

Translational genomics for engineered forage quality traits in alfalfa

**Richard A. Dixon, Fang Chen, Lisa Jackson, Jin Nakashima, Yongzhen Pang,
Gregory Peel, Gail Shadle, and Rui Zhou.
Plant Biology Division, Samuel Roberts Noble Foundation, 2510 Sam Noble
Parkway, Ardmore, Oklahoma 73401, USA**

Although alfalfa is the most important forage legume in the USA, it is a poor subject for genomic research. Barrel medic (*Medicago truncatula*) has been developed as a model legume for genomic studies, and its very close genetic relationship to alfalfa facilitates the direct transfer of genomic information to the target crop species. We have been using the wealth of genetic and genomic resources in *M. truncatula* to understand more about the biosynthesis of proanthocyanidins (PAs) and lignin, two classes of phenolic polymer that strongly impact forage quality.

PAs are oligomeric flavonoids, commonly found in seed coats. The flavanol (-)-epicatechin is the major component of *Medicago* PAs. We will summarize genomic approaches in *M. truncatula* to understand the late stages in PA biosynthesis and assembly, and the current status of our attempts to introduce PAs into alfalfa so as to reduce pasture bloat potential and improve protein utilization.

Lignin is a major polymeric component of plant secondary cell walls, synthesized from phenylpropanoid-derived monomers (monolignols). A major component of dietary fiber, lignin also has a negative impact on the digestibility of forages in ruminant animals, and in the processing of lignocellulosic biofuel crops. We have extensively utilized *Medicago* genome information for modifying lignin content and composition in alfalfa, and will summarize the applications of this work for forage and bioenergy research.