

**Revealing Genetic Relationships and the Scope of Diversity among Unimproved
Diploid Alfalfa Germplasm Using SSR Markers**

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Cultivated alfalfa has been selected from a taxonomic group called the *Medicago sativa-falcata* complex. The complex consists of several species and subspecies that do not have any hybridization barrier. Morphological traits such as flower color, pod shape and ploidy have traditionally been used for taxonomic classification, but the validity of taxa has not been investigated with genomic tools. Genetic diversity analyses in alfalfa have mainly been conducted to elucidate the genetic relationships of cultivated germplasm. The genetic basis of morphologically-based taxonomy, molecular diversity, and population structure of wild diploid accessions in the *M. sativa-falcata* complex are largely unknown. We have selected 384 individuals from 123 unimproved diploid alfalfa accessions from throughout the northern hemisphere that represent *M. sativa* subspecies *caerulea*, *falcata*, and *hemicycla*. We have genotyped selected individuals with SSR markers that are well distributed throughout the genome. High allelic diversity has been observed. SSR based population structure analyses has identified two clearly discrete subpopulations, corresponding to subsp. *falcata* and subsp. *caerulea*. The hybrid nature of subspecies *hemicycla* has also been confirmed based on its genome composition. The population structure among these diploid germplasm will be accounted for in subsequent analyses estimating linkage disequilibrium and identifying loci associated with biomass yield and stem cell wall composition.

References

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