

# Functional Plant Biology

## Contents

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### Special Issue: Legume Biology

*Foreword: Legume biology: the basis for crop improvement*

**Rajeev K. Varshney and Himabindu Kudapa** v–viii

This issue of *Functional Plant Biology* is dedicated to ‘Legume Biology’ research covering part of the work presented at VI International Conference on Legume Genetics and Genomics held at Hyderabad, India, in 2012. The 13 contributions cover recent advances in legume research in the context of plant architecture and trait mapping, functional genomics, biotic stress and abiotic stress.

*Review: FT genes and regulation of flowering in the legume Medicago truncatula*  
**Joanna Putterill, Lulu Zhang, Chin Chin Yeoh, Martin Balcerowicz, Mauren Jaudal and Erika Varkonyi Gasic**

1199–1207

The timing of flowering has major effects on crop productivity and plant adaptation. Here we review *FT* genes which encode important floral activators and discuss recent work in the model legume *Medicago* highlighting the importance of an *FT* ortholog *FTa1* in flowering. Our work and others shows that while *FT* orthologs promote flowering in many plants, there appears to be considerable diversity in the upstream pathways that regulate these genes.

Overexpression of miR160 affects root growth and nitrogen-fixing nodule number in *Medicago truncatula*  
**Pilar Bustos-Sanmamed, Guohong Mao, Ying Deng, Morgane Elouet, Ghazanfar Abbas Khan, Jérémie Bazin, Marie Turner, Senthil Subramanian, Oliver Yu, Martin Crespi and Christine Lelandais-Brière**

1208–1220

The phytohormone auxin plays fundamental roles in plant development, including the formation of symbiotic nitrogen-fixing nodules in legumes. This study shows that (i) microRNA160 represses the expression of five transcription factors of the auxin response factor family in *Medicago truncatula*; and (ii) that its overexpression in the root affects both root growth and nodule number. The miR160/ARF regulatory loop may thus be involved in auxin-dependent regulation of nodule organogenesis.

*Review: Functional genomics to study stress responses in crop legumes: progress and prospects*  
**Himabindu Kudapa, Abirami Ramalingam, Swapna Nayakoti, Xiaoping Chen, Wei-Jian Zhuang, Xuanqiang Liang, Guenter Kahl, David Edwards and Rajeev K. Varshney**

1221–1233

The majority of legume crops suffer from low level of crop productivity especially in developing countries due to their exposure to several stresses. Therefore, it is important to identify candidate genes and molecular mechanisms associated with resistance to these stresses. This article provides a critical appraisal on recent advances and potential of functional genomics for crop improvement in legume crops.

*Cover illustration:* Legumes (e.g. chickpea) are important food crops and are quite different from other plant species in that they have certain unique features, such as ability for symbiotic nitrogen fixation. Several biotic (e.g. pod borer) and abiotic (e.g. heat) are major constraints for legume productivity. The study of legume genetics, genomics and biology are all important in order to understand the limitations of yield of legume crops and to support our legume breeding programs. This special issue focuses on legume biology: the basis for crop improvement. Source: ICRISAT, Hyderabad.

