

## PB-3

Transcriptome Analysis of Korean Wild Soybean (*Glycine soja*) under Abiotic StressTae Kyeom Kim<sup>1</sup>, Ha Young Chung<sup>1</sup>, Jae Yoon Kim<sup>1\*</sup><sup>1</sup>Department of Plant Resources, Kongju National University, Yesan, Chungnam, Republic of Korea**[Introduction]**

The collection, research, and conservation of native wild species are essential researches for food security and increased species diversity of agricultural crops. In particular, the collection and research of various native wild species related to soybeans are being conducted, and the origin of the currently cultivated soybean (*Glycine max*) is *Glycine soja*, which is native to Korea. A domestic wild soybean (*Glycine soja*), is known to have higher resistance to abiotic stress than cultivated soybean (*Glycine max*). To adjust to abiotic stress, plants induce changes in gene expression by the complex networking of multiple genes. We performed high-throughput transcriptome analysis in the aerial part of the plant under drought, salinity, and flooding stress during the early growth stage of wild soybean.

**[Materials and Methods]**

*Glycine soja* was germinated in a greenhouse environment and transplanted into pots with the same bed soil and moisture content. At the time of V2, after treating abiotic stress (drought, salinity, and flooding) as a standard before treatment (control), the aerial part of the plant was sampled. Total RNA was extracted from all samples, High-throughput transcriptome analysis was performed through RNA-seq, and expression of candidate genes was analyzed through qRT-PCR.

**[Results and Discussion]**

In the aerial part of *Glycine soja*, DEG for drought (5/10 d: 4306/3873), salinity (24/48 h: 284/1826), flooding (7 d: 1059) treatments were detected using the untreated group as a control. Through KEGG pathway enrichment analysis, genes of the isoflavonoid biosynthesis pathway were up-regulated under most stress conditions, and the highest expression was especially observed in drought treatment. Additionally, the reliability and reconstruction for RNA-seq results of Isoflavonoid biosynthesis genes were verified by qRT-PCR. Isoflavonoids are functional natural substances found in abundance in legumes and play numerous roles in the interaction between plants and their environment. It is expected that the isoflavonoid biosynthesis genes, are up-regulated to confer resistance traits to abiotic stress in *Glycine soja*. Based on these results, a comparative analysis of the relationship between the abiotic stress adaptability of wild soybean and isoflavonoids at the metabolite and proteomic level is considered, and further studies are needed.

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