

Functional Plant Biology

Contents

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Editorial:

New developments for *Functional Plant Biology*

Rana Munns

Identification and characterisation of barley
(*Hordeum vulgare*) respiratory burst oxidase homologue
family members

**Damien J. Lightfoot, Annette Boettcher, Alan Little,
Neil Shirley and Amanda J. Able** 347–359

The authors describe the identification and preliminary characterisation of six barley respiratory burst oxidase homologues (RBOHs). The expression patterns of two of the RBOH transcripts (HvRBOHF1 and HvRBOHF2) within the early response of the plant to infection by necrotrophic fungal pathogens (*Pyrenophora teres* and *Rhynchosporium secalis*) are described. This study represents the first report of *RBOH* gene activity in response to necrotrophic fungal infection.

Copper pretreatment augments ultraviolet B toxicity in
the cyanobacterium *Anabaena doliolum*: a proteomic
analysis of cell death

**Poonam Bhargava, Arvind Kumar, Yogesh Mishra
and Lal Chand Rai** 360–372

This study provides proteomic characterisation of Cu-pretreatment induced augmentation of ultraviolet B toxicity in *Anabaena doliolum*. Of the three treatments given *Anabaena* (Cu, UV-B and Cu + UV-B), the Cu + UV-B treatment produced the greatest inhibition of physiological attributes than UV-B alone. Significant and reproducible alterations in Mn-SOD, Fe-SOD, PER, RuBisCo, PRK, Flv, PLC, PGK, PC, PC α chain, DnaK and NDPK were observed. However, Cu pretreated *Anabaena* on subjecting to high UV-B depicted a severe down-regulation of DnaK, NDPK and Flv, which appear responsible for augmentation of UV-B toxicity by Cu.

Identification and characterisation of a novel inorganic
carbon acquisition gene, *CIA7*, from an insertional
mutant of *Chlamydomonas reinhardtii*

Ruby A. Ynalvez and James V. Moroney 373–381

This paper describes the insertional mutant, *cia7* from *Chlamydomonas reinhardtii*, which grows poorly in a low CO₂ environment. The gene disrupted by the insert encodes a protein of unknown function, and has high similarity to conserved bacterial proteins. One possible role of CIA7 would be in the delivery or storage of a metal ion.

Expression of sucrose synthase in the developing
endosperm is essential for early seed development
in cotton

**Yong-Ling Ruan, Danny J. Llewellyn, Qing Liu,
Shou-Min Xu, Li-Min Wu, Lu Wang and
Robert T. Furbank** 382–393

Sucrose synthase (Sus) has long been considered to be an enzyme predominately involved in starch and protein biosynthesis at the storage phase of seed development. Here, we provide a set of biochemical, cellular and transgenic evidence that expression of Sus in the cellularising endosperm is critical for early embryo and seed development in cotton.

Cover illustration: Comparative shape of 12-day-old wild-type and transgenic *VvTLPI* somatic embryos of grapevine. (Left) Wild-type embryo showing cotyledon primordia (CP), vascular traces (VT), embryo axis (dashed line) and apical region (star). (Right) Transgenic embryo showing irregular shape and outgrowths on the epidermis indicating secondary embryo initiation (see François *et al.* pp. 394–402).

Overexpression of the *VvLTP1* gene interferes with somatic embryo development in grapevine

**Julie François, Magali Lallemand,
Pierette Fleurat-Lessard, Laurent Laquittaine,
Serge Delrot, Pierre Coutos-Thévenot and
Eric Gomès**

394–402

Grapevine (*Vitis vinifera* L.) embryo has an early developmental pattern, which differs from the one observed in model angiosperms. Promoter-*GUS* studies indicate that *VvLTP1* is a marker of grapevine protoderm establishment, and *p35S*-driven ectopic expression of *VvLTP1* reveals the importance of the correct spatial and temporal expression pattern of *VvLTP1* in grapevine somatic embryo early development.

Development of fruit cuticle in cherry tomato (*Solanum lycopersicum*)

**Eva Domínguez, Gloria López-Casado,
Jesús Cuartero and Antonio Heredia**

403–411

We provide a detailed description of the morphological and cuticle components changes in tomato fruit cuticle throughout fruit development and ripening. The techniques described allowed us to identify some key stages in fruit development and ripening for plant cuticle studies at the molecular level.

Nitrogen metabolism in durum wheat under salinity: accumulation of proline and glycine betaine

**Petronia Carillo, Gabriella Mastrolonardo,
Francesco Nacca, Danila Parisi, Angelo Verlotta
and Amodio Fuggi**

412–426

Protective compounds against salt stress seem to be ubiquitously required in all leaves of durum wheat. At high nitrate, proline accounts for more than 39% to the osmotic adjustment of old leaves. The contribution of glycine betaine is higher in young leaves and independent of nitrogen nutrition.

Comparative mapping of a QTL controlling black point formation in barley

**Timothy J. March, Jason A. Able, Kerrie Willsmore,
Carolyn J. Schultz and Amanda J. Able**

427–437

The dark discolouration of the embryo end of barley grain (known as black point) is a physiological disorder which appears to be controlled genetically. This study describes the use of comparative mapping to identify candidate genes within a QTL on chromosome 2H for the control of barley black point.