

Functional Plant Biology

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Viewpoint: Why are non-photosynthetic tissues generally ^{13}C enriched compared with leaves in C_3 plants? Review and synthesis of current hypotheses

Lucas A. Cernusak, Guillaume Tcherkez, Claudia Keitel, William K. Cornwell, Louis S. Santiago, Alexander Knohl, Margaret M. Barbour, David G. Williams, Peter B. Reich, David S. Ellsworth, Todd E. Dawson, Howard G. Griffiths, Graham D. Farquhar and Ian J. Wright 199–213

Non-photosynthetic, or heterotrophic, tissues in C_3 plants tend to be enriched in ^{13}C compared to the leaves that supply them with photosynthate. We review six hypotheses aimed at explaining this isotopic pattern. Direct tests of these hypotheses will provide insight into the mechanisms causing within-plant variation in carbon isotope composition.

Desiccation protects two Antarctic mosses from ultraviolet-B induced DNA damage

Johanna D. Turnbull, Simon Leslie and Sharon A. Robinson 214–221

This study shows that two cosmopolitan species of Antarctic mosses are remarkably tolerant of UV-B radiation especially whilst in the desiccated state, suggesting they are well equipped to survive under the ozone hole. Unfortunately, the endemic moss *Schistidium antarctici* is not as well protected raising biodiversity concerns for the dominant plant species in the Windmill Islands, East Antarctica.

Distinction and characterisation of submergence tolerant and sensitive rice cultivars, probed by the fluorescence OJIP rise kinetics

Ramani Kumar Sarkar and Debabrata Panda 222–233

The protection of chloroplast structural and functional ability upon exposure to complete submergence is critical to plant productivity and survival. The results indicate that several JIP-test parameters clearly distinguish between submergence tolerant and sensitive rice cultivars, and tolerance to submergence is not necessarily a means of tolerance to low light stress.

Heat tolerance and expression of protein synthesis elongation factors, EF-Tu and EF-1 α , in spring wheat

Urška Bukovnik, Jianming Fu, Miranda Bennett, P. V. Vara Prasad and Zoran Ristic 234–241

Expression (accumulation) of protein elongation factors, EF-Tu and EF-1 α was investigated in heat stressed plants of spring wheat cultivars Kukri and Excalibur. Heat-induced accumulation of both elongation factors was greater in Excalibur, the cultivar that showed better tolerance to heat stress. Results suggest that EF-Tu and EF-1 α may be of importance to wheat response to heat stress.

The predicted subcellular localisation of the sugarcane proteome

Renato Vicentini and Marcelo Menossi 242–250

To contribute to an understanding of the distribution of the proteome in sugarcane, the authors carried out the first in silico genome-wide subcellular localisation analysis for the sugarcane. They showed that many proteins were localised in multiple compartments, and the analysis allowed identification of proteins that could show dual targeting by the use of truncated forms.

Cover illustration: Moss, oxygen and ice shows a turf of *Schistidium antarctici* growing close to Casey Station, Antarctica. The moss is growing on the edge of meltlake, partially submerged by icy water. Bubbles of oxygen accumulate on the moss surface as it photosynthesises. The harsh conditions mean that moss growth is very slow (<1 mm per year) and turfs like these can be over 100 years old. These mosses were blowing bubbles before Amundsen reached the South Pole but recent changes to the environment, such as the ozone hole and higher UV-B radiation, are making life tougher for this species (see Turnbull *et al.* pp. 214–221). Photographed by Sharon Robinson 2008.

Proteomic analysis of ‘hybrid necrosis’ in wheat
(*Triticum aestivum*) leaves

**Xing Lai Pan, Qi Yan Jiang, Qian Ying Pan,
Xue Fei Wen, Yin Hong Shi, Yong Jie Wang,
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Shen Jie Wu, Yong Feng Chai, Chang Sheng Zhang,
Zong Xin Wu and Shi Hua Shen**

251–259

The so-called ‘hybrid necrosis’ genotype *Ne1ne1Ne2ne2* of a common wheat cross PZF1 dramatically shortened the leaf life-span by ~30–40 days by interfering with leaf protein stoichiometry, probably in an epigenetic way. The genotype *Ne1Ne1Ne2Ne2* will be used to investigate molecular triggers and cellular pathways in a future study.

Systemic effects on leaf glutathione metabolism and defence
protein expression caused by esca infection in grapevines

**Christophe Valtaud, Christine H. Foyer,
Pierrette Fleurat-Lessard and Andrée Bourbouloux**

260–279

In *Vitis vinifera*, fungi involved in esca induce systemic effects on glutathione metabolism before the appearance of visible damage in leaves. The expression of GSTs, the variation of the glutathione level and the ratio of GSSG to total glutathione can be used as early stress markers in field-grown vines.

A non-cell-autonomous mechanism for the control
of plant architecture and epidermal differentiation involves
intercellular trafficking of BREVIPEDICELLUS protein

**Yeonggil Rim, Jin-Hee Jung, Hyosub Chu,
Won Kyong Cho, Seon-Won Kim, Jong Chan Hong,
David Jackson, Raju Datla and Jae-Yean Kim**

280–289

Intercellular movement of BREVIPEDICELLUS (BP or KNAT1) the *Arabidopsis* homologue of KNOTTED1 was tissue-specific and took place through a selective pathway. Here, we provide evidence from complementation analyses using cell autonomous or non-cell-autonomous BP fusions that the intercellular trafficking of BP protein is important for plant architecture and epidermal differentiation.