

## Adaptive Responses of *Medicago truncatula* and *Medicago sativa* to Low Phosphorus Availability

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Alfalfa (*Medicago sativa* L.) is a perennial legume species capable of symbiotic nitrogen fixation and thus reduces the need for nitrogen fertilizers as part of a crop rotation system. Alfalfa has high forage quality and high biomass production potential that can be hindered from abiotic stresses including drought and nutrient deficiencies. Phosphorus (P) is one of the main nutrients required for plant growth but its availability may be limited in certain soils. Phosphorus is a non-renewable nutrient on Earth and some projections on a global scale anticipate that P fertilizer production could reach a peak as early as 2030. Therefore, P could become a limiting factor for agricultural production in the not too distant future. Adaptive responses of *M. truncatula* to low P availability may provide insights on strategies that can be exploited to enhance P acquisition and use efficiency in agricultural legumes including alfalfa. The availability of extensive resources in *M. truncatula* including an annotated genome sequence and HapMap accessions with available single nucleotide polymorphism (SNP) data, can be used to identify genes and/or sequence variation associated with biomass production and root growth under low P conditions. The objective of this study is to identify natural genetic diversity for P acquisition efficiency (PAE) and P use efficiency (PUE) in annual and perennial *Medicago* germplasm. Phenotypic screening strategies were implemented in both greenhouse and laboratory conditions in which plants were grown in varying P regimes and used to identify the optimal P levels to induce P-deficient vs. P-sufficient growth conditions. Considerable genetic variation for decreased shoot and root biomass yield in P-limiting conditions was observed. The extent of the P response on growth and development was genotype and species-dependent. In addition to the phenotypic screening, mining of the available SNP data is being pursued as a strategy to identify sequence variation in key genes that could result in sustained biomass yield under low P conditions. Further transcriptomic and P-profiling approaches under various P regimes will increase our understanding of the genetic mechanisms and key genes associated with P acquisition and use efficiency in the sampled genotypes contrasting for plant growth. These key P-related genes will serve as targets to develop molecular markers for their potential use in plant breeding applications. The breeding lines and populations developed would then be further evaluated in low P-field conditions to assess genetic gains from molecular breeding strategies. The long-term goal is to address a practical limitation of year-round forage production systems and reduce the need for expensive on-farm P fertilizers that directly impact biomass yield, the environment and on-farm profitability.

**Key words:** *Medicago*; phosphorus use efficiency; breeding; SNP