

# 分子生物学科・環境科学研究センター・ SUPER FORUM 共催セミナーのご案内

12月9日(火) 16:20～17:55 理学部3号館二階11番教室

## Potential application of one Arabidopsis reductase gene

時間: 16:20-17:05 (講演30分、質疑応答15分)  
主講: Prof. Ming-Tsair Chan (台湾 中央研究院)

## Molecular regulation of orchid floral morphogenesis

時間: 17:10-17:55 (講演30分、質疑応答15分)  
主講: Prof. Wen-Chieh Tsai (台湾 国立成功大学)

問い合わせ先:  
高木 優 (環境科学研究センター)



# Potential application of one *Arabidopsis* reductase gene



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### Research Focus

Orchid Biotechnology

Functional analysis of genes by transgenic plant genomic and proteomic approaches that hold potential for improving tolerance to abiotic and biotic stresses

### Abstract

Biotic and abiotic stresses have been shown to affect various aspects of the plant system including the formation of reactive oxygen species (ROS). ROS convert methionine into methionine sulfoxide (MetO) resulting in altered protein conformation and activity. MetO reductases (MSRs) catalyze the reduction of MetO back to methionine and thereby function as antioxidant repair enzymes. We found that MSRB7 was methyl viologen (MV)-inducible and could reduce R-form MetO to Met. Overexpressing transformants exhibited substantial tolerance to MV treatment, whereas MSRB7 knockdown plants were sensitive to MV. Furthermore, comparative proteomic analysis using cyanogen bromide (CNBr) digestion revealed that two MV-induced glutathione-S-transferases that are ROS-removal enzymes were more abundant in MSRB7-overexpressing plants than in the wild type. Co-immunoprecipitation, bimolecular fluorescence complementation, and the yeast two-hybrid assay showed that GSTF2 and GSTF3 interacted and co-precipitated with MSRB7. MSRB7 maintained the stability of GSTF2 and GSTF3 and restored GST activity. Overall, these results indicate that GST is a MSRB substrate and that MSRB7 may be important in plant adaptation to oxidative stress. Meanwhile, I will present the potential application of this gene family in crop protection.

Keywords: *A.thaliana*, methionine sulfoxide reductase B (MSRB), oxidative stress, glutathione transferase, methyl viologen, LC-MS/MS

# Molecular regulation of orchid floral morphogenesis



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### Research Focus

Orchid floral development

Orchid genomics and functional genomics

### Abstract

Containing more than 25,000 species, the Orchidaceae classified in class Liliopsida, order Asparagales is one of the largest angiosperm families. Associated with this enormous size is an extraordinary floral diversity. Orchids are extremely rich in species and speciation rates presumed to be exceptionally high. Orchidaceae represent an unusually coherent group among monocots, possessing several reliable floral morphological synapomorphies, including the presence of a gynostemium, or column, fused by the style and at least part of the androecium, a highly evolved petal called labellum. Because of the fine and delicate development of the gynostemium and labellum, the orchid flower presents obvious zygomorphy. Thus, the Orchidaceae can be used to testify the validity of the 'ABC model' and 'floral bilateral development' in the monocots and to study how MADS-box and Cycloidea genes are involved in defining the different highly specialized structures in orchid flowers.