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Transcriptomic Profiling of Sorghum Leaves Responsive to Waterlogging Stress at the Vegetative Stage

Ku-Hyun Kwon¹, Sang-Heon Choi¹, Dong-Gyu Lee¹, Swapan Kumar Roy¹, Soo-Jeong Kwon¹, Hyen-Chung Chun², Joo-Ho Kim³, Sung-Woo Cho⁴, Sun-Hee Woo^{1*}

¹Department of Crop Science, Chungbuk National University, Cheong-ju 28644, Korea

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

³Nonghyup Chemical, Okcheon 29008, Korea

⁴Department of Agronomy and Medicinal Plant Resources, Gyeongnam National University of Science and Technology, Jinju 52725, Korea

[Introduction]

Waterlogging stress is increased in the summer when the cultivation of paddy fields and the growing period of main crops are concentrated, and the frequency of the drought due to the waterlogging stress is increasing. However, the literature on waterlogging stress is very limited compared to the study of other environmental stresses. This study was carried out to investigate the mRNA expression patterns of Sorghum, which is one of the most crucial field crops in Korea.

[Materials and Methods]

The seeds of Sodamchal(*Sorghum bicolor* L.) were collected from RDA and conducted the experiment at greenhouse in the Chungbuk National University. In the early stage of growth, the soil was saturated with water (up to 3 cm) from the feed port at the bottom of the pot for 10 days. After that, total RNA was extracted from the leaves of the Sorghum leaves and RNA-seq was performed for mRNA analysis using extract total RNA.

[Results and Discussion]

The present study was aimed to profile transcriptome changes caused by waterlogging stress. The growth characteristics (plant height, stem length, SPAD value) were decreased notably under waterlogging stress. A total of 971 up-regulated transcripts showed differential expression under waterlogging stress while 1,201 down-regulated counts was obtained from 3-leaf stage. However, in the 5-leaf stage, a total of 1,691 transcripts counts were up-regulated whereas 1,863 were down-regulated. Gene-set analysis based on various functional annotation DB for transcripts in the comparison of 3-leaf and 5-leaf showed that the most of the genes were involved in metabolism, stress defense, photosynthesis, ion binding and membrane at each period. In addition, we selected the top 5 genes that differ in the level of the volume that is more than twice as high as the fold change. LOC8074608, 8084497, 110429605, 8078601, 8059588 genes were selected in the comparative analysis of 3-leaf stage, and LOC8062994, 8084497, 110431784, 8078601, 110429605 genes were selected in the analysis of 5th leaf stage.

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*Corresponding author: Tel. +82-043-261-2515, E-mail. shwoo@chungbuk.ac.kr