B-158

Fine mapping and transcriptomic analysis of near-isogenic lines to identify candidate genes for a major QTL for Phytophthora root and stem rot resistance

*Stephanie Karhoff**, Department of Translational Plant Sciences, The Ohio State University, Ohio, USA
Sung*woo Lee*, Department of Research Facilities, Chungnam National University, Daejeon, Republic of Korea
Rouf Mian, Department of Plant Physiology, USDA-ARS, North Carolina, USA
Anne Dorrance, Department of Plant Pathology, The Ohio State University, Ohio, USA
Leah McHale, Department of Horticulture and Crop Sciences, The Ohio State University, Ohio, USA

Phytophthora root and stem rot is a major yield-limiting disease in soybean [*Glycine max* (L). Merr.] caused by the soil-borne oomycete *Phytophthora sojae*. The widespread use of race specific *Rps* genes has led to a shift in pathogen virulence. Thus, there is an increased need for stronger partial resistance, which is polygenic and non-race specific. Quantitative trait loci (QTLs) are valuable resources for broad spectrum resistance. However, major QTLs are relatively rare in this pathosystem and the majority of QTLs explain less than 20% of the phenotypic variance. Previously, we identified a major QTL on Chromosome 18 which explains up to 45% of the phenotypic variance. The QTL interval contains 180 predicted genes and spans over 1,000 kb. Our goal is to provide a limited number of candidate genes for further functional analyses and to contribute to our growing knowledge of the trait's genetic architecture. To narrow our list of candidate genes, we have taken two approaches: first, we are assessing the expression profile of resistant and susceptible near isogenic lines (NIL) varying for the allele present at the QTL; second, we are fine-mapping the QTL. We used RNA-Seq to analyze differential gene expression of resistant and susceptible NILs 3, 24, and 48 hours after inoculation (hai). In total, among all comparisons, 45 of 7,966 unique genes differentially expressed are located within the QTL interval. Four of these 45 genes are differentially expressed in non-inoculated relative to inoculated treatment in resistant NILs only. In addition to analyzing transcriptional data, for fine mapping, 21 recombinant $BC_2S_{1:2}$ families were identified using the KASP genotyping platform and phenotyped for resistance to *P. sojae*. Ultimately, the identification of the gene(s) controlling this QTL will facilitate the use of the resistance source in breeding programs.