

Identification of boron (B) tolerance genes in barley and wheat

Thorsten Schnurbusch^{1,2}, Julie Hayes¹, Margaret Pallotta¹, Peter Langridge¹, Tim Sutton¹

Abstract

Boron (B) toxicity is an eminent limitation in regions of small grain cereal production worldwide, including parts of southern Australia. In recent years, much progress has been made by research groups in Australia investigating the physiological and molecular mechanisms involved in B toxicity tolerance in both barley (*Hordeum vulgare* L.) and wheat (*Triticum* L.). In barley, genes have been identified controlling B tolerance at two of the four known B toxicity tolerance loci. Progress has also been made towards the identification of genes involved in B toxicity tolerance in wheat. Here we describe the current status of B toxicity tolerance research in Australia.

The Algerian barley landrace Sahara 3771 proved of being highly tolerant to B and thus, represents one of the most B-tolerant barleys currently known. It carries four quantitative trait loci (QTL) conferring tolerance to toxic B conditions. One gene (*HvBot1*) underlying the tolerance QTL on chromosome 4H of barley has recently been identified and is a putative membrane-bound B transporter with similarity to bicarbonate transporters in animals; it functions as an efflux transporter to move B out of the plant (SUTTON et al. 2007). *Bot1* was the first B tolerance QTL to be identified in plants. In this work, we describe the identification of a second high B tolerance QTL in barley, mapping to the 6H B tolerance locus, *Bot3*. Higher tolerance to B in Sahara 3771 is mediated through lower transcript levels of *Bot3* in root tips of barley plants possibly owing to a repeat insertion into the promoter region approximately 2 kb upstream of the start codon. Moreover, we observed lower shoot B accumulation in a rice (*Oryza sativa* L.) mutant possessing a point mutation in the orthologous rice gene of *Bot3*. Based

upon our results we conclude that under high soil B *Bot3* entails lower shoot B accumulation and thus, effectually aids to higher B tolerance in Sahara 3771.

In bread and durum wheat, tolerance to high B is controlled by a major tolerance locus for reduced shoot B accumulation on the long arm of chromosome 7B (*Bo1*). It co-segregated with the co-dominant sequence tagged site (STS) molecular marker locus *Xaww5L7-7BL* in the Cranbrook×Halberd doubled haploid and Yallaroi×AUS14010 F₂ populations (SCHNURBUSCH et al. 2007, 2008). AWW5L7 proved to be highly predictive for the occurrence of *Bo1* in a set of 94 Australian bread wheat cultivars and breeding lines, indicating that *Bo1*-derived tolerance is prevalent in Australian bread wheat germplasm.

Keywords

Candidate gene, cloning, functional analysis, mapping, marker, QTL

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¹ Australian Centre for Plant Functional Genomics, School of Agriculture, Food and Wine, University of Adelaide, Waite Campus, Urrbrae, South Australia 5064, Australia

² Leibniz-Institute of Plant Genetics and Crop Plant Research (IPK), Genebank Department, Corrensstr. 3, D-06466 GATERSLEBEN

* Ansprechpartner: Dr. Thorsten SCHNURBUSCH, thor@ipk-gatersleben.de