
QTL mapping for zinc tolerance at the intra-specific level in *Arabidopsis halleri* using a F2 progeny

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Abstract

Arabidopsis halleri is a well-studied species for its ability to tolerate and hyperaccumulate metals, particularly zinc and cadmium. Deciphering the genetic architecture of these quantitative traits has only been done at the inter-specific level using *A. lyrata* ssp. *petraea* x *A. halleri* backcross and F2 progenies. The major QTL regions identified included candidate genes implied in the traits such as genes from the *hma4* (heavy-metal transporting ATPase 4) and the *mtp1* (metal tolerance protein 1) families. So far, no QTL mapping study has been done at the intra-specific level. We aimed at studying the genetic architecture of zinc tolerance and hyperaccumulation in an *A. halleri* F2 progeny (175 individuals) by crossing individuals coming from polluted and non-polluted soils. 384 single nucleotide polymorphism (SNP) markers issued from high-throughput sequencing of the genomes of parental plants have been developed and used for the genetic map construction. Growth parameters and photosynthetic yield were performed under control and polluted conditions in hydroponics (10 vs. 2000 μ M of ZnSO₄). One major QTL was identified for photosynthetic yield that explained about 30% of the variation for the trait. This QTL region does not co-localize with the known candidate genes for metal tolerance that have been identified so far at the inter-specific level. This suggests that, in *A. halleri*, molecular mechanisms involved in local adaptation to metal-polluted soils at the intra-specific level differ from those that distinguish the level of metal tolerance observed in the species from those observed in its non-tolerant close relatives.

Keywords: *Arabidopsis halleri*, zinc tolerance, QTL mapping, intraspecific F2 cross, Single Nucleotide Polymorphism

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