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Systematic identification of AtSUMO 1 substrates in *Arabidopsis*

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Objectives

To understand the biological roles of small ubiquitin-related modifier (SUMO), and SUMO substrates in plant, we performed a mass spectrometry-based proteomics.

Materials and Methods

1. Material

   Plant-*Arabidopsis thaliana* plants over-expressing His_6-$FLAG_3$ fused AtSUMO1 (HFAtSUMO1)

2. Methods

   Transgenic plants over-expressing HFAtSUMO1were treated with H_2O_2, ethanol, and heat shock. And then, SUMO substrates were identified by a mass spectrometry-based proteomics.

Results and Discussion

Post-translational modification by SUMO plays important regulatory roles in many cellular processes, such as sub-cellular localization, enzymatic activity, stability, and protein-protein interaction. Although many proteins modified by SUMO have been identified and characterized in yeast, mammals, and *Drosophila* recently, but yet SUMO substrates have been unknown in plant. In order to identify SUMO substrates in *Arabidopsis* using a proteomics approach and understand biological functions of SUMO, we constructed His_6-$FLAG_3$ fused AtSUMO1 (HFAtSUMO1) under the control of the CaMV35S promoter and transformed *Arabidopsis* plants. The seedlings of transgenic plants over-expressing HFAtSUMO1 showed growth inhibition phenotype on the abscisic acid (ABA) media. This result is consistent with earlier observation that over-expression of AtSUMO1 increased sumoylation levels attenuate abscisic acid (ABA)-mediated growth inhibition (Lois *et al*, 2003). When treated with H_2O_2, ethanol, and heat shock stress, large increased sumoylation pattern was detected in the transgenic plants overexpressing HFAtSUMO1. In the meeting, we will represent putative SUMO substrates identified by a mass spectrometry-based proteomics.

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