

Legume Focus: Model Species Sequenced, Mutagenesis Approaches Extended, and Debut of a New Model

Legumes (members of the plant family Fabaceae) have long been at the forefront of both applied and basic plant sciences. Legume species have been domesticated for thousands of years, and Mendel introduced one as a model system some 150 years ago. No less today, legume research is driven by efforts to meet the needs of humanity and the biosphere and by basic curiosity about how living things work. This is the fourth issue of *Plant Physiology* to focus on advances in legume biology, following special issues in 2003, 2005, and 2007. Below, we outline some highlights.

Elucidating the sequences and functions of the genomes of three legume species, *Medicago truncatula*, *Lotus japonicus*, and *Glycine max* (soybean), has been a more than decade-long effort, and now the genome sequences of these species are essentially complete. *M. truncatula* and *L. japonicus* are model systems that have relatively small diploid genomes, self fertility, short generation times, and are amenable to genetic manipulation. Soybean is an extremely important crop that has also become an important model. Collectively, the genome sequences of these three species are greater than the sum of their parts, because they can be compared with each other and are likely to be predictive of other agriculturally important legume crops. The three legumes are all part of the papilionoid subfamily, and their genes are found in large syntenic regions, which should facilitate positional cloning of genes from other related legumes. New technologies in high-throughput sequencing, highly multiplexed mapping techniques, and fledgling haplotype map projects will glean new information about the current model systems and emerging models as well. Moreover, new tools for legume mutagenesis and reverse genetics augment sequence data and are expanding experimental approaches to investigate gene and genome functions in development, as seen in the advances reported here.

Legumes have traditionally been key systems for investigating organismal interactions, especially interactions of roots with microbes. Although this has been a focus for decades, challenges remain. New findings have identified possible functions for microRNAs in the development of nitrogen-fixing nodules, but details of many roles are yet to be characterized. On an environmental scale, researchers are evaluating the capacity of legumes to respond to elevated [CO₂] with increased nitrogen fixation, but long-term studies and additional quantitative work are needed. Among deleterious organisms interacting with legume roots,

infection by the soybean cyst nematode results in major crop losses. Recent efforts to identify soybean genes involved in responses to this pest have advanced understanding, such that researchers are now poised to translate the advances for greater resistance.

Our current knowledge base and tools provide the means to engineer desired traits into seeds of crop legumes. For example, soybean oils are high in polyunsaturated fatty acids, resulting in low oxidative stability. Oxidation diminishes its food value as well as its utility as a biofuel and other industrial applications. This problem can be solved by hydrogenation of the unsaturated bonds in the oil fatty acids. However, hydrogenation results in the formation of trans-fats, which contribute to cardiovascular disease. Engineered changes in fatty acid biosynthesis can address these problems; thus, new technologies allow improvements in seed quality as well as in overall yield.

With the increasing volume of literature describing advances in our understanding of model systems, it is easy to acquire a sense that we are beginning to know a lot about legumes. However, legumes are a very large plant family, comprising about 700 genera and 20,000 species. Indeed, the model and crop legumes that are most heavily studied cluster in one large clade within the papilionoid subfamily, which includes less than half of the species diversity of legumes. *Chamaecrista fasciculata* is an emerging model for the mimoid clade of legumes. Nonpapilionoid models such as *C. fasciculata* will allow comparison with the existing model legumes with regard to development, genome evolution, and symbiosis with rhizobia. *C. fasciculata* also has considerable practical utility in the development of mixed prairie cropping systems containing native legumes, which are being studied as an alternative to crop-based systems for bioenergy.

We hope that through this Focus issue, readers will gain an appreciation of new tools and directions in legume biology. The articles within identify many questions and opportunities for continued work. We especially hope that students, postdocs, and educators will get a feel for the excitement and promise of a rapidly advancing field.

Mark R. O'Brien
Carroll P. Vance
Kathryn A. VandenBosch
Monitoring Editors
Plant Physiology