

Proteomic analysis of soybean leaf under waterlogging stress at early vegetative stage

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[Introduction]

Waterlogging (WL), a major environmental stress, is a severe constraint on crop growth and productivity in many regions and situations. Waterlogging can reduce the photosynthesis rate, induce oxidative stress, accelerate leaf senescence, inhibit plant growth and finally lead to crop yield loss. Though traditional breeding programs and biotechnological methods have been used to improve plant tolerance to waterlogging, few practical results have been obtained so far. Soybean is sensitive to various abiotic stresses, particularly waterlogging stress during the germination, early vegetative, and early reproductive stages. Proteomic analysis has been widely used to understand the function of differentially regulated proteins under abiotic stress, which is crucial for investigating the mechanisms of plant in response to stress. Several proteomic studies have examined the changes in the root system of soybean under waterlogging stress, revealing multiple pathways involved in stress perception and signal transduction.

[Materials and Methods]

The seeds of Soybean var. Uram were collected from the Rural Development Administration, Korea. Soil properties and growth characteristics of soybean cultivated in rice field were measured during the third and fifth leaf stage. In order to confirm the expression pattern of the protein, the soybean leaves (from three- 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]

The present study was conducted to investigate the morpho-physiological and proteome responses of three- and five leaf stage of soybean to WL stress. The domestic cultivar, Uram was used to test the waterlogging stress. In the experiment of 3-leaf stage soybean, stem length, chlorophyll contents were decreased when the plants were exposed to WL stress. The 5-leaf stage experiment was similar to the 3-leaf experiment. In the waterlogging for 4 days, the stem length and chlorophyll contents showed significant change among other treatments. Characteristic related to leaf showed treatments was smaller than control regardless to soils. The results observed from experiment 1, 2 and 3 were considered to be influenced by the waterlogging stress more in the 5-leaf stage soybean, and as the waterlogging treatment progressed, the waterlogging stress influenced the growth difference between control and treatment. A total of 30 protein spots were analyzed using LTQ-FI ICR MS. As a result, 9 proteins were up-regulated in the treatment group and 4 proteins were down-regulated. Analysis of LTQ-FI ICR MS showed that 50% of the proteins involved in RNA processing, translation, biological process. Malate dehydrogenase protein and Glyceraldehyde-3-phosphate dehydrogenase protein increased the level of protein expression in 3 and 5-leaf stage under waterlogging stress. These proteins are known to function as antistress agents. The expression of oxygen-evolving enhancer protein 1 related to photosynthesis was increased in treatment than control. Superoxide dismutase protein related to response to oxidative stress showed high expression level in 5-leaf stage treatment. These results suggest that waterlogging directly impairs photosynthesis and photorespiration.

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