## **Functional Plant Biology**

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## Contents

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Theoretical considerations about carbon isotope distribution in glucose of C <sub>3</sub> plants <i>Guillaume Tcherkez, Graham Farquhar, Franz Badeck</i> <i>and Jaleh Ghashghaie</i> 857–877	The authors of this paper examine the origin of the non-statistical intramolecular distribution of $^{13}$ C in glucose of C <sub>3</sub> plants, and take a modelling approach to investigate the relationships between the intramolecular distribution of $^{13}$ C in hexoses and the reactions of primary carbon metabolism. The model is used to estimate photorespiratory and day respiratory fractionations, which both appear to depend only weakly on the rate of ribulose-1,5-bisphosphate oxygenation.
<ul> <li><sup>23</sup>Na NMR microimaging: a tool for non-invasive monitoring of sodium distribution in living plants</li> <li><i>Markus Rokitta, Danielle Medek, James M. Pope and Christa Critchley</i> 879–887</li> </ul>	Knowledge of sodium distribution within salt-tolerant Australian native species could help to understand the physiological adaptations of salt-tolerant plants. <sup>23</sup> Na nuclear magnetic resonance (NMR) microimaging is presented in this paper as a method for quantifying sodium concentration in living plants. <sup>23</sup> Na NMR microimaging may become a unique tool for diagnosing salt tolerance and sensitivity at the macroscopic level.
Quantitative metabolic profiling by 1-dimensional <sup>1</sup> H-NMR analyses: application to plant genetics andfunctional genomicsAnnick Moing, Mickaël Maucourt, Christel Renaud,Monique Gaudillère, Renaud Brouquisse, BénédicteLebouteiller, Aurélie Gousset-Dupont, Jean Vidal,David Granot, Béatrice Denoyes-Rothan,Estelle Lerceteau-Köhler andDominique Rolin889–902	Metabolic profiling with 1-dimensional <sup>1</sup> H-NMR has been validated for quantification of soluble sugars, organic acids, amino acids and some secondary metabolites in fruit, root and leaf samples, and is described in this paper. The method was applied to a genetic study of strawberry fruit quality and functional studies of tomato hexokinase and <i>Arabidopsis</i> phospho <i>enol</i> pyruvate carboxylase transformants, to demonstrate its validity.
Effects of nitrogen supply on xylem cytokinin delivery, transpiration and leaf expansion of pea genotypes differing in xylem-cytokinin concentration <i>Ian C. Dodd, Chuong Ngo, Colin G. N. Turnbull and</i> <i>Christine A. Beveridge</i> 903–911	Branching mutants of <i>Pisum sativum</i> were grown at two levels of nitrogen to study the effects of N supply on xylem-cytokinin delivery, transpiration and leaf expansion. Similar leaf growth responses of all genotypes to N deprivation despite differences in absolute and relative xylem-cytokinin concentrations and deliveries suggests that shoot N status is more important in regulating leaf expansion than xylem-supplied cytokinins, but changes in xylem-supplied cytokinins may modify water use.

*Cover illustration*: Young vegetative plants of the *rms4* pea branching mutant (right) have lower xylem-cytokinin concentrations than wild type (WT, left) peas when sap is collected at transpirational flow rates (lower panel) yet have similar leaflet-cytokinin concentrations (upper panel) (see Dodd *et al.* pp. 905–913 for specific details on the plant phenotypes and conditions). Cover image courtesy of Dr Ian Dodd (University of Lancaster), Dr Christine Beveridge (University of Queensland) and the ARC Centre of Excellence for Integrative Legume Research.

Hydrogen peroxide is a common signal for darkness- and ABA-induced stomatal closure in <i>Pisum sativum</i> <i>Radhika Desikan, Man-Kim Cheung, Andrew Clarke,</i> <i>Sarah Golding, Moshe Sagi, Robert Fluhr,</i> <i>Christopher Rock, John Hancock</i> <i>and Steven Neill</i> 913–920	The requirement for $H_2O_2$ generation and action during stomatal closure induced by darkness and abscisic acid (ABA) was investigated in <i>Pisum sativum</i> . Dark- or ABA-induced stomatal closure was inhibited by the $H_2O_2$ -scavenging enzyme catalase, the antioxidant N-acetyl cysteine or by diphenylene iodonium, an inhibitor of NADPH oxidase. Confocal microscopy confirmed that $H_2O_2$ accumulation in guard cells was increased by darkness or ABA, and PCR identified several NADPH oxidase homologues in pea genomic DNA.
Do polyamines modulate the <i>Lotus glaber</i> NADPH oxidation activity induced by the herbicide methyl viologen? <i>Juan C. Cuevas, Diego H. Sánchez, María Marina and</i> <i>Oscar A. Ruiz</i> 921–928	These authors characterised the roles of zinc, spermine and spermidine as oxidative stress regulatory compounds by exposing <i>Lotus glaber</i> and tobacco plants to methyl viologen. In <i>L. glaber</i> , zinc and the polyamines inhibited NADPH oxidation and in tobacco, methyl viologen treatment induced free polyamines in intercellular fluids, supporting the notion that polyamine metabolism in the apoplast is involved in the physiological response to oxidative stress.
Determination of growth and maintenance coefficients by calorespirometry Sannali Matheson, Derek J. Ellingson, V. Wallace McCarlie, Bruce N. Smith, Richard S. Criddle, Laurence Rodier and Lee D. Hansen 929–939	This work describes a calorespirometric method for determining the coefficients of the correlation of specific respiration and growth rates. Validation of the method revealed agreement with accepted theory that growth coefficients increase with temperature in one species ( <i>Helianthus tuberosus</i> ) but disagreement in two other species ( <i>Convolvulus arvensis</i> and <i>Avena sativa</i> ). The decline in specific respiration and growth rates with age is caused by dilution-by-growth, not down- regulation of respiration rate by reduced demand.
Measurement of trace metal influx in plants: a case study with Co <i>Rob Reid and Juhong Liu</i> 941–947	The analysis of transport systems involved in the uptake of trace metals in plants is complicated by technical difficulties associated with measurement of uptake and by the likely presence of multiple broad specificity transporters. This paper addresses many of these problems, which have previously hampered the functional characterisation of genes that are potentially involved in trace-metal uptake.