

Functional Plant Biology

Contents

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Foreword

Review: Legume nodulation: successful symbiosis through short and long-distance signalling

Mark Kinkema, Paul T. Scott and

Peter M. Gresshoff

707–721

Kinkema *et al.* provide a detailed review of the molecular and physiological events regulating nodulation in legumes. They describe the events controlling root nodule formation, and present evidence for short- and long-distance signalling in various legumes.

Brassinosteroid-independent function of BRI1/CLV1 chimeric receptors

Anne Diévert, Matthew J. Hymes, Jianming Li

and Steven E. Clark

723–730

This paper makes a valuable contribution to our understanding of the mechanistic basis of receptor kinase signalling in plants, tackling the question of what mechanisms *Arabidopsis* Leucine-rich repeat (LRR) receptors employ to relay information across the plasma membrane. The authors propose that the BRASSINOSTEROID INSENSITIVE 1 (BRI1) extracellular domain has a homodimerisation capacity, and that the mutants we assess control dimerisation, and not hormone binding.

Review: Functional genomics of plant transporters in legume nodules

Vagner A. Benedito, Xinbin Dai, Ji He,

Patrick X. Zhao and Michael K. Udvardi

731–736

In recent decades, a combination of physiology, biochemistry, molecular and cell biology and genetics has provided a basic understanding of key transport processes in nitrogen-fixing legume nodules, particularly those involved in nutrient exchange between infected plant cells and their endosymbiotic rhizobia. This concise and timely review integrates existing biochemical and biophysical information on symbiosome membrane/nodule transporters with ongoing more progressive genomic and functional genomic analyses.

Review: Transcriptional snapshots provide insights into the molecular basis of arbuscular mycorrhiza in the model legume *Medicago truncatula*

Natalija Hohnjec, Kolja Henckel, Thomas Bekel,

Jerome Gouzy, Michael Dondrup,

Alexander Goesmann and Helge Küster

737–748

This review covers the rapidly evolving, very specialised and very exciting area of transcriptional genomics. The authors give a comprehensive, state-of-the-art account of gene expression analysis of the symbiosis between arbuscular mycorrhiza (AM) and the model legume *Medicago truncatula*. The review will be of value to AM biologists and those interested in transcriptional profiling in plant–microbe interactions.

Cover illustration: Soybean vascular tissue in stem revealing the channels of tissue communication. Photo by Mr Yu-Hsiang Lin (ARC Centre of Excellence for Integrative Legume Research, Brisbane).

Genetic suppressors of *Lotus japonicus har1-1* hypernodulation show altered interactions with *Glomus intraradices*

Jeremy Murray, Ryan Geil, Cameron Wagg, Bogumil Karas, Krzysztof Szczygłowski, and R. Larry Peterson

749–755

Murray *et al.* describe the root colonisation of a series of *Lotus japonicus* nodulation mutants by the arbuscular mycorrhiza, *Glomus intraradices*, identified from a genetic screen for suppressors of the hypernodulating *har1-1* mutant. They examine the associated structures (such as hyphae, appressoria and arbuscules) and describe the stage at which each mutant is impeded. The work helps our understanding of the *L. japonicus*–*G. intraradices* symbiosis, and the mutants are valuable in future characterization of the early stages of mycorrhization and nodulation. This is important in the dissection of the roles of these genes in regulation of the mycorrhization and in relating this genetic control to that of rhizobial symbiosis.

A *crispa* null mutant facilitates identification of a *crispa*-like pseudogene in pea

Frank Sainsbury, Alexander D. Tattersall, Michael J. Ambrose, Lynda Turner, T. H. Noel Ellis and Julie M. I. Hofer

757–763

This paper studies the role of *Phantastica* (*Phan*), and a closely related gene, *crispa*, in pea leaf development. The authors show that this second gene lies on a different chromosome, and is most likely a pseudogene, so has no role in conferring stipule adaxial identity. A new deletion mutant, *crispa-4* was identified, with radialised stipules and leaflets, indicating that *crispa* confers adaxial identity on both these organs in pea.

Survey sequencing of soybean elucidates the genome structure, composition and identifies novel repeats

Andrew Nunberg, Joseph A. Bedell, Mohammad A. Budiman, Robert W. Citek, Sandra W. Clifton, Lucinda Fulton, Deana Pape, Zheng Cai, Trupti Joshi, Henry Nguyen, Dong Xu and Gary Stacey

765–773

The work by Nunberg *et al.* reports on the survey sequencing (24000 DNA fragments and 29000 BAC end sequences) of soybean to create a useful DNA repeat sequence database, and provides interesting information on the distribution of different genomic elements throughout the DNA of this complex legume species. 248 different DNA repeats were identified, including novel repeats. The sequence methylation-filtration studies predict a 343-Mb hypomethylated, gene-rich space.

Differences in syntenic complexity between *Medicago truncatula* with *Lens culinaris* and *Lupinus albus*

Huyen T. T. Phan, Simon R. Ellwood, Rebecca Ford, Steve Thomas and Richard Oliver

775–782

Model organisms are widely used to provide technological knowledge for use in agronomically important but genomically less accessible crop plants. Phan *et al.* describe the development of PCR-based cross-species specific genetic markers for leguminous plants, to create genetic maps for *Lens* and *Lupinus* species and to reveal syntenic relations between the genome of these species and the model legume *Medicago truncatula*.

The Affymetrix *Medicago* GeneChip® array is applicable for transcript analysis of alfalfa (*Medicago sativa*)

Mesfin Tesfaye, Kevin A. T. Silverstein, Bruna Bucciarelli, Deborah A. Samac and Carroll P. Vance

783–788

This timely transcriptomics paper describes the results of experiments using the new *Medicago* GeneChip from Affymetrix. It is a useful reference on the technical basics of this new array. The authors investigate the utility of this new GeneChip by analysing the expression profiles of leaf and root RNA from *Medicago truncatula* and *M. sativa*, and provide useful information on the performance of this new array for transcriptional profiling.

Identification of candidate phosphorus stress induced genes in *Phaseolus vulgaris* through clustering analysis across several plant species

Michelle A. Graham, Mario Ramírez, Oswaldo Valdés-López, Miguel Lara, Mesfin Tesfaye, Carroll P. Vance and Georgina Hernandez

789–797

Graham *et al.* report an *in silico* approach for the identification of genes involved in adaptation of *Phaseolus vulgaris* and other legumes to phosphorus deficiency. Some 22 groups of genes from four legume species and *Arabidopsis thaliana* were identified as statistically over-represented in EST contigs from P-stressed tissues. By combining bioinformatics analysis with micro/macroarray technologies and clustering results across five species, 52 *P. vulgaris* candidate genes belonging to 19 categories were identified as induced by P-stress. Transport-related, stress (defence and regulation) signal transduction genes were abundant.