Chromosomal localization of genes mediating tolerance to boron in pea (Pisum sativum L.) using molecular markers

Abstract

Background: The use of molecular markers in linkage analysis facilitates the location of quantitative trait loci (QTLs) associated with characteristics of agronomic interest. The aim of this study was to identify molecular markers linked to QTLs associated with boron tolerance in Pisum sativum L. (pea).

Materials and Methods: A F_2 population derived from a cross between Alma (sensitive) and SA 310 (tolerant) containing 150 individuals was used. DNA was extracted from leaves and used as a template for PCR amplification. RFLP and RAPD markers were used to identify loci linked to boron tolerance.

Results: A total of 239 informative markers were identified, of which 164 were RFLP markers and 75 were RAPD markers. The results showed that two QTLs associated with boron tolerance were located on linkage groups A1 and A4. The QTLs were linked to RFLP markers PR-11 and PR-14 on linkage group A1, and to RAPD markers RFLP-12 and RAPD-15 on linkage group A4.

Conclusion: The results of this study provide valuable information for the development of molecular marker-assisted selection programs for boron tolerance in Pisum sativum L. and other genotypes with related traits.