segment size on yield in target environments.

The resulting germplasm from the fast track breeding strategy was evaluated for RFT using field and controlled environment frost tolerance screening methods. The adaptation of the developed germplasm was assessed by conducting yield trials in the environments where frost is a major risk to production in southern Australia. The performance of this germplasm under a range of frost events provided a better understanding of the conditions in which this source of tolerance is effective.

The results of this thesis highlighted challenges associated with RFT breeding in barley and wheat. The systematic way in which this work was approached through the development of screening methods, identification of genetic variation, genetic analysis and devising a breeding strategy to incorporate the tolerance into adapted germplasm provides a good example of how a cereal crop can be rapidly improved for a quantitative trait such as RFT.

Statement

This work contains no material which has been accepted for the award of any other degree

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Designed experiment, conducted research, analysed and interpreted data, wrote manuscript and acted as corresponding author.

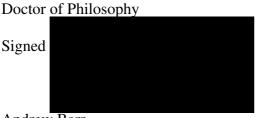


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