

**Quantitative Trait Loci and Candidate Gene Mapping of Aluminum
Tolerance in Diploid Alfalfa**

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Aluminum (Al) toxicity in acid soils is a major limitation to alfalfa (*Medicago sativa* subsp. *sativa* L.) production in the USA. Developing Al-tolerant alfalfa cultivars is one alternative to overcome this constraint. Accessions of wild diploid alfalfa (*M. sativa* subsp. *coerulea*) were found to be a source of useful genes for Al tolerance. Previously, two genomic regions associated with Al tolerance were identified in this diploid species using restriction fragment length polymorphism (RFLP) markers and single marker analysis. This study was conducted to identify additional QTLs and to flank the previously identified Al tolerance QTL with simple sequence repeats (SSR) markers. A genetic linkage map was constructed using EST-SSR markers in a population of 130 BC₁ lines derived from the cross between Al-sensitive and tolerant genotypes. Three putative QTLs on LGI, LGII and LGIII explaining 38%, 16% and 27% of the phenotypic variation, respectively, were identified. Six candidate gene markers designed from *Medicago truncatula* ESTs that showed homology to known Al-tolerance genes identified in other plant species were placed on the QTL map. A marker designed from a candidate gene known to be involved in the release of malic acid mapped near a marginally significant (LOD 2.83), QTL on LG I. The SSR markers flanking these QTLs will be useful for transferring them to cultivated alfalfa via marker-assisted selection and for pyramiding Al tolerance QTL.