A

Genetics of Boron Tolerance in Durum Wheat

by

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Thesis submitted for the degree of Doctor of Philosophy

in

Department of Plant Science

Waite Agricultural Research Institute

The University of Adelaide

April, 1996

Awarded 1996

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Abstract

Genetic studies of tolerance of durum wheat (*Triticum turgidum* L. var *durum*) to high concentrations of boron (B) were undertaken in order to identify genetic variation in response to B, the mode of gene action, number of genes and chromosomal locations of genes controlling tolerance to B.

Sources of B tolerance and the range of response of durum wheat to high concentrations of B were investigated by using filter paper soaked in solutions with high B concentrations and soil screening methods. Tolerant genotypes were identified among landrace lines, originating from Asian countries, but not in the agronomically adapted varieties. Significant differences between tolerant and sensitive genotypes were recorded for expression of symptoms of toxicity, dry matter production and shoot B concentrations when plants were grown in soils containing high concentrations of B. All parameters measured in high B soil showed high correlations with the root length of seedlings in high B filter paper. It was concluded that the root length of seedlings grown under high B conditions was an appropriate criterion for determining B tolerance in durum wheat.

Major genes were identified from the evaluation of F_2 and F_3 segregating populations derived from seven parents which represented four levels of tolerance. Single gene segregation resulted between:-

- tolerant x moderately tolerant (AUS 10105 (T) and AUS 10110 (T) x AUS 10344 (MT) and AUS 14010 (MT)) lines,
- moderately tolerant x moderately sensitive (AUS 10344 (MT) x Yallaroi (MS), AUS 14010 (MT) x AUS 10348 (MS) and Yallaroi (MS)) lines,
- moderately sensitive x sensitive (AUS 10348 (MS) x AUS 13244 (S)) lines.

Transgressive segregation resulted between:-

- moderately tolerant (AUS 10344) x moderately tolerant (AUS 14010) lines,
- moderately sensitive (AUS 10348) x moderately sensitive (Yallaroi) lines,
- moderately tolerant (AUS 10344) x moderately sensitive (AUS 10348) lines.

No segregation was observed in the cross between:-

- tolerant (AUS 10105) x tolerant (AUS 10110) lines.

Tolerance to B in durum wheat was controlled by three independent loci, which act additively, designated Bo_T1, Bo_T2 and Bo_T3 with the tolerance character being expressed as a partially dominant trait, depending on the concentration of applied B. Genotypes in respect to B tolerance were proposed as:-

- tolerant (T): Bo_T1 Bo_T2 Bo_T3 (AUS 10110, AUS 10105),
- moderately tolerant (MT): Bo_T1 bo_T2 Bo_T3 (AUS 10344) and bo_T1 Bo_T2 Bo_T3 (AUS 14010),
- moderately sensitive (MS): bo_T1 Bo_T2 bo_T3 (AUS 10348) and bo_T1 bo_T2 Bo_T3 (Yallaroi), and
- sensitive (S): bo_T1 bo_T2 bo_T3 (AUS 13244).

The chromosomal locations of genes controlling B tolerance were studied by aneuploid analysis using Langdon D-genome disomic substitution lines. It was found that Bo_T1 was located on chromosome 7B of AUS 10344 (MT), Bo_T2 on 7B of AUS 14010 (MT) and both genes on 7B of AUS 10110 (T). Linkage analysis using restriction fragment length polymorphisms indicated that Bo_T2 was likely to be located on the distal region of the long arm of chromosome 7B. Bo_T1 and Bo_T2 segregated independently of each other.

The results from this thesis demonstrated the range and sources of genetic variation for response to B. Tolerance to high concentrations of B is under simple genetic control as observed in bread wheat. High levels of tolerance can be transferred into sensitive commercial varieties via backcrossing and selection can be performed during seedling growth at early generations. These findings are being adopt in a durum wheat breeding program at the Waite Institute in South Australia.