

Functional Plant Biology

Contents

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Histone modifications at the grapevine *VvOMT3* locus, which encodes an enzyme responsible for methoxypyrazine production in the berry

Juri Battilana, Jake D. Dunlevy and Paul K. Boss 655–664

Methoxypyrazines are responsible for some herbaceous characters in wines of some grape varieties characters and this is determined by the differential expression of a methyltransferase gene known as *VvOMT3*. In order to investigate the chromatin arrangement of the *VvOMT3* gene, histone modifications were studied in the locus and these differed spatially between the skin and flesh tissues, temporally during fruit development and also amongst different *VvOMT3* alleles. This study provides evidence of histone tail modification of the *VvOMT3* locus in grapevine, which may play a role in the varietal, spatial and developmental regulation of the expression of this gene.

Combined effects of soil salinity and high temperature on photosynthesis and growth of quinoa plants (*Chenopodium quinoa*)

Verena I. Becker, Johannes W. Goessling, Bernardo Duarte, Isabel Caçador, Fulai Liu, Eva Rosenqvist and Sven-Erik Jacobsen 665–678

The Andean crop species *Chenopodium quinoa* (Willd.) can cope with combined salinity and high temperature stress, albeit these factors have partially contradictory implications on photosynthesis. Morphological and physiological analysis revealed high phenotypic plasticity of the canopy, resulting in improved leaf gas exchange and maintenance of photosynthesis. Quinoa is thereby a suitable candidate for agriculture in regions affected by salinity and high temperature.

Changes in leaf stomatal conductance, petiole hydraulics and vessel morphology in grapevine (*Vitis vinifera* cv. Chasselas) under different light and irrigation regimes

Silvina Dayer, Jorge Perez Peña, Katia Gindro, Laurent Torregrosa, Francine Voinesco, Liliana Martínez, Jorge A. Prieto and Vivian Zufferey 679–693

Hydraulic conductance in plants may be affected by environmental factors, which in turn, regulate gas exchanges and yield. Leaf stomatal conductance and specific hydraulic conductivity in petioles (K_{petiole}) were evaluated in grapevines under different radiation and water regimes. Results indicate that variations in K_{petiole} were modulated in the short-term by the expression of aquaporins and in a longer-term, by modifications in the anatomy of xylem vessels.

Overexpressing *OsMAPK12-1* inhibits plant growth and enhances resistance to bacterial disease in rice
Xiaorong Xiao, Zhijuan Tang, Xiuqiong Li, Yuhui Hong, Boling Li, Wenfang Xiao, Zhiliang Gao, Daozhe Lin, Chunxia Li, Lijuan Luo, Xiaolei Niu, Chaozu He and Yinhua Chen 694–704

Mitogen-activated protein kinases (MAPKs) play crucial roles in plant development and response to environmental stress. In our study, *OsMAPK12-1* – an alternatively spliced form of *BWMK1* – was found to respond to defence-related elicitors and positively modulates rice resistance against bacterial blight and streak disease whereas negatively regulates plant growth. Therefore, *OsMAPK12-1* showed a balance between rice pathogen resistance and vegetative growth which provided a basis for rice molecular breeding.

Cover illustration: A schematic diagram of ^{14}C flux in the *OsGSK5* overexpressor line under high salinity (Thitisaksakul *et al.* pp. 705–719). Arrows indicate the rate of change in ^{14}C uptake over the 2 h chase period. The values in blue boxes are from the null segregant (NS) plants, and the value in pink boxes are from the *OsGSK5* overexpression (OE) plants. Image conceived by Diane M. Beckles and Maysaya Thitisaksakul and created by Kwanjeera Wanichthanarak.

<p>Overexpression of <i>GSK3-like Kinase 5 (OsGSK5)</i> in rice (<i>Oryza sativa</i>) enhances salinity tolerance in part via preferential carbon allocation to root starch</p> <p>Maysaya Thitisaksakul, Maria C. Arias, Shaoyun Dong and Diane M. Beckles</p>	705–719	<p>The development of salt-tolerant rice cultivars is critical for its production in areas of high soil salinity. This study examined salt-adaptive mechanisms conferred by elevated levels of a regulatory protein OsGSK5, which enhanced rice salinity tolerance through the reallocation of carbon to root. This novel mechanism provides a target for rice breeders to develop cultivars that can withstand episodes of salinity.</p>
<p>Vernalisation mediated lncRNA-like gene expression in <i>Beta vulgaris</i></p> <p>Naiguo Liang, Dayou Cheng, Jie Cui, Cuihong Dai, Chengfei Luo, Tianjiao Liu and Junliang Li</p>	720–726	<p>A new complementary flowering model of sugar beet was proposed. Investigations confirmed that <i>AGLX2</i> was the first candidate lncRNA gene in <i>Beta vulgaris</i> and that the <i>BvRAV1-like</i> gene was expressed in response to vernalisation. Our findings opened up new possibility for future studies and further illuminated the molecular mechanism of vernalisation in sugar beet.</p>
<p>Performance of <i>Arabidopsis thaliana</i> under different light qualities: comparison of light-emitting diodes to fluorescent lamp</p> <p>Karin Köhl, Takayuki Tohge and Mark Aurel Schöttler</p>	727–738	<p>The change to LED systems for growing <i>Arabidopsis thaliana</i> raises questions concerning the reproducibility of results obtained under fluorescent light. We compared growth, photosynthesis and metabolite contents in <i>Arabidopsis</i> genotypes grown under two LED systems or fluorescent lamps. In conclusion, the effect caused by the change to LED was small compared to those of plant age and diurnal rhythm.</p>
<p>Molecular characterisation and expression profiling of calcineurin B-like (CBL) genes in Chinese cabbage under abiotic stresses</p> <p>Hee-Jeong Jung, Md. Abdul Kayum, Senthil Kumar Thamilarasan, Ujjal Kumar Nath, Jong-In Park, Mi-Young Chung, Yoonkang Hur and Ill-Sup Nou</p>	739–750	<p>The <i>CBL</i> genes act as calcium sensors present in plants, therefore, identification of candidate <i>CBL</i> gene(s) confer the responses against abiotic stresses. We have identified <i>BrCBL1-1</i>, <i>BrCBL9-1</i> and <i>BrCBL4-2</i> as candidate genes for cold, salt, and drought stresses, respectively. Our results will help the molecular breeders for developing abiotic stress tolerance Chinese cabbage cultivars through conventional or gene engineering.</p>