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Proteomic Analysis of Proteins in Cold-Stressed Rice Leaf Tissues

Dong-Gi Lee*, Noo-Ri Oh, Kyu Young Kang, Jeung Joo Lee[1], Byung-Hyun Lee

Division of Applied Life Science, [1]Department of Agricultural Biology, Gyeongsang National University, Jinju 660-701, Korea

Objectives

Low temperature is one of the most important environmental factors governing the distribution and productivity of cultivated crop plants. Although many studies have described extensively physiological and biochemical changes associated with cold stress, the molecular mechanisms involved in cold tolerance have still not been well elucidated. A potential way to better understand low temperature adaptation is to identify the proteins differentially expressed in cold conditions. The objective of this study was to identify differentially expressed proteins related to cold stress in rice plants.

Materials and Methods

Rice (*Oryza sativa* L. cv. Dongjinbyeo) were used in this experiment. The seedlings were grown hydroponically in a growth chamber on a 26°C. Rice plants were subjected to cold treatment for 0 to 120 h at 10 or 15°C, respectively. Total soluble proteins extracted from rice leaves were fractionated with 15% PEG, and the proteins in supernatants and precipitants were further separated by 2-dimensional polyacrylamide gel electrophoresis. The proteins spots up- or down-regulated were analyzed by MALDI-TOF mass spectrometry.

Results and Discussion

We investigated the proteins in rice leaves after exposure to low temperatures. Interesting protein spots derived from cold stress were identified by MALDI-TOF mass spectrometry. Among differentially expressed protein spots, several proteins involved in stress and defense mechanism were identified. One of them, enolase (2-phopho-D-glycerate hydrolase, EC 4.2.1.11), an essential glycolytic enzyme that catalyzes the interconversion of 2-phosphoglycerate to phosphoenolpyruvate, was increased dramatically in rice leaves subjected to cold treatment. In animal cells, enolase has been known to function as a transcription factor that represses the expression of *c-myc*. Recently, it has also been reported that mutation in the enolase gene of *Arabidopsis* impairs cold-responsive gene transcription. These results suggest a possibility that the rice enolase also has a regulatory function in controlling gene expression under cold stress. Further study with proteomic analysis of this protein will be helpful to understand the function of rice enolase under cold stress.

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*Corresponding author. Tel 055-751-5418 E-mail hyun@nongae.gsnu.ac.kr