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Transcriptome Analysis of Korean Wild Soybean (*Glycine soja)* Under Flooding Stress

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[Introduction]

The collection, research, and conservation of native wild species are essential researches for food security and increase in species diversity of crops. Soybean was domesticated and has been cultivated for a long time. Soybean breeding based on mendelian genetics has accelerated a decrease in genetic diversity. Soybean is exposed to flood stress due to intensive summer rains in Korea. *Glycine soja* is known as the origin of soybean cultivars and is widely found in East Asia such as Korea, Japan, and China. *G. soja* has a high genetic variation and is known to be very resistant to various biotic and abiotic stresses compared to cultivated soybeans. In this study, a high-throughput transcriptome analysis was conducted by applying water stress to *G. soja* through flooding treatment.

[Materials and Methods]

G. soja was germinated in a greenhouse environment and transplanted into pots with the same bed soil and moisture content. Flood treatment was performed for 7 days during V3 (third trifoliolate) period, and the control group did not receive any treatment. The top part of *G. soja* was sampled in 3 replicates, respectively, for the control group and the comparison group. Total RNA was extracted from all samples and used for RNA-seq. DEGs, GO, and KEGG analyses were performed. Additionally, the expression of candidate DEGs were validated by qRT-PCR.

[Results and Discussion]

A total average of 58,180,604 mapped reads including control were obtained from the shoots of *G. soja*, of which 61,010,639 (78-81%) were obtained in the flooding treatment. By performing DEGs analysis from the mapped reads, 524 up-regulated DEGs and 292 down-regulated DEGs were selected by cut-off based on log2FC > |2| and FDR < 0.05. GO and KEGG analyses were performed on the selected DEGs for functional annotation. Genes that can explain various mechanisms related to water stress were identified from the results of GO and KEGG analyses. The structural change mechanisms for cell wall expansion, alcoholic fermentation under anaerobic conditions, and aerenchyma development were high. In addition, qRT-PCR was performed by selecting the top 10 up-and down-regulated genes, respectively, from among the DEGs expressed by more than log2FC > |4|. Genes highly involved in flooding stress were identified. Through the above results, this study will contribute to improving the basic understanding of water stress resistance in Korean wild soybean and can be applied to cultivated soybeans.

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