



Soybean Proteomics: Application to Elucidation of Flooding-Tolerant Mechanisms

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Abstract:

Climate changes influence the magnitude and frequency of hydrological fluctuations, which create an unfavorable environment for the growth and development of crops. Because the accurate analysis of a large number of proteins promotes the knowledge of biological systems, gel-free/label-free proteomics has been performed on agricultural materials. Soybean, which is rich in protein and oil as well as phytochemicals, is cultivated in several climatic zones. However, its growth is markedly decreased by flooding stress. Proteomic techniques were used for understanding the flood-response and -tolerant mechanisms in soybean. Under flooding, soybean seedlings showed differential regulation of proteins involved in hormonal signal transduction, transcriptional control, glucose degradation/ sucrose accumulation, alcohol fermentation, gamma-aminobutyric acid shunt, reactive-oxygen species scavenging suppression, mitochondrial impairment, ubiquitin/ proteasome-mediated proteolysis, and cell-wall loosening. Although many flood-response mechanisms have been reported, flood-tolerant mechanisms have not been fully clarified for soybean because of limitations in germplasm with flooding tolerance. Subcellular localizations and post-translational modifications play important roles in stress tolerance to flooding stress. Based on the results from proteomic analyses, the roles of key proteins in crops related to stress tolerance were carefully confirmed with molecular biological techniques. These approaches contribute to not only understanding stress-tolerant mechanisms in crops, but also producing crops with environmental-stress tolerance.

Biography

Setsuko Komatsu is a Professor at Fukui University of Technology, Japan from 2018. Before this position, she was Chief of Field Omics Research Unit at National Institute of Crop Science and Professor at University of Tsukuba, Japan. Since 1990, she started working on plant proteomics using protein sequencer and mass spectrometry. Her main research interests are within the field of crop proteomics, phytohormone, biochemistry, and molecular biology with a special focus on signal transduction in cell.