

Identification of Aluminum Tolerance QTL in Tetraploid Alfalfa

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Abstract

Aluminum (Al) toxicity in acid soils is one of the factors limiting crop production. Alfalfa (*Medicago sativa* L.) is one of the most important forage legumes worldwide and is susceptible to Al toxicity. Al tolerance in alfalfa was identified in a diploid *Medicago sativa* subs. *caerulea* accession and has been successfully transferred to tetraploid germplasm. The goals of this study are to identify and confirm quantitative trait loci (QTL) for Al tolerance in tetraploid alfalfa. An F₁ mapping population from the cross between the Al tolerant genotype Altet-4 and the Al susceptible genotype NECS-141 was used for mapping. A total of 538 legume SSR primer pairs was used to construct a genetic linkage map for each of the eight groups of four homologous chromosomes. The composite map length was 826 cM and 745 cM for Altet-4 and NECS-141, respectively. Phenotypic characterization for Al tolerance was performed using a callus bio assay and a whole plant assay in media. A normal distribution and transgressive segregation was identified in both sets of phenotypic data indicating a quantitative inheritance. A total of 21 alleles with a positive effect on Al tolerance and 51 alleles with a negative effect were identified using single factor analysis of variance and the Kruskal-Wallis test. The identification of alleles contributing to Al tolerance enables the integration of molecular breeding strategies to accelerate the development of alfalfa cultivars which are productive in acid and Al toxic soils.