The Expression Patterns of Thai Moderately Salt Tolerant Rice and High Salt Tolerant Rice in Response to Salt Stress

Kongngern, K. *
Salt-Tolerant Rice Research Group, Department of Biology, Khon Kaen University, Khon Kaen, Thailand

Homwonk, C.
Salt-Tolerant Rice Research Group, Department of Biology, Khon Kaen University, Khon Kaen, Thailand

Theerakulpisut, P
Salt-Tolerant Rice Research Group, Department of Biology, Khon Kaen University, Khon Kaen, Thailand

Roytrakul, R
Genome Institute, National Center for Genetic Engineering and Biotechnology, National Science and Technology Development Agency, Klong Luang, Pathumthani, Thailand

Abstract

Rice is an important crop worldwide. It is the most widely consumed staple food for a large part of the world's human population especially in Asia. However, the big problem on agricultural lands was soil salinity. In this research, we compared the proteomic profile of two rice leaf sheaths under salt stress, Thai moderately salt tolerant rice (Leaung Anan) and high salt tolerant rice (Pokkali). Seeds were grown in hydroponic culture for 21 days before NaCl was introduced initially at the level of 12 dS m-1 for 10 days. Then the leaf sheath proteomes were analyzed by 1D-SDS-PAGE and NanoLC-MS/MS. In this study 873 proteins were detected. Among these proteins, 219 proteins were known proteins and the other proteins were unnamed and unknown proteins. By using Mev software, we found that only 31 proteins in treated plants of both rice cultivars significantly expressed, 21 proteins were up-regulated and 10 proteins were down-regulated. Interestingly, the intensity of the 3 proteins in the Leaung Anan more expressed than in the Pokkali. The results indicate that the up-regulated proteins were more expressed in less tolerant rice may play an important role in helping rice to survive under salt stress.

Keywords

Mass spectrometry, proteomics, rice leaf sheaths, salt stress.