Abstract Submission Instructions

Abstracts are limited to **one page** with 1 inch margins on all sides. Name of presenting author should be underlined and e-mail of the presenting author should be included. A template is provided below. Title should be in 14 pt arial, authors in 12 pt arial, affiliation and addresses in 10 pt arial. Abstract text in 12 pt arial font.

Proteomics of Arabidopsis Redox Proteins in Response to MeJA

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Protein redox regulation is increasingly recognized as an important switch of protein activity in yeast, bacteria, mammals and plants. In this study, we identified proteins with potential thiol switches involved in jasmonate signaling, which is essential for plant defense. Methyl jasmonate (MeJA) treatment led to enhanced production of hydrogen peroxide in *Arabidopsis* leaves and roots, indicating *in vivo* oxidative stress. With monobromobimane (mBBr) labeling to capture oxidized sulfhydryl groups and 2D gel separation, a total of 35 protein spots that displayed significant redox and/or total protein expression changes were isolated. Using LC-MS/MS, the proteins in the spots were identified. By comparative analysis of mBBr and SyproRuby gel images, we were able to differentiate proteins that were redox responsive from proteins that displayed abundance changes in response to MeJA. Identification of redox proteins and their cysteine residues involved in the redox regulation allows for a deeper understanding of the jasmonate signaling networks.

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