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Proteomic analysis of cold-responsive proteins in rice leaves

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Cold stress is one of the major abiotic stresses in agriculture worldwide. To examine the response of rice to cold stress, changes in protein expression were analyzed using a proteomic approach. To investigate dose- and time-dependant response, three-weeks-old rice seedlings were subjected to a cold stress of 4°C or 10°C for 12 to 72 h. Total proteins of leaf tissues were extracted and separated by two-dimensional gel electrophoresis (2-DE). More than 1000 proteins spots were reproducibly detected on 2-DE gels including 43 that were up-regulated and 4 were down-regulated under 4°C treatment, 47 that were up-regulated and 7 were down-regulated under 10°C treatment, respectively. All of differentially expressed protein spots were subjected to matrix-assisted laser desorption/ionization-time of flight-mass spectrometry (MALDI-TOF) followed by database searching which allowed the identification of 34 protein spots under 4°C treatment, 27 protein spots under 10°C treatment, respectively. These proteins are involved in redox regulation, reactive oxygen species scavenging, signal transduction, and nitrogen and amino acid metabolism-related proteins. Proteins involved in transcription factor or in plant defense mechanism were also identified and will be discussed.