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A Proteomic Analysis of Proteins in Cold-Stressed Rice Leaf and Root Tissues

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Objectives

When exposed to low temperatures, plants respond with changes in their pattern of gene expression and protein products. This ability to adapt has an impact on the distribution and survival of the plant, and on crop yields. Identification of proteins expressed in plants in response to low temperature will provide important clues for molecular breeding of cold tolerant crop plants. We have studied low temperature damage response of rice plants by proteomic approach.

Materials and Methods

- Materials : Rice (*Oryza sativa* L. cv. Dongjinbyeo) was used in this experiment. The plants were grown for 1~3 weeks in a growth chamber at 30℃ under 16 h light/8h dark.

- Methods : For cold treatment, rice plants were subjected to cold treatment for 0 h to 120 h. Total soluble proteins were extracted from leaf and root tissues. The soluble proteins were fractionated with 15% PEG. Protein profiles after cold treatment were analyzed by two-dimensional gel electrophoresis (2-DE). Protein spots were visualized by staining with silver nitrate. Differential expressed spots were identified by peptide mass fingerprinting using matrix assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF-MS) and peptide sequencing to obtain fragment ion-tag data using nanoelectrospray MS/MS.

Results and Discussion

After cold treatment, 109 of the 221 spots were identified. The identified proteins were classified into carbohydrate metabolism, cellular metabolism, detoxification enzyme, heat shock protein, nucleotide metabolism, plant defence, protein kinase, protein synthesis and transcription factors. Four of therm, isoflavon reducase homolog, enolase, Hsp 70 and calreticulin obtained partial sequence information by nanoelectrospray MS/MS. In animal cells, enolase has been known to function as a transcription factor and calretuculin is a major Ca^{2+} binding/buffering protein of the endoplasmic reticulum (ER) lumen and as such, is involved in several of the processes that comprise cellular Ca^{2+} homeostasis, including Ca^{2+} storage in the ER. These results suggest a possibility that the above proteins have protective function from cold stress or regulatory function in controlling gene expression under cold stress.

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