M-05

Transcriptomic and genomic approaches to identify soybean genes responsible for UV-B stress

*Jungmin Ha**, Department of Plant Science, Seoul National University, Seoul, Republic of Korea
Sangrea Shim, Department of Agricultural Biotechnology, Seoul National University, Seoul, Republic of Korea
Moon Young Kim, Department of Environmental Engineering, Seoul National University, Seoul, Republic of Korea
Suk-Ha Lee, Department of Plant Genomics, Seoul National University, Seoul, Republic of Korea

The depletion of the ozone layer in the stratosphere has led to increased ultraviolet B (UV-B) light levels. The direct absorption of high-intensity ultraviolet B (UV-B) induces complex abiotic stresses in plants, including excessive light exposure, heat, and dehydration. However, UV-B stress signaling mechanisms and responsible genes in plants including soybean (*Glycine max* [L.]) remain poorly understood. We surveyed overall transcriptional responses of two soybean genotypes, UV-B-sensitive Cheongja 3 and UV-B-resistant Buseok, to continuous UV-B irradiation for 0 (control), 0.5, and 6 h using RNA-seq analysis. UV-B-resistant Buseok utilized phosphatidic acid-dependent signaling pathways in response to UV-B exposure at high fluence rates, and genes involved in its downstream pathways were upregulated in this genotype. In addition, the DEGs for TIR-NBS-LRR and heat shock proteins are positively activated. Furthermore, we investigated quantitative trait loci (QTL) associated with resistance to supplementary UV-B stress using Genotype-by-sequencing (GBS) of 174 soybean RIL population derived from Cheongja 3 and Buseok. As the results of phenotypic evaluation, the mean range of damage leaf degree was 50.3%, paternal UV-B resistance Buseok showed 26.8% damage degree, and maternal UV-B sensitive Cheongja 3 exhibited 62.4 damage degrees (%). Total high quality 1,561 SNPs were obtained and used for construction of genetic map using Joinmap 4.1. Two QTLs, UVBR12-1 and UVBR15-1, were newly detected in this study and the candidate genes on chr 12 and chr 15 need to be examined more as UV-B stress responsible genes. Our two approaches could be applied to breed high adaptable soybean under continuous climate changes in the future.