Combining Transcriptome Analyses and Virus Induced Gene Silencing to Identify Genes in the *Rpp4*-mediated Asian Soybean Rust Resistance Pathway.

Aguida Morales Embrapa-soja
Jamie A. O'Rourke 2USDA-Agricultural Research Service, Plant Science Research Unit
Aluízio Borém Vicosa Federal University
Ricardo Vilela Abdelnoor Embrapa soja
Kerry F. Pedley (USDA-ARS Foreign Disease-Weed Science Research Unit); Steven A. Whitham (Iowa State University); Michelle A. Graham (USDA-ARS Corn Insects and Crop Genetics Research Unit)

Six Asian Soybean Rust (ASR) resistance loci have been identified and mapped in soybean genome: *Rpp1* (*Resistance to Phakopsora pachyrhizi 1*), *Rpp2*, *Rpp3*, *Rpp4*, *Rpp5* and *Rpp6*. Of particular interest is *Rpp4*, which has remained stable and confers resistance against *Phakopsora pachyrhizi* isolates from around the world. Sequencing of the region harboring *Rpp4* in the susceptible cultivar Williams 82 (Wm82) and the resistant cultivar (PI459025B) genotype identified a cluster of CC-NBS-LRR resistance genes. Meyers et al. (2009) developed Virus Induced Gene Silencing constructs from the LRR regions of the Wm82 *Rpp4* candidate genes to confirm that orthologous genes were responsible for resistance in the resistant parent (PI459025B). In this study, RNA samples extracted from the same *Rpp4* LRR silenced and empty vector treated plants, also infected with *P. pachyrhizi* (described by Meyer et al., 2009) were compared using the GeneChip® Soybean Genome Array (Affymetrix®). Since the plant samples differed only in the expression of *Rpp4*, comparisons of these samples would identify genes downstream of *Rpp4* in the signaling pathway. In total, 383 differentially expressed probes were identified, many with functions related to defense. While the time point analyzed was late in defense signaling, bioinformatic approaches were useful in characterizing the defense response and identify transcription factors regulating the response.

Poster Number: 86