

**Genetic Mapping of Factors Influencing Alfalfa Biomass  
Accumulation Under Drought-Stress.**

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Identifying genetic factors influencing alfalfa (*Medicago sativa* L.) biomass production under drought stress will provide knowledge to design tools for developing cultivars that can remain more productive in drought-prone environments. Two tetraploid alfalfa F<sub>1</sub>BC<sub>1</sub> linkage mapping populations derived from a cross between two subspecies genotypes of *M. sativa* (i.e. ssp. *sativa* var. Chilean and ssp. *falcata*, var. Wisfall), and previously genotyped with 286 EST-SSRS and 43 SNP markers, were evaluated in this study. Seeded plots of maternal half-sib families of each F<sub>1</sub>BC<sub>1</sub> genotype were characterized for shoot biomass production under water-stress conditions over two regrowth cycles in each of three years (2005-2007) at Las Cruces, NM. Field plots were destructively harvested for root biomass measurements (25 cm soil depth) in August 2007. Study plots experienced severe water stress conditions, with leaf relative water contents as low as 50% at solar noon, and significant reductions in photosynthesis and stomatal conductance. Both the Chilean and Wisfall mapping population parents possessed favorable and unfavorable alleles for root and shoot biomass production. Marker alleles accounted for up to 18% of the yield variance in a given harvest. Markers in alfalfa linkage groups 1, 5, and 8 exhibited the most consistent effects on biomass production under water stress. Markers in linkage groups 3, 6, and 8 had the greatest influence on root biomass production. These mapping populations are also being evaluated for biomass production at Burneyville, OK, with results to be forthcoming.