

Comparative proteomic analysis revealing the tolerance mechanism associated with waterlogging stress in sesame

Hyun-Jin Jung¹, Jang-Hwan Yu¹, Swapan Kumar Roy¹, Ju-Young Choi¹, Soo-Jeong Kwon¹, Hyen-Chung Chun², Seong-Woo Cho³, Yoon-Sup So¹, Yong-Gu Cho¹, Sun-Hee Woo^{1*}

¹Dept. of Crop Science, Chungbuk National University, Cheongju 28644, Korea

²Crop Production Technology Research Div., National Institute of Crop Science, RDA, Miryang 50424, Korea

³Dept. of Crop Science and Biotechnology, Chonbuk National University, Jeonju 54896, Korea

[Introduction]

Sesame is typically considered drought-tolerant but susceptible to waterlogging, a property that can be ascribed to its suspected origin in Africa or India and its subsequent dispersal to tropical or semitropical regions. Low yield may be attributed to several reasons, but waterlogging is a primary factor that has a severe effect in countries such as China and Korea due to changing climate. In the case of Korea, the demand for cultivation area of the crops in the paddy field is increasing. At the same time, rainfall is concentrated in the summer season, which is the primary growth period of the plant, and the precipitation amount of the specific period is increased according to the abnormal weather, and the frequency of the waterlogging is rising. Protein is an essential molecule that participates in enzymes that act as catalysts for various chemical reactions in cells, hormones with regulatory functions, in vivo reactions and energy metabolism. These proteins are very diverse in different kinds of plants and also in various organs in plants, and the expression pattern varies depending on the growth stage of the plant and the environment in which the plant is located.

[Materials and Methods]

To observe the changes in the morpho-physiological changes of sesame leaf, the pot experiment was conducted in the greenhouse with controlled environment. During the ten-leaf stage and the flowering stage, the sesame plants were exposed to waterlogging stress for two and three days. At every stage, the morphological and physiological parameters were measured. For proteomics study, the proteins were extracted from the leaf samples and separated by 2-D PAGE. The proteins were identified by LTQ-FI ICR mass spectrometry and the bioinformatics of the identified proteins were performed by using various bioinformatics tools.

[Results and Discussions]

Waterlogging is a common adverse environmental condition that limits plant growth and one of the major abiotic stresses affect in sesame (*Sesamum indicum* L.) yields resulting in increases of relative ion leakage, lipid peroxidation and in vivo H₂O₂ content. The purpose of this study was to explore the protein expression patterns of sesame leaves under waterlogging stress. The plant height, stem length, chlorophyll content exhibited gradually decrease while chlorophyll and H₂O₂ content increased significantly in response to waterlogging stress. More than 300 protein spots were detected on 2-DE from 10-leaf growth stage and 20 protein spots were differentially altered, and their abundance was significantly responsive to waterlogging treatment, with more than a 1.5-fold change in intensity. In case of flowering stage, more than 400 protein spots were identified and a total of 31 protein spots that exhibited more than a 1.5-fold changes in intensity. Of 31 proteins 16 proteins were found to be up-regulated and 15 proteins were down-regulated under waterlogging stress. These findings shed light on the complex mechanisms underlying waterlogging tolerance in sesame.

[Acknowledgements]

This work was supported by a grant from the Agenda project (No. PJ01228605) of the Rural Development Administration, Republic of Korea.

*Corresponding author: E-mail, shwoo@chungbuk.ac.kr