

PB-23

Expression Analyses of the Candidate Genes about *Phytophthora sojae* Resistance on Chromosome 2 in Soybean (*Glycine max* L.)

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[Introduction]

In recent years, the soybean cultivation area produced on paddy fields has increased from 6,335 ha in 2017 to 12,590 ha in 2022. Phytophthora root rot (PRR) caused by *Phytophthora sojae* in soybean is a prevalent disease around humid conditions like poorly drained paddy soil. The object of this study is to find resistant genes related to *P. sojae* by performing qRT-PCR and analyzing the expression in candidate genes.

[Materials and Methods]

The study was conducted with two isolates of *P. sojae*, Gimje (GJ) 3053 and Andong (AD) 3617, collected from major soybean production areas in Korea. The samples were contained from above and below the treated hypocotyl tissues in 'Jungmo3009ho' and 'Seonpung' at 0, 3, 6, 12, and 24 hours after inoculation. Gene expression was determined by qRT-PCR using SYBR Green premix EX Taq on QuantStudio 5 System (ABI/Life Technologies).

[Results and Discussion]

The linkage disequilibrium (LD) blocks were found from AX-90455181 (15,056,628bp) to AX-90475572 (15,298,872bp) of Chromosome 2 through genome-wide association study (GWAS) with 207 Korean soybean genotypes. Among the 28 genes in these genetic regions, the following candidate genes were selected for transcript variations compared to the reference genome 'Williams 82', *Glyma.02g149200* (Phenazine biosynthesis protein), *Glyma.02g148400* (Hepatoma-derived growth factor-related), and *Glyma.02g150200* (Piezo non-specific cation channel). There was no significant difference in the relative expression level of three genes in 'Jungmo3009ho' and 'Seonpung'. Therefore, it is necessary to find other genetic regions for breeding *P. sojae*-resistant soybean cultivars.

[Acknowledgement]

This research is supported by Rural Development Administration and the project name is "Development of elite line and analysis of related genes for soybean root-rot disease resistance (PJ01576202)".

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