

Examining Genetic Relationships among Alfalfa Cultivars (Fall Dormancy 2-6) and Historical Sources of Medicago Germplasm with Amplified Fragment Length Polymorphisms (AFLPs)

Isadora Jiménez, Jennifer Ariss and George Vandemark, USDA-ARS, Prosser, WA 99350

(AFLPs) were used to examine both genetic relationships between alfalfa populations and genetic similarity within populations. Forty seven populations consisting of 38 cultivars ranging from fall dormancy 2-6 and the nine historically recognized sources of *Medicago* germplasm in North American were examined using four different AFLP primer pairs. Four bulk DNA samples consisting of total DNA extracted from 20 plants/bulk were examined for each population. A total of 410 AFLP markers ranging in size from 50-500 bp were detected, of which 396 (96.6%) were polymorphic. A dendrogram from the analysis suggests that the historical sources of germplasm are quite diverse from all the alfalfa cultivars examined. Among the nine original sources of *Medicago* germplasm the highest mean genetic similarity between bulks within a population was observed for *M. varia*, while the lowest was observed for *M. falcata*. The highest mean genetic similarity between bulks within an alfalfa cultivar was observed for Magnum IV, while the lowest was observed for Amerigraze. The highest genetic similarity between historical germplasm sources was between *M. varia* and Peruvian, while the lowest similarity was between *M. falcata* and African. The highest mean genetic similarity among the nine original sources of *Medicago* germplasm and alfalfa cultivars was observed between *M. varia* and Imperial, while the lowest mean genetic similarity was between *M. falcata* and Dual. The highest mean genetic similarity between cultivars was between Magnum IV and Magnum V, while the lowest mean genetic similarity was between Vernema and 53V08. The use of AFLPs to amplify DNA from a pooled sample of 20 tetraploid, and likely highly heterozygous, plants resulted in complex yet informative fingerprints. Marker analysis of bulked plant samples may prove to be an efficient approach for detecting associations between markers and phenotypes in alfalfa.