

Comparative proteome analysis of azuki bean leaves at early vegetative and reproductive stage under waterlogging stress

Hae-Ryong Jeong¹, Swapan Kumar Roy¹, Soo-Jeong Kwon¹, Sang-Heon Choi¹, Hyen-Chung Chun², Seong-Woo Cho³, 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]

Waterlogging of soil is a major limiting factor for crop growth in humid regions. Prolonged rainy period or heavy rainfall in the field with poor soil drainage significantly reduces the seed yield of grain legumes. The growth and seed yield of Azuki bean are adversely affected by waterlogging of the soil. Azuki bean is sensitive to various abiotic stresses, particularly waterlogging stress during early vegetative, and early reproductive stages. Several morpho-physiological studies have been conducted in Azuki bean but the proteomic study under waterlogging stress is still limited in this plant.

[Materials and Methods]

The seeds of Azuki bean were collected from the Rural Development Administration, Korea. Soil properties and growth characteristics of Azuki bean were measured during the second and fifth leaf stage. To confirm the expression pattern of the protein, the Azuki bean leaves (from two- and five leaf stage) were collected and sampled to extract the protein. 2-DE electrophoresis was performed to confirm the protein separation and LTQ-FI ICR MS was applied to identify the proteins. The functional categorization and clustering analysis were performed using the updated bioinformatics tools.

[Results and Discussions]

To explore the morpho-physiological and unravel the molecular tolerance mechanism of two- and five leaf stage of Azuki bean to waterlogging stress. The plant height, stem length, chlorophyll contents were decreased when the plants were exposed to waterlogging stress. In the 2-leaf stage, more than 400 protein spots were detected on 2-D gels, and quantitative image analysis revealed a total of 43 protein spots that exhibited more than a 1.5-fold changes in intensity whereas 23 differentially expressed proteins were successfully analyzed using LTQ-FI ICR MS analysis. Among these proteins, a total of 14 proteins showed increased expression, and 9 proteins showed decreased expression in the treated samples compared to their levels in untreated seedlings. However, in the 5-leaf stage proteome, 29 protein spots were found to be expressed differentially upon waterlogging stress, with more than 1.5-fold differences in abundances between the control and waterlogging-treated samples. A total of 16 proteins were increased significantly while 13 proteins were decreased abundances. The abundance of the most identified protein species from the leaves that function in stress response and metabolism was significantly enhanced, while protein species involved in transcription and regulation were severely reduced.

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