

Transcriptional profiling of potential regulatory factors modulating defense mechanisms in soybean under *P. sojae* infection.

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Quantitative resistance which is controlled by multiple genes is a durable means of disease control, and has been shown in soybean. The overall objective of the project is to identify the mechanisms among plant and pathogen genes that determine quantitative resistance in soybean against *Phytophthora sojae*. Microarray technology was used to examine the global expression profiles in this pathosystem as to unravel the complex networks of pathways that appear to regulate plant defense against infection. Linear mixed model analysis (LMMA) and false discovery rate (FDR) control was used to identify genes that varied in expression among cultivars over a range of time after pathogen infection. Results of this study will be presented.