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Volume 43 Issue 8 2016

Review: Understanding the regulation of iron nutrition: can it contribute to improving iron toxicity tolerance in rice?

Geoffrey Onaga, Khady Nani Dramé and Abdelbagi M. Ismail

709–726

Molecular mechanisms underlying iron nutrition and regulation are not fully exploited for rice improvement against Fe-toxicity. It is vital to understand these mechanisms to unravel effective pathways for improving rice tolerance. A hypothetical genetic model for Fe toxicity tolerance in rice is presented, and key genes and proteins involved are discussed to provide future prospects for improved rice tolerance to Fe toxicity.

Rapid stomatal response to fluctuating light: an under-explored mechanism to improve drought tolerance in rice

Mingnan Qu, Saber Hamdani, Wenzhen Li, Shimei Wang, Jiuyou Tang, Zhuo Chen, Qingfeng Song, Ming Li, Honglong Zhao, Tiangen Chang, Chengcai Chu and Xinguang Zhu

727–738

Stomatal dynamics in response to fluctuating light can affect water use efficiency and carbon assimilation. This work demonstrated a robust correlation between stomatal delays and drought tolerance through large-scale field investigation to 204 rice mini-core population, and highlighted the importance of natural variation of stomatal movements on leaf economics for breeding programs targeting drought resistance in rice.

*Salinity tolerances of three succulent halophytes (*Tecticornia* spp.) differentially distributed along a salinity gradient*

Louis Moir-Barnetson, Erik J. Veneklaas and Timothy D. Colmer

739–750

The distribution of halophytes in saline landscapes is often correlated with varying levels of soil salinity. Three stem-succulent (i.e. reduced and fused leaves) *Tecticornia* species that occupy different habitats at an inland salt marsh of north-western Australia, differed in survival at extreme salinity (2000 mM NaCl) but had comparable physiological responses and growth tolerances of moderate to high salinity (10–1200 mM NaCl). Knowledge of halophyte responses to extreme salinity has implications in the context of understanding adaptation and community structure in saline environments.

Separating species and environmental determinants of leaf functional traits in temperate rainforest plants along a soil-development chronosequence

Matthew H. Turnbull, Kevin L. Griffin, Nikolaos M. Fyllas, Jon Lloyd, Patrick Meir and Owen K. Atkin

751–765

In this research we measured ways in which rainforest trees and shrubs change their leaf function in response to massive changes in soil nutrient availability along a 120 000 year soil chronosequence in New Zealand. Leaf density/thickness and photosynthetic rates were most strongly affected by changes in species along the gradient, while leaf phosphorus and nitrogen content were most strongly influenced by changes in nutrient availability along the gradient. This work indicates that a large proportion of plant physiological response at the community level is based on changes in species, and not a direct response of individual species to environment *per se* – this should be considered when making predictions of responses of plants to short-term environmental change.

Integrated transcriptomics and metabolomics reveal induction of hierarchies of resistance genes in potato against late blight

**Kalenahalli N. Yogendra
and Ajjamada C. Kushalappa**

766–782

Potato production is threatened worldwide by late blight disease. A metabolo-transcriptomics approach revealed hierarchies of resistance genes triggered following pathogen invasion, including receptors, MAP kinases, phytohormones and transcription factor genes that regulated the downstream genes to biosynthesise phenylpropanoids, flavonoids, fatty acids and alkaloid metabolites to reinforce secondary cell walls, deterring pathogen advancement. These genes can be used in breeding following validation.

Identification of novel stress-responsive biomarkers from gene expression datasets in tomato roots

**Almudena Ferrández-Ayela, Ana Belén Sánchez-García,
Cristina Martínez-Andújar, Zoltan Kevei,
Miriam L. Gifford, Andrew J. Thompson,
Francisco Pérez-Alfocea
and José Manuel Pérez-Pérez**

783–796

In nature and in the field, plants and crops are commonly exposed to different stresses. By screening public gene expression data, we identified several conserved stress-responsive genes in tomato roots that could be used as biomarkers to rapidly evaluate the response of salt-tolerant cultivars and wild species for which sufficient genetic information is not yet available.

Effects of plant growth stage and leaf aging on the response of transpiration and photosynthesis to water deficit in sunflower

**Fety Nambinina Andrianasolo, Pierre Casadebaig,
Nicolas Langlade, Philippe Debaeke
and Pierre Maury**

797–805

Water deficit in sunflower is a major concern regarding the context of producing oilseed crops with limited water inputs. We analysed the transpiration and photosynthesis processes under water deficit and found that transpiration was more affected than photosynthesis, but sensitivity depended on leaf age, plant growth stage and genotype. Our results could help to improve phenotyping methods and crop modelling under water deficit.