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

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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 aim to compare the expression patterns 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. By using 1D-SDS-PAGE, NanoLC-MS/MS, and MEV software. We found that among the 219 proteins, 18 proteins showed significantly differing expression patterns in both rice cultivars, while other proteins did not meet the statistical criteria analyzed by MEV software. The 18 proteins showed significantly differing expression patterns in both rice cultivars. Interestingly, some proteins, such as Os05g0364500, which functions as a Chaperone protein, were upregulated in PX but down-regulated in LA. In contrast, some proteins, such as pr1-like protein, which functions as protein kinase activity, and Os03g0418800, which functions as nuclear transport factor2 domain-containing protein, were up-regulated in LA but down-regulated in PX. The results indicate that the up-regulated proteins were more expressed in tolerant rice, which may play an important role in helping rice to survive under salt stress.

Keywords : mass spectrometry, proteomics, rice leaf sheaths, salt stress

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