

PB-002

Analysis of Differentially Expressed Genes in Tolerant and Susceptible Soybean Cultivars Under Flooding Stress

Sanjeev Kumar Dhungana¹, Hong-Sik Kim^{1*}, Beom-Kyu Kang¹, Jeong-Hyun Seo¹, Hyun-Tae Kim¹, Sang-Ouk Shin¹, Jae-Hyeon Oh², In-Youl Baek¹

¹Upland Crop Breeding Research Division, Department of Southern Area Crop Science, National Institute of Crop Science, R.D.A., Miryang 50424, Korea

²Gene Engineering Division, Department of Agricultural Biotechnology, National Institute of Agricultural Sciences, R.D.A., Jeonju 54874, Korea

[Introduction]

Flooding stress is one of the major abiotic stresses that cause a huge loss in soybean yield worldwide. Molecular information on the gene expression pattern of tolerant and susceptible genotypes under flooded condition could be valuable to improve the flooding tolerance in soybean. The objective of this study was to analyze the differentially expressed genes (DEGs) under flooding condition revealed by RNA-sequencing (RNA-Seq).

[Materials and Methods]

The seedlings of flood-tolerant ('Paldalkong' and 'Danbaekkong') and flood-susceptible ('NTS1116') cultivars were grown in a well-watered condition up to the V1 – V2 stage and flood-stressed by inundating ~10 cm water for 14 days. The total RNA was extracted from the leaf tissues of tolerant and susceptible cultivars collected at 14 days after flooding. Pooled samples of three biological replicates were prepared for each cultivar and stress condition and were sent to Macrogen, Korea for RNA-Seq and DEGs analysis.

[Results and Discussion]

A total of 22,468 genes were differentially expressed in the flood-stressed condition compared to the well-watered condition, in which 13,729, 13,405, and 13,160 DEGs were found in 'Paldalkong', 'Danbaekkong', and 'NTS1116', respectively. A higher number of some of the previously reported flooding tolerance-related genes such as expansin, glutathione S-transferase, and sugar efflux transporter were up-regulated in the tolerant cultivars than in the susceptible cultivar. The number of some transcription factors of basic leucine zipper domain (bZIP) and myeloblastosis (MYB) families were also higher in the tolerant cultivars than in the susceptible cultivar. The molecular information about the DEGs of tolerant and susceptible cultivars obtained in this study could be valuable in understanding the tolerance mechanism and to improve the flooding tolerance in soybean.

[Acknowledgements]

This research was supported by the RDA Agenda Project (No. PJ01186801).

*Corresponding author: Tel. +82-55-350-1226, E-mail, kimhongs@korea.kr