

## Comparative Proteome Analysis of Sorghum (*Sorghum bicolor* L.) Seedlings in Response to Waterlogging Stress

Hae-Ryong Jeong<sup>1</sup>, Min-Heon Yun<sup>1</sup>, Jang-Hwan Yoo<sup>1</sup>, Hyun-Jin Jung<sup>1</sup>, Hyung-Jun Park<sup>1</sup>, Swapan Kumar Roy<sup>1</sup>, Soo-Jeong Kwon<sup>1</sup>, Hyen Chung Chun<sup>2</sup>, Ki Yuol Jung<sup>2</sup>, Seong-Woo Cho<sup>3</sup> and Sun-Hee Woo<sup>1\*</sup>

<sup>1</sup>Dept. of Crop Science, Chungbuk National University, Cheong–ju 28644, Korea

<sup>2</sup>National Institute of Crop Science, RDA, Miryang 50424, Korea

<sup>3</sup>Dept. of Crop Science and Biotechnology, Chonbuk National University, Jeon–ju 54896, Korea

### [Introduction]

Waterlogging is the major obstacle for sustainable agriculture. In addition, plants subjected to waterlogging suffer from substantial yield losses. Soil waterlogging always leads to oxygen deprivation that restricts aerobic respiration and is accompanied by a decrease in soil pH. Proteomics, defined as the systematic analysis of the proteins expressed by the genome, is not only a powerful molecular tool for describing complete proteomes at the organelle, cell, organ, or tissue level, but also for comparing proteomes under different physiological conditions, such as exposure to waterlogging or other stressful environmental factors.

### [Material and Method]

This experiment was carried out from June to November, 2016 in the greenhouses of farms attached to the Chungbuk National University. On June 13, the seeds of the domestic Sorghum cultivar, Nam-pung chal (Milyang No. 4) were sown directly into a Wagner pot filled with 2.5 kg of soil mixed with 2: 1 ratio of soils of the farm. The samples were collected from the leaves of Sorghum after 10 days of treatment and morpho-physiological analysis was performed using the samples. For proteome analysis, the leaves were collected, immediately frozen in liquid nitrogen and stored at  $-80^{\circ}\text{C}$  until protein extraction. Then protein was extracted from the collected leaves and performed 2-D PAGE.

### [Result and Discussion]

This study was performed to explore the molecular changes in the vegetative stage (3-leaf stage and 5-leaf) of sorghum under waterlogging stress. A total of 375 protein spots were identified using the Progenesis sameSpot software program. Of 375 protein spots, a total of 74 differentially expressed protein spots were analyzed using LTQ-FT-ICR MS. Among them, a total of 20 proteins were up-regulated while 5 proteins were down-regulated. Mass spectrometry (MS) results showed that about 50% of the proteins involved in carbohydrate metabolic process, metabolic process, and cellular metabolic compound salvage. The level of protein expression of malate dehydrogenase and glyceraldehyde-3-phosphate dehydrogenase protein related to carbohydrate metabolic process increased in both 3 and 5-leaf stage under waterlogging stress. These proteins are known to function as antistress agents against waterlogging stress. It is considered that the expression levels of the proteins are increased in response to waterlogging stress. The expression of oxygen-evolving enhancer protein 1 protein related to photosynthesis was slightly increased in the treated group than in the control group. However, the expression level was increased in the 5-leaf stage compared to the 3-leaf stage. Probable phospholipid hydroperoxide glutathione peroxidase protein and superoxide dismutase protein related to response to oxidative stress showed the highest expression level in 5-leaf stage treatment. This suggests that the production of reactive oxygen species by the waterlogging stress was the most abundant in the 5-leaf treatment group, and the expression of the antioxidant defense protein was increased.

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\*Corresponding author: Tel. 043–261–2515, E–mail, shwoo@chungbuk.ac.kr