

Functional Plant Biology

Contents

Volume 38 Issue 1 2011

Viewpoint: Natural $^{15}\text{N}/^{14}\text{N}$ isotope composition in C_3 leaves: are enzymatic isotope effects informative for predicting the ^{15}N -abundance in key metabolites?

Guillaume Tcherkez

1–12

In this paper, the fundamentals of the natural ^{15}N -abundance in leaf metabolites are given. Using a model that takes into account enzymatic isotope effects, it was shown that $\delta^{15}\text{N}$ in major metabolites (e.g. glutamate and glutamine) depends on key fluxes such as photorespiration and the nitrate reduction input.

Transcription profiling of the isoflavone phenylpropanoid pathway in soybean in response to *Bradyrhizobium japonicum* inoculation

**Lisette Pregelj, Joanne R. McLanders,
Peter M. Gresshoff and Peer M. Schenk**

13–24

Isoflavones are legume-specific secondary metabolites that function as defence compounds, signal molecules and regulators of gene expression during plant–microbe interactions. They are synthesised by a branch of the core phenylpropanoid pathway, using several isoenzymes within each enzymatic step. Gene-specific reverse transcriptase PCR was used to quantify expression of isoflavone synthesis genes in soybean roots and hypocotyls, with and without inoculation with *Bradyrhizobium japonicum*. Results were compared with mutants lacking the functional nodulation regulator GmNARK.

Bioinformatic studies of the wheat glutaredoxin gene family and functional analysis of the *ROXY1* orthologues

**Mark Ziemann, Mrinal Bhawe
and Sabine Zachgo**

25–34

ROXYs are land plant-specific glutaredoxins that were shown to participate in *Arabidopsis* in stress-related and flower developmental processes by modifying TGA transcription factors post-translationally. Isolation of ROXYs from the hexaploid wheat was followed up by complementation and yeast interaction studies suggesting a conserved molecular function in *Arabidopsis* and wheat.

The *hyp-1* gene is not a limiting factor for hypericin biosynthesis in the genus *Hypericum*

**Ján Košuth, Andrija Smelcerovic, Thomas Borsch,
Sebastian Zuehlke, Katja Karppinen,
Michael Spiteller, Anja Hohtola
and Eva Čellárová**

35–43

The expression of the candidate *hyp-1* gene proposed to play a role in hypericin biosynthesis was studied in 15 *Hypericum* species with varying ability to synthesize this naphthodianthrone. Detection of the *hyp-1* gene transcripts in both, hypericin-producing as well as hypericin-lacking species questions the role of the *hyp-1* gene product.

miR398 regulation in rice of the responses to abiotic and biotic stresses depends on *CSD1* and *CSD2* expression

**Yuzhu Lu, Zhen Feng, Liying Bian, Hong Xie
and Jiansheng Liang**

44–53

This is the first report of the function of miR398 in rice, which told how rice miR398 mediated responses to a wide range of abiotic and biotic stresses through regulating its target genes, *Os-CSD1* and *Os-CSD2*. The contrary phenotype between transgenic lines over-expressing *Os-miR398* and miR398-resistant form of *Os-CSD2* was also observed clearly. And thus the molecular response was investigated thoroughly in rice.

Cover illustration: *Hypericum* species are important sources of secondary metabolites with wide range of pharmacological activities including anti-cancer or anti-depressant (see Košuth *et al.* pp. 35–43; Photograph by Ján Košuth). Leaves of some *Hypericum* species lacking (top row) and possessing (bottom row) dark nodules as sites for hypericin accumulation. Arrows indicate distribution of these structures on the leaf lamina. Size bar represents 250 micrometers.

Effects of growth temperature on photosynthetic gas exchange characteristics and hydraulic anatomy in leaves of two cold-climate *Poa* species
**Danielle E. Medek, John R. Evans,
Marcus Schortemeyer and Marilyn C. Ball**

54–62

Interrelationships between hydraulic anatomy and photosynthesis were studied in two grasses, subantarctic *Poa foliosa* and alpine *Poa hothamensis*. The results showed that nitrogen plays a central role in maintaining assimilation rates when constrained either by enzymatic activity at low temperatures or by hydraulic limitations at high temperatures and evaporative demands.

Is fruit anatomy involved in variation in fruit starch concentration between *Actinidia deliciosa* genotypes?
**Simona Nardoza, Ian C. Hallett,
Rosannah McCartney, Annette C. Richardson,
Elspeth A. MacRae, Guglielmo Costa
and Michael J. Clearwater**

63–74

This study examines how variation in fruit anatomy contributes to differences in fruit starch accumulation between high and low dry matter kiwifruit genotypes. We show for the first time that variation in the volumetric ratio of the two principal outer-pericarp cell types contributes to variation in starch content between the genotypes, thus creating a link between anatomical traits and fruit taste.

A white mutant of Malay apple fruit (*Syzygium malaccense*) lacks transcript expression and activity for the last enzyme of anthocyanin synthesis, and the normal expression of a MYB transcription factor
**Panumas Kotepong, Saichol Ketsa
and Wouter G. van Doorn**

75–86

The fruit skin of mature Malay apple is purple. Cyanidin-3-*O*-glucoside accounted for a large proportion of the anthocyanin content. Its accumulation was correlated with increased activity of UDP-glucose : flavonoid 3-*O*-glucosyltransferase (F3GT). No anthocyanins were found in the skin of a white mutant fruit. It contained transcripts of seven anthocyanin biosynthesis genes, except *F3GT*. It also did not show F3GT activity. A MYB transcription factor, highly homologous to *Arabidopsis* MYBs involved in anthocyanin synthesis, was also lacking.