Functional Plant Biology

Contents

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Viewpoint: Natural $^{15}$N/$^{14}$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 $^{15}$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 Bhave 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 Smelerovic, 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 Nie 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 Nardozza, 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.