

Medicago genomics and functional genomics

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Legumes are second only to grasses in importance to humans as a source of food, feed for livestock, and raw materials for industry. The Noble Foundation is committed to the improvement of legumes for pastures. This includes enhancing the nutritional value of legumes as well as increasing the tolerance or resistance of legumes to abiotic and biotic stress. Although alfalfa, *Medicago sativa*, is the most important forage legume in the USA, it is a poor model for genetic and genomic research. However, its close relative, *Medicago truncatula* (or simply *Medicago*), which has a comparatively small diploid genome is an ideal model for legume genomics. The Noble Foundation has played a leading role in the establishment of *Medicago* as a model and is using it to identify target genes for legume breeding programs. This talk will review progress of the international *Medicago* genome sequencing effort as well as our work on the development and use of tools for *Medicago* functional genomics, which include: a gene expression atlas for *Medicago truncatula*; platforms for high-throughput qRT-PCR analysis of transcription factor and miRNA genes; and fast neutron deletion and *Tnt1* transposon insertion mutant populations for forward and reverse genetics. Examples will be presented of how these tools are being utilized to reveal the molecular basis of symbiotic nitrogen fixation, seed development, and plant response to drought stress.