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## Investigation of Drought Resistance Characteristics of Wild-type Soybean *Glycine soja* through Comparative Analysis of Transcriptome and Proteome

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### [Introduction]

Soybean (*Glycine max*) has been improved through a very long breeding history. Because cultivated soybean has very narrow genetic variation, the search for new genetic resources for abiotic stress resistance is limited. Wild species with high genetic variation can be useful tools for exploring new resistance traits. The *Glycine soja*, the wild ancestor of the *Glycine max*, has a high genetic variation and shows strong resistance to various stresses. Recently, due to climate change, the damage caused by water stress in summer has been increasing, and in particular, drought can cause fatal damage to soybean seedlings and the flowering period. This study compared the transcriptome and proteome data of *Glycine soja* under drought treatment.

### [Materials and Methods]

*Glycine soja* was drought-treated at the V3 (Third trifoliolate) stage in a greenhouse environment with a 14/10-hour photoperiod and a temperature of 25°C. At 5 and 10 days after treatment (DAT), RNA and protein were extracted from above-ground parts and performed to RNA-seq and LC-MS/MS, respectively. RNA-seq data were used to analyze differentially expressed genes (DEGs) and alternative splicing (AS), and LC-MS/MS data were used to search for differentially expressed proteins (DEPs). Samples that were used for transcriptome and proteomic analysis were processed and collected independently.

### [Results and Discussion]

A total of 4,024/4,095 (DAT+5/10) DEGs from mapped reads were selected. When comparing the transcripts between samples by treatment time, the expression of 73 genes changed as the treatment time increased. In the case of AS events, an average of 2,098 (DAT+5) and 2,616 (DAT+10) were confirmed by treatment time, and 567 AS events showed a difference as the treatment time increased. As for the occurrence of AS events, skipped exon (SE) occurred the most in all comparison conditions, and differences in expression were identified in an average of 123 genes. A total of 578 DEPs were detected in the protein after 10 days of drought treatment, and 142 of them were confirmed in DEGs as well. However, most DEGs and DEPs showed different expression patterns. Gene ontology analysis of co-profiled genes and proteins suggested that genes and proteins involved in stomatal regulation, antioxidant response, and ion binding response were modulated. A multi-omics approach will provide even more complementary and decisive information for understanding the response mechanisms of wild soybean drought tolerance.

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