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Cold-induced Proteins in the Fibrous Roots of Sweetpotato by Proteomic Analysis

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Objectives

Sweetpotato (*Ipomoea batatas* Lam.) is an attractive crop to provide staple food and important industrial materials for human being in the 21st century. The understanding of its adaptability to low temp will be contribute to develop transgenic sweetpotato with enhanced tolerance to low temperature by molecular breeding. In this study, we aim to isolate and characterize cold-responsive genes in fibrous roots of sweetpotato using a proteomic approach.

Materials and Methods

Sweetpotato (cv. White Star) was grown on growth chamber under 28°C in a 14 h-light/10 h dark cycle. Six week-old plants were treated with cold at 4°C for 12 h. Proteins from fibrous roots were prepared for 2D-gel electrophoresis, stained with silver nitrate and analyzed by Progenesis Workstation software. Identification and peptide sequencing were obtained by MALDI-TOF-MS and ESI-Q-TOP.

Results and Discussion

2D-gel analysis of fibrous root proteins reveals about 1,100 protein spots. Protein spot changes were scored only when they were at least three times reproducibly observed in five independent experiments. In this criterion, 17 proteins were induced and no protein repressed by more than a factor of 1.5. Among them 6 proteins including BTF3 and centrin were identified. Using the CODEHOP PCR primer prediction program, partial cDNAs of BTF3, centrin and dimethylmenaquinone methyltransferase were cloned. Further detail experiments for cloned genes will provide understanding of their functions regarding cold defense mechanism in sweetpotato.

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