

High Resolution Melting Analysis for SNP Genotyping in Diploid and Tetraploid Alfalfa (*Medicago sativa* L.)

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Abstract

Single nucleotide polymorphism (SNP) represents the most abundant type of genetic polymorphism in plant genomes. SNPs markers are valuable tools for linkage and association mapping, map-based cloning, molecular breeding, and genetic analysis of complex traits of agronomic importance. Current challenges for SNP genotyping in polyploid outcrossing species include multiple alleles per loci and lack of high-throughput methods suitable for variant detection. In this study, we developed a high-resolution melting (HRM) analysis system for SNP genotyping in diploid and tetraploid alfalfa. The sensitivity and utility of this technology is demonstrated by identification of the parental genotypes and segregating progeny from multiple populations based on unique melting curve profiles due to differences in allelic composition at multiple loci. HRM is a fast and efficient approach for SNP discovery and genotyping, useful in polyploid species with uncharacterized genomes.