

PB-3

Transcriptomic Profiling of Resistant and Susceptible Soybean Genotypes Following Inoculation of *Phytophthora sojae*

Hee Jin You¹, Jeongsun Lee¹, Sungwoo Lee^{1*}

¹Department of Crop Science, College of Agriculture and Life Sciences, Chungnam National University, Daejeon 34134, Republic of Korea.

[Abstract]

Our previous study identified a resistance locus to *Phytophthora sojae* (isolate 2457) in an interval of 3.8-4.7 Mbp on chromosome 3 via genetic mapping using a 'Daepung'×'Daewon' recombinant inbred population. Since differential gene expression between Daepung (susceptible) and Daewon (resistant) after inoculation of *P. sojae* is unknown, RNA sequencing was carried out to compare transcriptomic changes between the two genotypes following inoculation with *P. sojae* isolate 2457. The two varieties were inoculated using hypocotyl inoculation at the VC stage and stem tissue of 1 cm above and below of the inoculated site were sampled at 0, 6, 12 hours after inoculation (hai), respectively. Differentially expressed genes (DEGs) under same cultivar in different time point and Daepung vs. Daewon in same time point were investigated. In comparison of Daepung vs. Daewon at 12 hai, a total of 3,513 DEGs were identified, including two nucleotide-binding site-leucine rich repeat (NBS-LRR) genes (Glyma.03g034800 and Glyma.03g034900) that are located in the previously reported resistance locus on chromosome 3. In addition, 14,966 DEGs were detected between 0 vs. 6 hai, containing one of candidate genes (Glyma.03g035300). This gene was upregulated by up to 4-fold in Daewon and Daepung. Additional results will be further discussed in the presentation. This study will provide valuable information for soybean crop improvement.

[Acknowledgement]

This study was funded by the Agriculture Science & Technology Research and Development Program (Project No. PJ01574402), Rural Development Administration, South Korea.

*Corresponding author: Tel. +82-42-821-5727 E-mail. sungwoolee@cnu.ac.kr