

Functional Plant Biology

Contents

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Diversity and plasticity of C₄ photosynthesis in
Eleocharis (Cyperaceae)

**Lesley R. Murphy, João Barroca,
Vincent R. Franceschi, Raymond Lee,
Eric H. Roalson, Gerald E. Edwards
and Maurice S. B. Ku**

571–580

This paper describes the diversity and plasticity of C₄ photosynthesis in the genus *Eleocharis*. The authors present anatomical, physiological and biochemical data showing different photosynthetic patterns in three amphibious *Eleocharis* species, and show that two of these express different types of photosynthesis in response to growth under terrestrial and submerged conditions. The work highlights the value of *Eleocharis* as a model system for studying the evolution, regulation and environmental responses of C₄ photosynthesis at physiological and molecular levels.

Diurnal expression of five protein phosphatase type 2C
genes in the common ice plant, *Mesembryanthemum*
crystallinum

**Ko Sato, Hiroaki Ohsato, Shunsuke Izumi,
Saori Miyazaki, Hans J. Bohnert,
Hiromitsu Moriyama and Toshiyuki Fukuhara** 581–588

This work extends our knowledge of diurnal regulation and possible circadian rhythms of genes involved in crassulacean acid metabolism (CAM). The authors characterise the expression of five protein phosphatase type 2C (PP2C) genes in *Mesembryanthemum crystallinum*, a eu-halophytic species with a developmentally programmed switch from C₃ to CAM photosynthesis. The expression patterns of these genes indicate that they play a role in the diurnal regulation of protein phosphorylation during CAM photosynthesis.

Desiccation-tolerance specific gene expression in leaf
tissue of the resurrection plant *Sporobolus stapfianus*

**Tuan Ngoc Le, Cecilia K. Blomstedt, Jianbo Kuang,
Jennifer Tenlen, Donald F. Gaff, John D. Hamill
and Alan D. Neale** 589–600

Le *et al.* use a novel approach to identify genes that may play a role in desiccation tolerance strategies in the resurrection plant *Sporobolus stapfianus*. By comparison of mRNA levels in detached or attached leaf tissue, they identify four genes that are up-regulated specifically in desiccation-tolerant tissue. Putative functions of these genes in desiccation tolerance are then discussed.

Ascorbate and glutathione metabolism during
development and desiccation of orthodox and
recalcitrant seeds of the genus *Acer*

Stanislawa Pukacka and Ewelina Ratajczak 601–613

Pukacka and Rataczak tackle the important issue of the mechanisms underlying desiccation tolerance of orthodox seeds and study the ascorbate–glutathione system during seed development in two *Acer* species of differing desiccation tolerance. Desiccation-tolerant seeds of Norway maple (*Acer platanoides*) have higher concentrations of glutathione and greater redox status of glutathione and ascorbate than recalcitrant seeds of sycamore maple (*A. pseudoplatanoides*), indicating that the ascorbate–glutathione cycle plays an important role in the acquisition of desiccation tolerance and protein maturation.

Cover illustration: Plant natriuretic peptides open stomata and retard ABA induced closure. (See Wang *et al.*, pp. 645–653).

Cell wall disassembly events in boysenberry
(*Rubus* hybrid) fruit development

**Ariel Roberto Vicente, Ann Powell, L. Carl Greve
and John M. Labavitch** 614–623

Fruit softening is associated with dramatic modifications in the cell wall. A feature of boysenberry ripening is that the early period of colour change overlaps with the end of the fruit expansion phase. Vicente *et al.* analyse the changes in cell wall structure and composition, and the activities of cell-wall-degrading enzymes during ripening of the highly perishable boysenberry fruit. They propose that the enzymes involved in pectin matrix disassembly are the best candidates for future manipulation of late fruit softening.

Is erratic bud-break in grapevines grown in warm winter areas related to disturbances in mitochondrial respiratory capacity and oxidative metabolism?

**Francisco J. Pérez, Sebastián Rubio
and J. Ormeño-Núñez** 624–632

Pérez *et al.* study endodormancy and bud-break in grapevines grown in contrasting winter environments. They investigate the relationship between the phenomenon of erratic bud-break and mitochondrial respiratory capacity under oscillating winter temperatures during bud dormancy and propose that warmer winter temperatures and subsequent increases in H₂O₂ levels are associated with erratic breaking of latent buds.

A bioinformatic approach to the identification of a conserved domain in a sugarcane legumain that directs GFP to the lytic vacuole

**Mark A. Jackson, Anne L. Rae, Rosanne E. Casu,
Christopher P. L. Grof, Graham D. Bonnett
and Donald J. Maclean** 633–644

Sugarcane has great potential as a biofactory for the production of valuable products such as industrial proteins. These authors utilised the central vacuole of storage parenchyma cells as a storage site for a heterologous protein. They conclude that the putative N-terminal propeptide (NTPP) of sugarcane legumain contains a motif of five amino acids which directs GFP to the vacuole and they identify by sequence comparison similar motifs in legumain from other species. In addition, they tentatively identify another potential signal at the C-terminus of these proteins, within a putative C-terminal propeptide (CTPP).

Plant natriuretic peptide active site determination and effects on cGMP and cell volume regulation

**Yu Hua Wang, Chris Gehring, David M. Cahill
and Helen R. Irving** 645–653

This paper addresses the interesting and important area of the interactions between classical hormones and small peptide molecules, and in particular, the role of a small plant natriuretic peptide (PNP) in cell volume regulation. The authors use synthetic peptides representing different segments of PNP and an *in vivo* assay to test the ability of these fragments to mimic PNP action. They show that PNP acts through a cGMP-dependent mechanism and that in some circumstances PNP affects ABA induced responses.

Expression of a human tRNA isopentenyltransferase in tobacco reveals a developmental role for tRNA isopentenyladenosine

**Anna Golovko, Folke Sithon, Elisabeth Tillberg
and Björn Nicander** 654–661

Tobacco plants transformed with a human tRNA-modifying enzyme, tRNA isopentenyltransferase, are characterised and the resulting plant phenotype indicates that key regulatory processes are affected. tRNA maturation processes are also affected, as tRNAs containing isopentenyladenosine increase in transgenic plants. This is the first study highlighting the important roles in plant development played by tRNA containing isopentenyladenosine.