Characterization of Perennial *Medicago* Germplasm Diversity Using Molecular Markers

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Alfalfa is one of the most important cultivated forage legumes worldwide. Knowledge of the extent of variation in a species is crucial for successful exploitation of its natural genetic diversity. In this study, we evaluated the genetic diversity of 190 perennial Medicago accessions that were mostly collected from the wild in the Former Soviet Union area. Multiple accessions from *M. sativa* subsp. *caerulea* and *M. sativa* subsp. *falcata* were included in the genetic diversity analysis and phenotypic evaluations. SSR markers were used to genotype eight individuals from each accession. Both clustering and population structure analysis indicate the alfalfa subspecies *M. sativa* subsp. *caerulea* and *M. sativa* subsp. *falcata* have significant genetic differences between them and the germplasm pools can be clearly distinguished using molecular markers. A population structure was present in both subspecies with the grouping of sub-populations being highly correlated with the geographic origin of the accessions. Characterization of novel alfalfa germplasm is essential to manage the germplasm collection, to identify alfalfa germplasm with positive alleles for traits of interest, to select parents for mapping desirable traits, and to implement association mapping approaches and identify functional association taking into account the population structure.