<p>Review: VIGS technology: an attractive tool for functional genomics studies in legumes  <b>Stéphanie Pflieger, Manon M. S. Richard, Sophie Blanchet, Chouaib Mezjadi and Valérie Geffroy</b></p>	1234–1248	<p>VIGS (virus-induced gene silencing) technology is a powerful technology for determining the function of unknown genes in species recalcitrant to stable genetic transformation. Here we provide an overview of the VIGS systems available for legumes, and present their successful applications in functional genomics studies. We also discuss the limitations and future challenges of VIGS technology in legumes.</p>
<p>Transcriptome profiling of peanut (<i>Arachis hypogaea</i>) gynophores in gravitropic response  <b>Hai-fen Li, Xiao-Ping Chen, Fang-he Zhu, Hai-Yan Liu, Yan-Bin Hong and Xuan-Qiang Liang</b></p>	1249–1260	<p>The gravitropic response of peanut gynophore plays an essential role in peanut pod development and, thus, plays an important role in pod yield. Transcriptome analysis was conducted using a high-density peanut microarray to identify candidate genes and pathways related to peanut gynophore gravitropism, leading to an enhanced understanding of this process.</p>
<p>Exploiting a fast neutron mutant genetic resource in <i>Pisum sativum</i> (pea) for functional genomics  <b>Claire Domoney, Maggie Knox, Carol Moreau, Mike Ambrose, Sarah Palmer, Peter Smith, Vangelis Christodoulou, Peter G. Isaac, Matthew Hegarty, Tina Blackmore, Martin Swain and Noel Ellis</b></p>	1261–1270	<p>Deletion mutants can be used in both forward and reverse genetic screens to discover genes controlling the biology of important plant and seed traits. Here we describe the use of mutants in pea in providing a route to gene isolation and the identification of mutations in genes with non-obvious phenotypes such as those altering seed composition or quality. This mutant resource broadens further the tools available for gene discovery in pea.</p>
<p>Review: Plant–aphid interactions with a focus on legumes  <b>Lars G. Kamphuis, Katherine Zulak, Ling-Ling Gao, Jonathan Anderson and Karam B. Singh</b></p>	1271–1284	<p>Aphids are sap-sucking insects that cause significant yield losses in agriculture. This review focuses on the progress made in understanding plant defense responses against aphid infestation particularly in legumes. Over the last decade, increased research efforts have been made to understand how aphids manipulate the plant to establish a successful feeding site. Progress in this area is described.</p>
<p>Review: Understanding the molecular defence responses of host during chickpea–<i>Fusarium</i> interplay: where do we stand?  <b>Sumanti Gupta, Anirban Bhar and Sampa Das</b></p>	1285–1297	<p>Comparative functional genomic studies involving chickpea and wilt disease causing fungus, <i>Fusarium oxysporum</i> are conducted to enrich present understanding of <i>Fusarium</i>–legume interplay. This report describes the differential pattern of molecular responses associated with wilt disease in susceptible and resistant chickpea. Molecular information deciphered from the present case study is expected to promote the development of legume crop protection strategies.</p>
<p>A survey of genes involved in <i>Arachis stenosperma</i> resistance to <i>Meloidogyne arenaria</i> race 1  <b>Carolina V. Morgante, Ana C. M. Brasileiro, Philip A. Roberts, Larissa A. Guimaraes, Ana C. G. Araujo, Leonardo N. Fonseca, Soraya C. M. Leal-Bertioli, David J. Bertioli and Patricia M. Guimaraes</b></p>	1298–1309	<p>Root-knot nematodes are parasites that infect a number of crops and cause significant economic losses. The use of resistant cultivars is a promising practice to reduce the use of nematicides, which are toxic to environment. Although peanut is susceptible to the nematode <i>Meloidogyne arenaria</i>, resistance is observed in its wild relative, <i>Arachis stenosperma</i>. We investigated the molecular mechanisms of this resistance, and identified 16 <i>A. stenosperma</i> genes potentially involved in plant defence, thus, provided additional resources for peanut breeding.</p>

*Perspective: Water: the most important ‘molecular’ component of water stress tolerance research*

**Vincent Vadez, Jana Kholova,**

**Mainassara Zaman-Allah and Nouhoun Belko** 1310–1322

The current genomic-centered era brings a belief that drought tolerance genes will soon be unraveled, although molecular genetics research on drought often overlooks water. Deciphering the molecular basis of water stress adaptation should focus on traits affecting plant water budget. Here we survey these traits, their interactions among them and with the environment, and provide a framework using crop simulation modeling to guide their use in crop improvement.

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Evaluation of five peanut (*Arachis hypogaea*) genotypes to identify drought responsive mechanisms utilising candidate-gene approach

**Phat M. Dang, Charles Y. Chen**

**and C. Corley Holbrook** 1323–1333

Drought can significantly reduce peanut yield and increase the likelihood of aflatoxin contamination. Selections of drought tolerant peanuts have been difficult because of strong environment  $\times$  and genotype interactions. The goal of this research was to identify potential molecular mechanism(s) utilising peanut genotypes with contrasting drought responses through a candidate-gene approach. The identification of drought regulated genes, determination of their specific gene-expression patterns, and the association with the levels of drought tolerance will provide a basis for drought tolerant plant selection in peanut breeding programs.

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Heat-stress-induced reproductive failures in chickpea (*Cicer arietinum*) are associated with impaired sucrose metabolism in leaves and anthers

**Neeru Kaushal, Rashmi Awasthi, Kriti Gupta,**

**Pooran Gaur, Kadambot H. M. Siddique**

**and Harsh Nayyar** 1334–1349

Heat stress induces reproductive failures in various crops, the underlying biochemical mechanisms are not known. The present work demonstrates that heat stress impairs sucrose metabolism in male reproductive organs of chickpea to impair their functioning. Selecting genotypes having superior sucrose metabolism in male components under heat stress would improve heat tolerance in this crop.

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Variation in carbon isotope discrimination and its relationship with harvest index in the reference collection of chickpea germplasm

**Lakshmanan Krishnamurthy, Junichi Kashiwagi,**

**Satoshi Tobita, Osamu Ito, Hari D. Upadhyaya,**

**Cholenahalli L. L. Gowda, Pooran M. Gaur,**

**Madavalam S. Sheshshayee, Sube Singh,**

**Vincent Vadez and Rajeev K. Varshney** 1350–1361

The variation in carbon isotope discrimination ( $\Delta^{13}\text{C}$ ), an integrator of plant behaviour indicating drought tolerance, was studied using a reference collection of chickpea germplasm. High  $\Delta^{13}\text{C}$  was associated with early maturity, moderate shoot biomass production, high seed yield and high harvest index (HI). There were indications that  $\Delta^{13}\text{C}$ 's association with grain yield was indirectly through final shoot biomass and HI.